

(12) NACH DEM VERTRAG ÜBER DIE INTERNATIONALE ZUSAMMENARBEIT AUF DEM GEBIET DES
PATENTWESENS (PCT) VERÖFFENTLICHTE INTERNATIONALE ANMELDUNG

(19) Weltorganisation für geistiges Eigentum
Internationales Büro



(43) Internationales Veröffentlichungsdatum
23. Oktober 2003 (23.10.2003)

PCT

(10) Internationale Veröffentlichungsnummer
WO 03/087386 A2

- (51) Internationale Patentklassifikation⁷: C12P 13/12, C12N 9/10, 1/15, 15/63 (74) Anwalt: SCHWEIGER Georg; Reitstötter, Kinzebach & Partner (GbR), Sternwartstrasse 4, 81679 München (DE).
- (21) Internationales Aktenzeichen: PCT/EP03/04010 (81) Bestimmungsstaaten (*national*): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW.
- (22) Internationales Anmeldedatum: 16. April 2003 (16.04.2003)
- (25) Einreichungssprache: Deutsch
- (26) Veröffentlichungssprache: Deutsch
- (30) Angaben zur Priorität: 102 17 058.4 17. April 2002 (17.04.2002) DE (84) Bestimmungsstaaten (*regional*): ARIPO-Patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW), eurasisches Patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), europäisches Patent (AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO, SE, SI, SK, TR), OAPI-Patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).
- (71) Anmelder (*für alle Bestimmungsstaaten mit Ausnahme von US*): BASF AKTIENGESELLSCHAFT [DE/DE]; 67056 Ludwigshafen (DE).
- (72) Erfinder; und
- (75) Erfinder/Anmelder (*nur für US*): KRÖGER, Burkhard [DE/DE]; Im Waldhof 1, 67117 Limburgerhof (DE). ZELDER, Oskar [DE/DE]; Franz-Stützel-Str. 8, 67346 Speyer (DE). KLOPPROGGE, Corinna [DE/DE]; Diemersteinstrasse 3, 67065 Ludwigshafen (DE). SCHRÖDER, Hartwig [DE/DE]; Benzstr. 4, 69226 Nussloch (DE). HÄFNER, Stefan [DE/DE]; Luitpoldstr. 11, 67063 Ludwigshafen (DE).
- Veröffentlicht:
— ohne internationalen Recherchenbericht und erneut zu veröffentlichen nach Erhalt des Berichts
- Zur Erklärung der Zweibuchstaben-Codes und der anderen Abkürzungen wird auf die Erklärungen ("Guidance Notes on Codes and Abbreviations") am Anfang jeder regulären Ausgabe der PCT-Gazette verwiesen.

WO 03/087386 A2

(54) Title: METHODS FOR PRODUCING SULPHUROUS FINE CHEMICALS

(54) Bezeichnung: VERFAHREN ZUR HERSTELLUNG VON SCHWEFELHALTIGEN FEINCHEMIKALIEN

(57) Abstract: The invention relates to methods for producing sulphurous fine chemicals, in particular L-methionine, by fermentation, using bacteria, in which a nucleotide sequence that codes for a methionine synthase (metF) gene is expressed.

(57) Zusammenfassung: Die Erfindung betrifft Verfahren zur fermentativen Herstellung von schwefelhaltigen Feinchemikalien, insbesondere L-Methionin, unter Verwendung von Bakterien, in denen eine für ein Methionin-Synthase (metF)-Gen kodierende Nukleotidsequenzen exprimiert wird.

Verfahren zur Herstellung von schwefelhaltigen Feinchemikalien

Beschreibung

Gegenstand der Erfindung ist ein Verfahren zur fermentativen Herstellung von schwefelhaltigen Feinchemikalien, insbesondere L-Methionin, unter Verwendung von Bakterien, in denen eine für ein Methionin-Synthase (methH)-Gen kodierende Nukleotidsequenz exprimiert wird.

Stand der Technik

Schwefelhaltige Feinchemikalien, wie zum Beispiel Methionin, Homocystein, S-Adenosyl-Methionin, Glutathion, Cystein, Biotin, Thiamin, Liponsäure werden über natürliche Stoffwechselprozesse in Zellen hergestellt und werden in vielen Industriezweigen verwendet, einschließlich der Nahrungsmittel-, Futtermittel-, Kosmetik- und pharmazeutischen Industrie. Diese Substanzen, die zusammen als "schwefelhaltige Feinchemikalien" bezeichnet werden, umfassen organische Säuren, sowohl proteinogene als auch nicht-proteinogene Aminosäuren, Vitamine und Cofaktoren. Ihre Produktion erfolgt am zweckmäßigsten im Großmaßstab mittels Anzucht von Bakterien, die entwickelt wurden, um große Mengen der jeweils gewünschten Substanz zu produzieren und sezernieren. Für diesen Zweck besonders geeignete Organismen sind coryneforme Bakterien, gram-positive nicht-pathogene Bakterien.

Es ist bekannt, dass Aminosäuren durch Fermentation von Stämmen coryneformer Bakterien, insbesondere *Corynebacterium glutamicum*, hergestellt werden. Wegen der großen Bedeutung wird ständig an der Verbesserung der Herstellverfahren gearbeitet. Verfahrensverbesserungen können fermentationstechnische Maßnahmen, wie zum Beispiel Rührung und Versorgung mit Sauerstoff, oder die Zusammensetzung der Nähmedien, wie zum Beispiel die Zuckerkonzentration während der Fermentation, oder die Aufarbeitung zum Produkt, beispielsweise durch Ionenaustauschchromatographie, oder die intrinsischen Leistungseigenschaften des Mikroorganismus selbst betreffen.

Über Stammselektion sind eine Reihe von Mutantenstämmen entwickelt worden, die ein Sortiment wünschenswerter Verbindungen aus der Reihe der schwefelhaltigen Feinchemikalien produzieren. Zur Verbesserung der Leistungseigenschaften dieser Mikroorganismen hinsichtlich der Produktion eines bestimmten Moleküls werden Methoden der Mutagenese, Selektion und Mutantenauswahl angewendet. Dies ist jedoch ein zeitaufwendiges und schwieriges Verfahren. Auf

diese Weise erhält man z.B. Stämme, die resistent gegen Antimetabolite oder Hemmstoffe, wie z. B. die Methionin-Analoga α -Methyl-Methionin, Ethionin, Norleucin, N-Acetylnorleucin, S-Trifluoromethylhomocystein, 2-Amino-5-heptenoinsäure, Seleno-Methionin, Methioninsulfoximin, Methoxin, 1-Aminocyclopentan-Carboxylsäure oder auxotroph für regulatorisch bedeutsame Metabolite sind und schwefelhaltige Feinchemikalien, wie z. B. L-Methionin, produzieren.

Seit einigen Jahren werden ebenfalls Methoden der rekombinanten DNA-Technik zur Stammverbesserung von L-Aminosäure produzierender Stämme von *Corynebacterium* eingesetzt, indem man einzelne Aminosäure-Biosynthesegene amplifiziert und die Auswirkung auf die Aminosäure-Produktion untersucht.

Die WO-A-02/10209 beschreibt ein Verfahren zur fermentativen Herstellung von L-Methionin unter Verwendung L-Methionin produzierender coryneformer Bakterien, worin wenigstens das methH-Gen überexprimiert ist, sowie die kodierende methH-Sequenz aus *C. glutamicum* ATCC 13032.

Kurze Beschreibung der Erfindung

Der Erfindung lag die Aufgabe zugrunde, ein neues Verfahren zur verbesserten fermentativen Herstellung von schwefelhaltige Feinchemikalien, insbesondere L-Methionin, bereitzustellen.

Gelöst wird obige Aufgabe durch Bereitstellung eines Verfahrens zur fermentativen Herstellung einer schwefelhaltigen Feinchemikalie, umfassend die Expression einer heterologen Nukleotidsequenz, welche für ein Protein mit methH-Aktivität kodiert, in einem coryneformen Bakterium.

Ein erster Gegenstand der Erfindung ist ein Verfahren zur fermentativen Herstellung wenigstens einer schwefelhaltigen Feinchemikalie, welches folgende Schritte umfasst:

- a) Fermentation einer die gewünschte schwefelhaltige Feinchemikalie produzierenden coryneformen Bakterienkultur, wobei in den coryneformen Bakterien zumindest eine heterologe Nukleotidsequenz exprimiert wird, welche für ein Protein mit Methionin-Synthase (methH) –Aktivität kodiert;
- b) Anreicherung der schwefelhaltigen Feinchemikalie im Medium oder in den Zellen der Bakterien, und

- c) Isolieren der schwefelhaltigen Feinchemikalie, welche vorzugsweise L-Methionin umfasst.

- 5 Vorzugsweise besitzt obige heterologe methH-kodierende Nukleotidsequenz zur methH-kodierenden Sequenz aus *Corynebacterium glutamicum* ATCC 13032 eine Sequenzhomologie vom weniger als 70% aufweist. Die methH-kodierende Sequenz ist vorzugsweise aus einem der folgenden Organismen von Liste I abgeleitet:

Liste I

10

| | |
|--|------------|
| <i>Streptomyces coelicolor</i> | ATCC 10147 |
| <i>Anabaena</i> sp. | ATCC 27892 |
| <i>Synechocystis</i> sp. | ATCC 27184 |
| <i>Prochlorococcus marinus</i> | PCC 7118 |
| <i>Thermus thermophilus</i> | ATCC 27634 |
| <i>Bacillus halodurans</i> | ATCC 21591 |
| <i>Bacillus stearothermophilus</i> | ATCC 12980 |
| <i>Vibrio cholerae</i> | ATCC 39315 |
| <i>Sinorhizobium meliloti</i> | ATCC 4399 |
| <i>Escherichia coli</i> K12 | ATCC 55151 |
| <i>Salmonella typhimurium</i> | ATCC 15277 |
| <i>Salmonella typhi</i> | ATCC 12839 |
| <i>Pseudomonas fluorescens</i> | ATCC 13525 |
| <i>Pseudomonas aeruginosa</i> | ATCC 17933 |
| <i>Nitrosomonas europaea</i> | ATCC 19718 |
| <i>Bordetella pertussis</i> | ATCC 9797 |
| <i>Clorobium tepidum</i> | ATCC 49652 |
| <i>Deinococcus radiodurans</i> | ATCC 13939 |
| <i>Clostridium acetobutylicum</i> | ATCC 824 |
| <i>Caulobacter crescentus</i> | ATCC 19089 |
| <i>Homo sapiens</i> | |
| <i>Vibrio fischeri</i> | ATCC 33715 |
| <i>Agrobacterium tumefaciens</i> str. C58 (Cereon) | ATCC 33970 |
| <i>Ralstonia solanacearum</i> | ATCC 25237 |

ATCC: American Type Culture Collection, Rockville, MD, USA

PCC: Pasteur Culture Collection of Cyanobacteria. Paris Frankreich

- 15 Die erfindungsgemäß eingesetzte methH-kodierende Sequenz umfasst vorzugsweise eine kodierende Sequenz gemäß SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35,

37, 39, 41, 43, 45, 47, 49 und 51 oder eine dazu homologe Nukleotidsequenz, welche für ein Protein mit methH-Aktivität kodiert.

5 Die erfindungsgemäß eingesetzte methH-kodierende Sequenz kodiert außerdem vorzugsweise für ein Protein mit methH-Aktivität, wobei das Protein eine Aminosäuresequenz gemäß SEQ ID NO:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50 und 52 oder eine dazu homologe Aminosäuresequenz, welche für ein Protein mit methH-Aktivität steht, umfasst.

10 Die kodierende methH-Sequenz ist vorzugsweise eine in coryneformen Bakterien replizierbare oder eine stabil in das Chromosom integrierte DNA oder eine RNA.

Gemäß einer bevorzugten Ausführungsform wird das erfindungsgemäße Verfahren durchgeführt, indem man

15

- a) einen mit einem Plasmidvektor transformierten Bakterienstamm einsetzt der wenigstens eine Kopie der kodierenden methH-Sequenz unter der Kontrolle regulativer Sequenzen trägt, oder
- b) einen Stamm einsetzt, in dem die kodierende methH-Sequenz in das Chromosom des Bakteriums integriert wurde.

20

Es ist weiterhin bevorzugt, die kodierende methH-Sequenz für die Fermentation zu überexprimieren.

25

Außerdem kann es wünschenswert sein, Bakterien zu fermentieren, in denen zusätzlich wenigstens ein weiteres Gen des Biosyntheseweges der gewünschten schwefelhaltigen Feinchemikalie oder eines damit assoziierten Biosynthese- oder sonstigen Stoffwechselweges, verstärkt ist; und / oder

in denen wenigstens ein Stoffwechselweg zumindest teilweise ausgeschaltet sind, der die Bildung der gewünschten schwefelhaltigen Feinchemikalie verringert.

30

Außerdem kann es wünschenswert sein, Bakterien zu fermentieren, in denen zusätzlich wenigstens ein weiteres Gen des Biosyntheseweges der gewünschten schwefelhaltigen Feinchemikalie durch Stoffwechselmetabolite in seiner Aktivität nicht in unerwünschter Weise beeinflusst wird.

Gemäß einer weiteren Ausführungsform des erfindungsgemäßen Verfahrens werden deshalb coryneforme Bakterien fermentiert, in denen gleichzeitig wenigstens eines der Gene, ausgewählt unter

5

- a) dem für eine Aspartatkinase kodierenden Gen *lysC*,
- b) dem für eine Aspartat-Semialdehyd-Dehydrogenase kodierenden Gen *asd*
- c) dem für die Glycerinaldehyd-3-Phosphat Dehydrogenase kodierenden Gen *gap*,
- d) dem für die 3-Phosphoglycerat Kinase kodierenden Gen *pgk*,
- 10 e) dem für die Pyruvat Carboxylase kodierenden Gen *pyc*,
- f) dem für die Triosephosphat Isomerase kodierenden Gen *tpi*,
- g) dem für die Homoserin O-Acetyltransferase kodierenden Gen *metA*,
- h) dem für die Cystathionin-gamma-Synthase kodierenden Gen *metB*,
- i) dem für die Cystathionin-gamma-Lyase kodierenden Gen *metC*,
- 15 j) dem für die Serin-Hydroxymethyltransferase kodierenden Gen *glyA*,
- k) dem für die O-Acetylhomoserin-Sulphydrylase kodierenden Gen *metY*,
- l) dem für die Methylen-Tetrahydrofolat-Reduktase kodierenden Gen, *metF*
- m) dem für die Phosphoserin-Aminotransferase kodierenden Gen *serC*
- n) dem für die Phosphoserin-Phosphatase kodierenden Gen *serB*,
- 20 o) dem für die Serine Acetyl-Transferase kodierenden Gen *cysE*,
- p) dem für die Homoserin-Dehydrogenase kodierenden Gen *hom*,

überexprimiert ist.

- 25 Gemäß einer anderen Ausführungsform des erfindungsgemäßen Verfahrens werden coryneforme Bakterien fermentiert, in denen gleichzeitig wenigstens eines der Gene ausgewählt unter Genen der oben genannten Gruppe a) bis p) mutiert ist, insbesondere so dass die korrespondierenden Proteine, verglichen mit nicht mutierten Proteinen, in geringerem Maße oder nicht durch Stoffwechselmetabolite in ihrer Aktivität beeinflusst werden und dass insbesondere die erfindungsgemäße Produktion der Feinchemikalie nicht beeinträchtigt wird. Durch die Mutation kann
- 30 das Protein auch eine höhere Aktivität (Sunstratumsatz) und/oder Sunstratspezifität besitzen und damit die Produktion der gewünschten Feinchemikalie fördern.

Gemäß einer anderen Ausführungsform des erfindungsgemäßen Verfahrens werden coryneforme Bakterien fermentiert, in denen gleichzeitig wenigstens eines der Gene, ausgewählt unter

- q) dem für die Homoserine-Kinase kodierenden Gen *thrB*,
- r) dem für die Threonin Dehydratase kodierenden Gen *ilvA*,
- 5 s) dem für die Threonin Synthase kodierenden Gen *thrC*
- t) dem für die Meso-Diaminopimelat D-Dehydrogenase kodierenden Gen *ddh*
- u) dem für die Phosphoenolpyruvat-Carboxykinase kodierenden Gen *pck*,
- v) dem für die Glucose-6-Phosphat-6-Isomerase kodierenden Gen *pgi*,
- w) dem für die Pyruvat-Oxidase kodierenden Gen *poxB*,
- 10 x) dem für die Dihydrodipicolinat Synthase kodierenden Gen *dapA*,
- y) dem für die Dihydrodipicolinat Reduktase kodierenden Gen *dapB*; oder
- z) dem für die Diaminopicolinat Decarboxylase kodierenden Gen *lysA*

abschwächt ist, insbesondere durch Verringerung der Expressionsrate des korrespondierenden Gens, oder durch Expression eines Proteins mit geringerer Aktivität (Substratumsatz).

15

Gemäß einer anderen Ausführungsform des erfindungsgemäßen Verfahrens werden coryneforme Bakterien fermentiert, in denen gleichzeitig wenigstens eines der Gene der obigen Gruppen q) bis z) mutiert ist, so dass die enzymatische Aktivität des korrespondierenden Proteins teilweise oder vollständig verringert wird.

20

Vorzugsweise werden in dem erfindungsgemäßen Verfahren Mikroorganismen der Art *Corynebacterium glutamicum* eingesetzt.

25 In einer weiteren Ausführungsform des Verfahrens werden solche Mikroorganismen eingesetzt, die Resistenz gegenüber wenigstens einen Methionin-Biosynthesehemmer aufweisen. Solche Hemmer sind, ohne darauf beschränkt zu sein, Methionin-Analoga, wie α -Methyl-Methionin, Ethionin, Norleucin, N-Acetylnorleucin, S-Trifluoromethylhomocystein, 2-Amino-5-heptenoisäure, Seleno-Methionin, Methioninsulfoximin, Methoxin, und 1-Aminocyclopentan-Carboxylsäure.

30

Ein weiterer Gegenstand der Erfindung betrifft ein Verfahren zur Herstellung eines L-Methionin-haltigen Tierfuttermittel-Additivs aus Fermentationsbrühen, welches folgende Schritte umfasst

7

- 5
- a) Kultivierung und Fermentation eines L-Methionin produzierenden Mikroorganismus in einem Fermentationsmedium;
 - b) Entfernung von Wasser aus der L-Methionin haltigen Fermentationsbrühe;
 - c) Entfernung der während der Fermentation gebildeten Biomasse in einer Menge von 0 bis 100 Gew.-%; und
 - d) Trocknung der gemäß b) und/oder c) erhaltenen Fermentationsbrühe, um das Tierfuttermittel-Additiv in der gewünschten Pulver- oder Granulatform zu erhalten.

10 Gegenstand der Erfindung sind ebenfalls die erstmalig aus obigen Mikroorganismen isolierten kodierenden methH-Sequenzen, die davon kodierten Methionin-Synthasen sowie die funktionalen Homologen dieser Polynukleotide bzw. Proteine.

15 Gegenstand der Erfindung sind insbesondere auch die zur Durchführung obiger Verfahren notwendigen Expressionskonstrukte und Mikroorganismen.

Weitere Gegenstände der Erfindung sind somit insbesondere:

20 - das Plasmid pCIS lysC thr311ile, kodierend für lysC thr311ile oder ein funktionales Äquivalent davon, d.h. eine lysC-Mutante mit vergleichbarer, gegenüber dem Wildtyp erhöhter Aspartatkinase-Aktivität;

25 - ein Wirtsorganismus transformiert mit dem Plasmid pCIS lysC thr311ile, insbesondere ausgewählt unter Mikroorganismen der Gattung Corynebacterium, insbesondere der Art C. glutamicum, wie der transformierte Stamm LU1479 lysC 311ile;

30 - das Plasmid pC Phsdh methH_Sc, kodierend für methH aus Streptomyces coelicolor;

- ein Wirtsorganismus gemäß obiger Definition, transformiert mit einem Plasmid, kodierend für exogenes methH; insbesondere transformiert mit dem Plasmid pC Phsdh methH_Sc;

- ein Wirtsorganismus gemäß obiger Definition mit Resistenz gegen wenigstens einen Methionin-Biosynthesehemmstoff, wie der transformierte Stamm LU1479 lysC 311ile ET-16, gege-

benenfalls transformiert mit einer exogenen kodierenden meth Sequenz, wie der transformierte Stamm LU1479 lysC 311ile ET-16 pC Phsdh meth_Sc.

Detaillierte Beschreibung der Erfindung

5

a) Allgemeine Begriffe

Als Proteine mit der biologischen Aktivität der Methionine-Synthase, kurz auch als methH genannt (systematische Bezeichnung: 5-Methyltetrahydrofolat-Homocystein S-Methyltransferase ;EC 10 2.1.1.13), werden solche Proteine bezeichnet, die in der Lage sind Homocystein unter Verwendung der Cofaktoren 5-Methyltetrahydrofolat (MTHF), Cobalamin (Vitamin B12) und S-Adenosyl-Methionin zu Methionin und Tetrahydrofolat umzusetzen. Während der Cofaktor 5-Methyltetrahydrofolat stöchiometrisch in die Reaktion mit eingeht (1mol MTHF/1Mol Methionin gebildet) wird, wie in der Literatur beschrieben, S-Adenosyl-Methionin substöchiometrisch umgesetzt. Cobalamin hingegen ist katalytisch an der Umsetzung beteiligt. Dem Fachmann sind weitere Details des methH-Proteins bekannt. (Banerjee R.V., Matthews R.G. FASEB J. 4:1450-1459, 1990, Ludwig ML. Matthews RG. Annual Review of Biochemistry. 66:269-313, 1997, Drennan CL. Matthews RG. Ludwig ML. Current Opinion in Structural Biology. 4:919-29, 1994). Der Fachmann unterscheidet die Aktivität der Cobalamin-abhängigen 5-Methyltetrahydrofolat-Homocystein S-Methyltransferase von der der Cobalamin-unabhängigen 5-Methyltetrahydro-Pteroyltryglutamat-Homocystein S-Methyltransferase (EC 2.1.1.14) auch metE genannt. Der Fachmann kann die enzymatische Aktivität von methH durch Enzymtests nachweisen, Vorschriften dafür können sein: Jarrett JT. Goulding CW. Fluhr K. Huang S. Matthews RG. Methods in Enzymology. 281:196-213, 1997.

25

Im Rahmen der vorliegenden Erfindung umfasst der Begriff „schwefelhaltige Feinchemikalie“ jegliche chemische Verbindung, die wenigstens ein Schwefelatom kovalent gebunden enthält und durch ein erfindungsgemäßes Fermentationsverfahrens zugänglich ist. Nichtlimitierende Beispiele dafür sind Methionin, Homocystein, S-Adenosyl-Methionin, insbesondere Methionin, und S-Adenosyl-Methionin.

30

Im Rahmen der vorliegenden Erfindung umfassen die Begriffe L-Methionin, Methionin, Homocystein und S-Adenosylmethionin auch die korrespondierenden Salze, wie z. B. Methionin-Hydrochlorid oder Methionin-Sulfat.

- 5 "Polynukleotide" bezeichnet im allgemeinen Polyribonukleotide (RNA) und Polydeoxyribonukleotide (DNA), wobei es sich um nicht modifizierte RNA oder DNA oder modifizierte RNA oder DNA handeln kann.

- Unter "Polypeptiden" versteht man erfindungsgemäß Peptide oder Proteine, die zwei oder mehr
10 über Peptidbindungen verbundene Aminosäuren enthalten.

- Der Begriff „Stoffwechselmetabolit“ bezeichnet chemische Verbindungen, die im Stoffwechsel von Organismen als Zwischen- oder auch Endprodukte vorkommen und die neben ihrer Eigenschaft als chemische Bausteine auch modulierende Wirkung auf Enzyme und ihre katalytische
15 Aktivität haben können. Dabei ist aus der Literatur bekannt, dass solche Stoffwechselmetabolite sowohl hemmend als auch stimulierend auf die Aktivität von Enzymen wirken können (Biochemistry, Stryer, Lubert, 1995 W. H. Freeman & Company, New York, New York.). In der Literatur ist auch beschrieben, dass es möglich ist durch Maßnahmen wie Mutation der genomischen DNA durch UV-Strahlung, ionisierender Strahlung oder mutagene Substanzen und nachfolgender
20 Selektion auf bestimmte Phänotypen in Organismen solche Enzyme zu produzieren, in denen die Beeinflussung durch Stoffwechselmetabolite verändert wurde (Sahm H. Eggeling L. de Graaf AA. Biological Chemistry 381(9-10):899-910, 2000; Eikmanns BJ. Eggeling L. Sahm H. Antonie van Leeuwenhoek. 64:145-63, 1993-94). Diese veränderten Eigenschaften können auch durch gezielte Maßnahmen erreicht werden. Dabei ist dem Fachmann bekannt, in Genen für
25 Enzyme auch gezielt bestimmte Nukleotide der für das Protein kodierenden DNA so zu verändern, dass das aus der exprimierten DNA-Sequenz resultierende Protein bestimmte neue Eigenschaften aufweist, so zum Beispiel, dass die modulierende Wirkung von Stoffwechselmetaboliten gegenüber dem nicht veränderten Protein verändert ist
- 30 Enzyme können derart in ihrer Aktivität beeinflusst werden, dass es zu einer Verringerung der Reaktionsgeschwindigkeit, oder zu einer Veränderung der Affinität gegenüber dem Substrat oder zu einer Änderung der Reaktionsgeschwindigkeiten kommt

Die Begriffe "exprimieren" bzw. "Verstärkung" oder "Überexpression" beschreiben im Kontext der Erfindung die Produktion bzw. Erhöhung der intrazellulären Aktivität eines oder mehrerer Enzyme in einem Mikroorganismus, die durch die entsprechende DNA kodiert werden. Dazu kann man beispielsweise ein Gen in einen Organismus einbringen, ein vorhandenes Gen durch ein
5 anderes Gen ersetzen, die Kopienzahl des Gens bzw. der Gene erhöhen, einen starken Promotor verwenden oder ein Gen verwenden, das für ein entsprechendes Enzym mit einer hohen Aktivität kodiert und man kann gegebenenfalls diese Maßnahmen kombinieren.

b) Erfindungsgemäße methH-Proteine

10

Erfindungsgemäß mit umfasst sind ebenfalls "funktionale Äquivalente" der konkret offenbarten methH-Enzyme aus Organismen obiger Liste I.

15 "Funktionale Äquivalente" oder Analoga der konkret offenbarten Polypeptide sind im Rahmen der vorliegenden Erfindung davon verschiedene Polypeptide, welche weiterhin die gewünschte biologische Aktivität, wie z.B. Substratspezifität, besitzen.

20 Unter "funktionalen Äquivalenten" versteht man erfindungsgemäß insbesondere Mutanten, welche in wenigstens einer der oben genannten Sequenzpositionen eine andere als die konkret genannte Aminosäure aufweisen aber trotzdem eine der oben genannten biologischen Aktivitäten besitzen. "Funktionale Äquivalente" umfassen somit die durch eine oder mehrere Aminosäure-Additionen, -Substitutionen, -Deletionen und/oder -Inversionen erhältlichen Mutanten, wobei die genannten Veränderungen in jeglicher Sequenzposition auftreten können, solange sie zu einer Mutante mit dem erfindungsgemäßen Eigenschaftsprofil führen. Funktionale Äquivalenz ist
25 insbesondere auch dann gegeben, wenn die Reaktivitätsmuster zwischen Mutante und unverändertem Polypeptid qualitativ übereinstimmen, d.h. beispielsweise gleiche Substrate mit unterschiedlicher Geschwindigkeit umgesetzt werden.

30 "Funktionale Äquivalente" umfassen natürlich auch Polypeptide welche aus anderen Organismen zugänglich sind, sowie natürlich vorkommende Varianten. Beispielsweise lassen sich durch Sequenzvergleich Bereiche homologer Sequenzregionen festlegen und in Anlehnung an die konkreten Vorgaben der Erfindung äquivalente Enzyme ermitteln.

„Funktionale Äquivalente“ umfassen ebenfalls Fragmente, vorzugsweise einzelne Domänen oder Sequenzmotive, der erfindungsgemäßen Polypeptide, welche z.B. die gewünschte biologische Funktion aufweisen.

- 5 „Funktionale Äquivalente“ sind außerdem Fusionsproteine, welche ein der oben genannten Polypeptidsequenzen oder davon abgeleitete funktionale Äquivalente und wenigstens eine weitere, davon funktionell verschiedene, heterologe Sequenz in funktioneller N- oder C-terminaler Verknüpfung (d.h. ohne gegenseitigen wesentliche funktionelle Beeinträchtigung der Fusionsproteinteile) aufweisen. Nichtlimitierende Beispiele für derartige heterologe Sequenzen sind z.B. Signalpeptide, Enzyme, Immunoglobuline, Oberflächenantigene, Rezeptoren oder Rezeptorliganden.

- 15 Erfindungsgemäß mit umfasst „funktionale Äquivalente“ sind Homologe zu den konkret offenbarten Proteinen. Diese besitzen, beispielsweise über die gesamte Länge, wenigstens 30%, oder etwa 40%, 50 %, vorzugsweise wenigstens etwa 60 %, 65%, 70%, oder 75% ins besondere wenigsten 85 %, wie z.B. 90%, 95% oder 99%, Homologie zu einer der konkret offenbarten Sequenzen, berechnet nach dem Algorithmus von Pearson und Lipman, Proc. Natl. Acad. Sci. (USA) 85(8), 1988, 2444-2448. Der Homologiegrad spiegelt insbesondere den Grad der Identität zwischen veränderter und nicht veränderter Sequenz wider.

- 20 Homologe der erfindungsgemäßen Proteine oder Polypeptide können durch Mutagenese erzeugt werden, z.B. durch Punktmutation oder Verkürzung des Proteins. Der Begriff „Homolog“, wie er hier verwendet wird, betrifft auch eine variante Form des Proteins, die als Agonist oder Antagonist der Protein-Aktivität wirkt.

- 25 Homologe des erfindungsgemäßen Proteine können durch Screening kombinatorischer Banken von Mutanten, wie z.B. Verkürzungsmutanten, identifiziert werden. Beispielsweise kann eine variierte Bank von Protein-Varianten durch kombinatorische Mutagenese auf Nukleinsäureebene erzeugt werden, wie z.B. durch enzymatisches Ligieren eines Gemisches synthetischer Oligonukleotide. Es gibt eine Vielzahl von Verfahren, die zur Herstellung von Banken potentieller Homologer aus einer degenerierten Oligonukleotidsequenz verwendet werden können. Die chemische Synthese einer degenerierten Gensequenz kann in einem DNA-Syntheseautomaten durchgeführt werden, und das synthetische Gen kann dann in einen geeigneten Expressions-

vektor ligiert werden. Die Verwendung eines degenerierten Gensatzes ermöglicht die Bereitstellung sämtlicher Sequenzen in einem Gemisch, die den gewünschten Satz an potentiellen Proteinsequenzen codieren. Verfahren zur Synthese degenerierter Oligonukleotide sind dem Fachmann bekannt (Z.B. Narang, S.A. (1983) Tetrahedron 39:3; Itakura et al. (1984) Annu. Rev. Biochem. 53:323; Itakura et al., (1984) Science 198:1056; Ike et al. (1983) Nucleic Acids Res. 11:477).

Zusätzlich können Banken von Fragmenten des Protein-Codons verwendet werden, um eine variierte Population von Protein-Fragmenten zum Screening und zur anschließenden Selektion von Homologen eines erfindungsgemäßen Proteins zu erzeugen. Bei einer Ausführungsform kann eine Bank von kodierenden Sequenzfragmenten durch Behandeln eines doppelsträngigen PCR-Fragmentes einer kodierenden Sequenz mit einer Nuklease unter Bedingungen, unter denen ein Nicking nur etwa einmal pro Molekül erfolgt, Denaturieren der doppelsträngigen DNA, Renaturieren der DNA unter Bildung doppelsträngiger DNA, die Sense-/Antisense-Paare von verschiedenen genickten Produkten umfassen kann, Entfernen einzelsträngiger Abschnitte aus neu gebildeten Duplices durch Behandlung mit S1-Nuclease und Ligieren der resultierenden Fragmentbank in einen Expressionsvektor erzeugt werden. Durch dieses Verfahren kann eine Expressionsbank hergeleitet werden, die N-terminale, C-terminale und interne Fragmente mit verschiedenen Größen des erfindungsgemäßen Proteins kodiert.

Im Stand der Technik sind mehrere Techniken zum Screening von Genprodukten kombinatorischer Banken, die durch Punktmutationen oder Verkürzung hergestellt worden sind, und zum Screening von cDNA-Banken auf Genprodukte mit einer ausgewählten Eigenschaft bekannt. Diese Techniken lassen sich an das schnelle Screening der Genbanken anpassen, die durch kombinatorische Mutagenese erfindungsgemäßer Homologer erzeugt worden sind. Die am häufigsten verwendeten Techniken zum Screening großer Genbanken, die einer Analyse mit hohem Durchsatz unterliegen, umfassen das Klonieren der Genbank in replizierbare Expressionsvektoren, Transformieren der geeigneten Zellen mit der resultierenden Vektorenbank und Exprimieren der kombinatorischen Gene unter Bedingungen, unter denen der Nachweis der gewünschten Aktivität die Isolation des Vektors, der das Gen codiert, dessen Produkt nachgewiesen wurde, erleichtert. Recursive-Ensemble-Mutagenese (REM), eine Technik, die die Häufigkeit funktioneller Mutanten in den Banken vergrößert, kann in Kombination mit den Screeningtests verwendet

werden, um Homologe zu identifizieren (Arkin und Yourvan (1992) PNAS 89:7811-7815; Delgrave et al. (1993) Protein Engineering 6(3):327-331

c) Erfindungsgemäße Polynukleotide

5

Gegenstand der Erfindung sind ebenso Nukleinsäuresequenzen (einzel- und doppelsträngige DNA- und RNA-Sequenzen, wie z.B. cDNA und mRNA), kodierend für eines der obigen meth-Enzyme und deren funktionalen Äquivalenten, welche z.B. auch unter Verwendung künstlicher Nukleotidanaloga zugänglich sind.

10

Die Erfindung betrifft sowohl isolierte Nukleinsäuremoleküle, welche für erfindungsgemäße Polypeptide bzw. Proteine oder biologisch aktive Abschnitte davon kodieren, sowie Nukleinsäurefragmente, die z.B. zur Verwendung als Hybridisierungs-sonden oder Primer zur Identifizierung oder Amplifizierung von erfindungsgemäßer kodierenden Nukleinsäuren verwendet werden können.

15

Die erfindungsgemäßen Nukleinsäuremoleküle können zudem untranslatierte Sequenzen vom 3'- und/oder 5'-Ende des kodierenden Genbereichs enthalten

20

Ein "isoliertes" Nukleinsäuremolekül wird von anderen Nukleinsäuremolekülen abgetrennt, die in der natürlichen Quelle der Nukleinsäure zugegen sind und kann überdies im wesentlichen frei von anderem zellulären Material oder Kulturmedium sein, wenn es durch rekombinante Techniken hergestellt wird, oder frei von chemischen Vorstufen oder anderen Chemikalien sein, wenn es chemisch synthetisiert wird.

25

Die Erfindung umfasst weiterhin die zu den konkret beschriebenen Nukleotidsequenzen komplementären Nukleinsäuremoleküle oder einen Abschnitt davon.

30

Die erfindungsgemäß Nukleotidsequenzen ermöglichen die Erzeugung von Sonden und Primern, die zur Identifizierung und/oder Klonierung von homologer Sequenzen in anderen Zelltypen und Organismen verwendbar sind. Solche Sonden bzw. Primer umfassen gewöhnlich einen Nukleotidsequenzbereich, der unter stringenten Bedingungen an mindestens etwa 12, vorzugsweise mindestens etwa 25, wie z.B. etwa 40, 50 oder 75 aufeinanderfolgende Nukleotide eines

Sense-Stranges einer erfindungsgemäßen Nukleinsäuresequenz oder eines entsprechenden Antisense-Stranges hybridisiert.

Weitere erfindungsgemäße Nukleinsäuresequenzen sind abgeleitet von SEQ ID NO:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49 oder 51 und unterscheiden sich davon durch Addition, Substitution, Insertion oder Deletion einzelner oder mehrerer Nukleotide, kodieren aber weiterhin für Polypeptide mit dem gewünschten Eigenschaftsprofil. Dies können Polynukleotide sein, die zu obigen Sequenzen, beispielsweise über die gesamte Länge, in mindestens etwa 50%, 55%, 60%, 65%, 70%, 80% oder 90%, vorzugsweise in mindestens etwa 95%, 96%, 97%, 98% oder 99% der Sequenzpositionen identisch sind.

Erfindungsgemäß umfasst sind auch solche Nukleinsäuresequenzen, die sogenannte stumme Mutationen umfassen oder entsprechend der Codon-Nutzung eines speziellen Ursprungs- oder Wirtsorganismus, im Vergleich zu einer konkret genannten Sequenz verändert sind, ebenso wie natürlich vorkommende Varianten, wie z.B. Spleißvarianten oder Allelvarianten, davon. Gegenstand sind ebenso durch konservative Nukleotidsubstitutionen (d.h. die betreffende Aminosäure wird durch eine Aminosäure gleicher Ladung, Größe, Polarität und/oder Löslichkeit ersetzt) erhältliche Sequenzen.

Gegenstand der Erfindung sind auch die durch Sequenzpolymorphismen von den konkret offenbarten Nukleinsäuren abgeleiteten Moleküle. Diese genetischen Polymorphismen können zwischen Individuen innerhalb einer Population aufgrund der natürlichen Variation existieren. Diese natürlichen Variationen bewirken üblicherweise eine Varianz von 1 bis 5 % in der Nukleotidsequenz eines Gens.

Weiterhin umfasst die Erfindung auch Nukleinsäuresequenzen, welchen mit oben genannten kodierenden Sequenzen hybridisieren oder dazu komplementär sind. Diese Polynukleotide lassen sich bei Durchmusterung von genomischen oder cDNA-Banken auffinden und gegebenenfalls daraus mit geeigneten Primern mittels PCR vermehren und anschließend beispielsweise mit geeigneten Sonden isolieren. Eine weitere Möglichkeit bietet die Transformation geeigneter Mikroorganismen mit erfindungsgemäßen Polynukleotiden oder Vektoren, die Vermehrung der Mikroorganismen und damit der Polynukleotide und deren anschließende Isolierung. Darüber hinaus können erfindungsgemäße Polynukleotide auch auf chemischem Wege synthetisiert

werden.

Unter der Eigenschaft, an Polynukleotide „hybridisieren“ zu können, versteht man die Fähigkeit eines Poly- oder Oligonukleotids unter stringenten Bedingungen an eine nahezu komplementäre Sequenz zu binden, während unter diesen Bedingungen unspezifische Bindungen zwischen nicht-komplementären Partnern unterbleiben. Dazu sollten die Sequenzen zu 70-100%, vorzugsweise zu 90-100%, komplementär sein. Die Eigenschaft komplementärer Sequenzen, spezifisch aneinander binden zu können, macht man sich beispielsweise in der Northern- oder Southern-Blot-Technik oder bei der Primerbindung in PCR oder RT-PCR zunutze. Üblicherweise werden dazu Oligonukleotide ab einer Länge von 30 Basenpaaren eingesetzt. Unter stringenten Bedingungen versteht man beispielsweise in der Northern-Blot-Technik die Verwendung einer 50 – 70 °C, vorzugsweise 60 – 65 °C warmen Waschlösung, beispielsweise 0,1x SSC-Puffer mit 0,1% SDS (20x SSC: 3M NaCl, 0,3M Na-Citrat, pH 7,0) zur Elution unspezifisch hybridisierter cDNA-Sonden oder Oligonukleotide. Dabei bleiben, wie oben erwähnt, nur in hohem Maße komplementäre Nukleinsäuren aneinander gebunden. Die Einstellung stringenter Bedingungen ist dem Fachmann bekannt und ist z.B. in Ausubel et al., Current Protocols in Molecular Biology, John Wiley & Sons, N.Y. (1989), 6.3.1-6.3.6. beschrieben.

c) Isolierung der kodierenden methH-Gene

20

Die für das Enzym Methionin-Synthase (EC 2.1.1.13) kodierenden methH Gene aus den Organismen obiger Liste I sind in an sich bekannter Weise isolierbar.

Zur Isolierung der methH-Gene oder auch anderer Gene der Organismen aus obiger Liste I wird zunächst eine Genbank dieses Organismus in Escherichia coli (E. coli) angelegt. Das Anlegen von Genbanken ist in allgemein bekannten Lehrbüchern und Handbüchern ausführlich beschrieben. Als Beispiel seien das Lehrbuch von Winnacker: Gene und Klone, Eine Einführung in die Gentechnologie (Verlag Chemie, Weinheim, Deutschland, 1990), oder das Handbuch von Sambrook et al.: Molecular Cloning, A Laboratory Manual (Cold Spring Harbor Laboratory Press, 1989) genannt. Eine sehr bekannte Genbank ist die des E. coli K-12 Stammes W3110, die von Kohara et al. (Cell 50, 495-508 (198)) in λ -Vektoren angelegt wurde.

Zur Herstellung einer Genbank von Organismen der Liste I in *E. coli* können Cosmide, wie der Cosmidvektor SuperCos I (Wahl et al., 1987, Proceedings of the National Academy of Sciences USA, 84: 2160-2164), aber auch Plasmide, wie pBR322 (BoliVal; Life Sciences, 25, 807-818 (1979)) oder pUC9 (Vieira et al., 1982, Gene, 19: 259-268), verwendet werden. Als Wirte eignen sich besonders solche *E. coli* Stämme, die restriktions- und rekombinationsdefekt sind. Ein Beispiel hierfür ist der Stamm DH5 α mc α r, der von Grant et al. (Proceedings of the National Academy of Sciences USA, 87 (1990) 4645-4649) beschrieben wurde. Die mit Hilfe von Cosmiden klonierten langen DNA-Fragmente können anschließend wiederum in gängige, für die Sequenzierung geeignete Vektoren subkloniert und anschließend sequenziert werden, so wie es z. B. bei Sanger et al. (proceedings of the National Academy of Sciences of the United States of America, 74: 5463-5467, 1977) beschrieben ist.

Die erhaltenen DNA-Sequenzen können dann mit bekannten Algorithmen bzw. Sequenzanalyse-Programmen, wie z. B. dem von Staden (Nucleic Acids Research 14,217-232(1986)), dem von Marck (Nucleic Acids Research 16, 1829-1836 (1988)) oder dem GCG-Programm von Butler (Methods of Biochemical Analysis 39, 74-97 (1998)), untersucht werden.

Die für die metH-Gene kodierenden DNA-Sequenzen von Organismen gemäß obiger Liste I wurden gefunden. Insbesondere wurden DNA-Sequenzen gemäß SEQ ID NO:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49 und 51 gefunden. Weiterhin wurde aus diesen vorliegenden DNA-Sequenzen mit den oben beschriebenen Methoden die Aminosäuresequenzen der entsprechenden Proteine abgeleitet. Durch SEQ ID NO:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50 und 52 sind die sich ergebenden Aminosäuresequenzen der metH Genprodukte dargestellt.

Kodierende DNA-Sequenzen, die sich aus den Sequenzen gemäß SEQ ID NO:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49 und 51 durch die Degeneration des genetischen Kodes ergeben, sind ebenfalls Gegenstand der Erfindung. In gleicher Weise sind DNA-Sequenzen, die mit diesen Sequenzen oder davon abgeleiteten Sequenzteilen hybridisieren, Gegenstand der Erfindung.

Anleitungen zur Identifizierung von DNA-Sequenzen mittels Hybridisierung findet der Fachmann unter anderem im Handbuch "The DIG System Users Guide für Filter Hybridization" der Firma

- Boehringer Mannheim GmbH (Mannheim, Deutschland, 1993) und bei Liebl et al. (International Journal of Systematic Bacteriology (1991) 41: 255-260). Anleitungen zur Amplifikation von DNA-Sequenzen mit Hilfe der Polymerase-Kettenreaktion (PCR) findet der Fachmann unter anderem im Handbuch von Gait: Oligonukleotide synthesis: A Practical Approach (IRL Press, Oxford, UK, 1984) und bei Newton und Graham: PCR (Spektrum Akademischer Verlag, Heidelberg, Deutschland, 1994).

- Weiterhin ist bekannt, dass Änderungen am N- und/oder C- Terminus eines Proteins dessen Funktion nicht wesentlich beeinträchtigen oder sogar stabilisieren können. Angaben hierzu findet der Fachmann unter anderem bei Ben-Bassat et al. (Journal of Bacteriology 169: 751-757 (1987)), bei O'Regan et al. (Gene 77: 237-251 (1989)), bei Sahin-Toth et al. (Protein Sciences 3: 240-247 (1994)), bei Hochuli et al. (Biotechnology 6: 1321-1325 (1988)) und in bekannten Lehrbüchern der Genetik und Molekularbiologie.
- Aminosäuresequenzen, die sich in entsprechender Weise aus den SEQ ID NO:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50 und 52 ergeben, sind ebenfalls Bestandteil der Erfindung.

d) Erfindungsgemäß verwendete Wirtszellen

- Weitere Gegenstände der Erfindung betreffen als Wirtszelle dienende Mikroorganismen, insbesondere coryneforme Bakterien, die einen Vektor, insbesondere Pendelvektor oder Plasmidvektor, der wenigstens ein meth Gen erfindungsgemäßer Definition trägt, enthalten oder in denen ein erfindungsgemäßes meth Gen exprimiert bzw. verstärkt ist.

- Diese Mikroorganismen können schwefelhaltige Feinchemikalien, insbesondere L-Methionin, aus Glucose, Saccharose, Lactose, Fructose, Maltose, Melasse, Stärke, Cellulose oder aus Glycerin und Ethanol herstellen. Vorzugsweise sind dies coryneforme Bakterien, insbesondere der Gattung Corynebacterium. Aus der Gattung Corynebacterium ist insbesondere die Art Corynebacterium glutamicum zu nennen, die in der Fachwelt für ihre Fähigkeit bekannt ist, L-Aminosäuren zu produzieren.

Als Beispiele für geeignete Stämme coryneformer Bakterien sind solche der Gattung *Corynebacterium*, insbesondere der Art *Corynebacterium glutamicum* (*C. glutamicum*), wie

Corynebacterium glutamicum ATCC 13032,

Corynebacterium acetoglutamicum ATCC 15806,

5 *Corynebacterium acetoacidophilum* ATCC 13870,

Corynebacterium thermoaminogenes FERM BP-1539,

Corynebacterium melassecola ATCC 17965

oder

10 der Gattung *Brevibacterium*, wie

Brevibacterium flavum ATCC 14067

Brevibacterium lactofermentum ATCC 13869 und

Brevibacterium divaricatum ATCC 14020 zu nennen;

oder davon abgeleitete Stämme, wie

15 *Corynebacterium glutamicum* KFCC10065

Corynebacterium glutamicum ATCC21608

welche ebenfalls die gewünschte Feinchemikalie oder deren Vorstufe(n) produzieren.

Mit der Abkürzung KFCC ist die Korean Federation of Culture Collection gemeint, mit der Abkür-

20 zung ATCC die American type strain culture collection und mit der Abkürzung FERM die Sammlung des National institute of Bioscience and Human-Technology, Agency of Industrial Science and Technology, Japan.

e) Durchführung der erfindungsgemäßen Fermentation

25

Erfindungsgemäß wurde festgestellt, dass coryneforme Bakterien nach Überexpression eines *methH* Gens aus Organismen der Liste I in vorteilhafter Weise schwefelhaltige Feinchemikalien, insbesondere L-Methionin, produzieren.

30 Zur Erzielung einer Überexpression kann der Fachmann unterschiedliche Maßnahmen einzeln oder in Kombination ergreifen. So kann die Kopienzahl der entsprechenden Gene erhöht werden, oder es kann die Promotor- und Regulationsregion oder die Ribosomenbindungsstelle, die sich stromaufwärts des Strukturgens befindet, mutiert werden. In gleicher Weise wirken Expres-

- sionskassetten, die stromaufwärts des Strukturgens eingebaut werden. Durch induzierbare Promotoren ist es zusätzlich möglich, die Expression im Verlaufe der fermentativen L-Methionin-Produktion zu steigern. Durch Maßnahmen zur Verlängerung der Lebensdauer der mRNA wird ebenfalls die Expression verbessert. Weiterhin wird durch Verhinderung des Abbaus des Enzymproteins ebenfalls die Enzymaktivität verstärkt. Die Gene oder Genkonstrukte können entweder in Plasmiden mit unterschiedlicher Kopienzahl vorliegen oder im Chromosom integriert und amplifiziert sein. Alternativ kann weiterhin eine Überexpression der betreffenden Gene durch Veränderung der Medienzusammensetzung und Kulturführung erreicht werden.
- 5
- 10 Anleitungen hierzu findet der Fachmann unter anderem bei Martin et al. (Biotechnology 5, 137-146 (1987)), bei Guerrero et al. (Gene 138, 35-41 (1994)), Tsuchiya und Morinaga (Bio/Technology 6, 428-430 (1988)), bei Eikmanns et al. (Gene 102, 93-98 (1991)), in der Europäischen Patentschrift 0472869, im US Patent 4,601,893, bei Schwarzer und Pöhler (Biotechnology 9, 84-87 (1991)), bei Remscheid et al. (Applied and Environmental Microbiology 60, 126-132
- 15 (1994)), bei LaBarre et al. (Journal of Bacteriology 175, 1001-1007 (1993)), in der Patentanmeldung WO 96/15246, bei Malumbres et al. (Gene 134, 15-24 (1993)), in der japanischen Offenlegungsschrift JP-A-10-229891, bei Jensen und Hammer (Biotechnology and Bioengineering 58, 191-195 (1998)), bei Makrides (Microbiological Reviews 60 : 512-538 (1996)) und in bekannten Lehrbüchern der Genetik und Molekularbiologie.
- 20
- Gegenstand der Erfindung sind deshalb auch Expressionskonstrukte, enthaltend unter der genetischen Kontrolle regulativer Nukleinsäuresequenzen eine für ein erfindungsgemäßes Polypeptid kodierende Nukleinsäuresequenz; sowie Vektoren, umfassend wenigstens eines dieser Expressionskonstrukte. Vorzugsweise umfassen solche erfindungsgemäßen Konstrukte 5'-stromaufwärts von der jeweiligen kodierenden Sequenz einen Promotor und 3'-stromabwärts eine Terminatorsequenz sowie gegebenenfalls weitere übliche regulative Elemente, und zwar jeweils operativ verknüpft mit der kodierenden Sequenz. Unter einer „operativen Verknüpfung“ versteht man die sequentielle Anordnung von Promotor, kodierender Sequenz, Terminator und gegebenenfalls weiterer regulativer Elemente derart, dass jedes der regulativen Elemente seine
- 25
- 30 Funktion bei der Expression der kodierenden Sequenz bestimmungsgemäß erfüllen kann. Beispiele für operativ verknüpfbare Sequenzen sind Aktivierungssequenzen sowie Enhancer und dergleichen. Weitere regulative Elemente umfassen selektierbare Marker, Amplifikationssignale, Replikationsursprünge und dergleichen. Geeignete regulatorische Sequenzen sind z.B. be-

schrieben in Goeddel, Gene Expression Technology: Methods in Enzymology 185, Academic Press, San Diego, CA (1990).

5 Zusätzlich zu den artifiziellen Regulationssequenzen kann die natürliche Regulationssequenz vor dem eigentlichen Strukturgen noch vorhanden sein. Durch genetische Veränderung kann diese natürliche Regulation gegebenenfalls ausgeschaltet und die Expression der Gene erhöht oder erniedrigt werden. Das Genkonstrukt kann aber auch einfacher aufgebaut sein, das heißt es werden keine zusätzlichen Regulationssignale vor das Strukturgen insertiert und der natürliche Promotor mit seiner Regulation wird nicht entfernt. Statt dessen wird die natürliche Regulationssequenz so mutiert, dass keine Regulation mehr erfolgt und die Genexpression gesteigert oder verringert wird. Die Nukleinsäuresequenzen können in einer oder mehreren Kopien im Genkonstrukt enthalten sein.

15 Beispiele für brauchbare Promotoren sind: die Promotoren, *ddh*, *amy*, *lysC*, *dapA*, *lysA* aus *Corynebacterium glutamicum*, aber auch gram-positiven Promotoren SPO2 wie sie in *Bacillus Subtilis* and Its Closest Relatives, Sonenshein, Abraham L., Hoch, James A., Losick, Richard; ASM Press, District of Columbia, Washington und Patek M. Eikmanns B.J., Patek J. Sahm H. Microbiology. 142 1297-309, 1996 beschrieben sind, oder aber auch *cos*-, *tac*-, *trp*-, *tet*-, *trp-tet*-, *lpp*-, *lac*-, *lpp-lac*-, *lacIq*-, T7-, T5-, T3-, *gal*-, *trc*-, *ara*-, SP6-, *lambda-PR*- oder *lambda-PL*-Promotor, die vorteilhafterweise in gram-negativen Bakterien Anwendung finden. Bevorzugt ist auch die Verwendung induzierbarer Promotoren, wie z.B. licht- und insbesondere temperaturinduzierbarer Promotoren, wie der *P_{HP}*-Promotor. Prinzipiell können alle natürlichen Promotoren mit ihren Regulationssequenzen verwendet werden. Darüber hinaus können auch synthetische Promotoren vorteilhaft verwendet werden.

25 Die genannten regulatorischen Sequenzen sollen die gezielte Expression der Nukleinsäuresequenzen ermöglichen. Dies kann beispielsweise je nach Wirtsorganismus bedeuten, dass das Gen erst nach Induktion exprimiert oder überexprimiert wird, oder dass es sofort exprimiert und/oder überexprimiert wird.

30 Die regulatorischen Sequenzen bzw. Faktoren können dabei vorzugsweise die Expression positiv beeinflussen und dadurch erhöhen oder erniedrigen. So kann eine Verstärkung der regulatorischen Elemente vorteilhafterweise auf der Transkriptionsebene erfolgen, indem starke

Transkriptionssignale wie Promotoren und/oder "Enhancer" verwendet werden. Daneben ist aber auch eine Verstärkung der Translation möglich, indem beispielsweise die Stabilität der mRNA verbessert wird.

- 5 Die Herstellung einer Expressionskassette erfolgt durch Fusion eines geeigneten Promotors, einer geeigneten Shine-Dalgarno-Sequenz mit einer methH-Nukleotidsequenz sowie einem geeigneten Terminationssignal. Dazu verwendet man gängige Rekombinations- und Klonierungstechniken, wie sie beispielsweise in Current Protocols in Molecular Biology, 1993, John Wiley & Sons, Incorporated, New York New York, PCR Methods, Gelfand, David H., Innis, Michael A., Sninsky, John J. 1999, Academic Press, Incorporated, California, San Diego, ., PCR Cloning Protocols, Methods in Molecular Biology Ser., Vol. 192, 2nd ed., Humana Press, New Jersey, Totowa. T. Maniatis, E.F. Fritsch und J. Sambrook, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY (1989) sowie in T.J. Silhavy, M.L. Berman und L.W. Enquist, Experiments with Gene Fusions, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY (1984) und in Ausubel, F.M. et al., Current Protocols in Molecular Biology, Greene Publishing Assoc. and Wiley Interscience (1987) beschrieben sind.

- Das rekombinante Nukleinsäurekonstrukt bzw. Genkonstrukt wird zur Expression in einem geeigneten Wirtsorganismus vorteilhafterweise in einen wirtsspezifischen Vektor inseriert, der eine optimale Expression der Gene im Wirt ermöglicht. Vektoren sind dem Fachmann wohl bekannt und können beispielsweise aus "Cloning Vectors" (Pouwels P. H. et al., Hrsg, Elsevier, Amsterdam-New York-Oxford, 1985) entnommen werden. Unter Vektoren sind außer Plasmiden auch alle anderen dem Fachmann bekannten Vektoren, wie beispielsweise Phagen, Transposons, IS-Elemente, Phasmide, Cosmide, und lineare oder zirkuläre DNA zu verstehen. Diese Vektoren können autonom im Wirtsorganismus repliziert oder chromosomal repliziert werden.

- Zur Verstärkung wurden erfindungsgemäße methH Gene beispielhaft mit Hilfe von episomalen Plasmiden überexprimiert. Als Plasmide eignen sich solche, die in coryneformen Bakterien repliziert werden. Zahlreiche bekannte Plasmidvektoren, wie z. B. pZ1 (Menkel et al., Applied and Environmental Microbiology (1989) 64: 549-554), pEKEx1 (Eikmanns et al., Gene 102: 93-98 (1991)) oder pHS2-1 (Sonnen et al., Gene 107: 69-74 (1991)) beruhen auf den kryptischen Plasmiden pHM1519, pBL1 oder pGA1. Andere Plasmidvektoren, wie z. B. pCLIK5MCS, oder solche, die auf pCG4 (US-A 4,489,160) oder pNG2 (Serwold-Davis et al., FEMS Microbiology

Letters 66, 119-124 (1990)) oder pAG1 (US-A 5,158,891) beruhen, können in gleicher Weise verwendet werden.

- 5 Weiterhin eignen sich auch solche Plasmidvektoren mit Hilfe derer man das Verfahren der Genamplifikation durch Integration in das Chromosom anwenden kann, so wie es beispielsweise von Remscheid et al. (Applied and Environmental Microbiology 60,126-132 (1994)) zur Duplikation bzw. Amplifikation des *hom-thrB*-Operons beschrieben wurde. Bei dieser Methode wird das vollständige Gen in einen Plasmidvektor kloniert, der in einem Wirt (typischerweise *E. coli*), nicht aber in *C. glutamicum* replizieren kann. Als Vektoren kommen beispielsweise pSUP301 (Simon et al., Bio/ Technology 1,784-791 (1983)), pK18mob oder pK19mob (Schäfer et al., Gene 145,69-73 (1994)), Bernard et al., Journal of Molecular Biology, 234: 534-541 (1993)), pEM1 (Schrumpf et al. 1991, Journal of Bacteriology 173: 4510-4516) oder pBGS8 (Spratt et al., 1986, Gene 41: 337-342) in Frage. Der Plasmidvektor, der das zu amplifizierende Gen enthält, wird anschließend durch Transformation in den gewünschten Stamm von *C. glutamicum* überführt.
- 10 Methoden zur Transformation sind beispielsweise bei Thierbach et al. (Applied Microbiology and Biotechnology 29, 356-362 (1988)), Dunican und Shivnan (Biotechnology 7, 1067-1070 (1989)) und Tauch et al. (FEMS Microbiological Letters 123,343-347 (1994)) beschrieben.
- 15

- Enzyme können durch Mutationen in den korrespondierenden Genen derart in ihrer Aktivität beeinflusst werden, dass es zu einer teilweisen oder vollständigen Verringerung der Reaktionsgeschwindigkeit der enzymatischen Reaktion kommt. Beispiele für solche Mutationen sind dem Fachmann bekannt (Motoyama H. Yano H. Terasaki Y. Anazawa H. Applied & Environmental Microbiology. 67:3064-70, 2001, Eikmanns BJ. Eggeling L. Sahm H. Antonie van Leeuwenhoek. 64:145-63, 1993-94.)
- 20

- 25 Zusätzlich kann es für die Produktion von schwefelhaltige Feinchemikalien, insbesondere L-Methionin, vorteilhaft sein, neben einer Expression bzw. Verstärkung eines erfindungsgemäßen *metH*-Gen eines oder mehrere Enzyme des Methionin-Biosyntheseweges oder eines damit assoziierten (d.h. in einem funktionelle Zusammenhang stehenden) Biosynthese – oder sonstigen Stoffwechselweges, wie des Cystein-, Lysin- oder Threonin-Stoffwechselwegs, wie insbesondere der Aspartatsemialdehyd-Synthese, der Glykolyse, der Anaplerotik, des Pentose-Phosphat-Stoffwechsels, des Zitronensäure-Zyklus oder des Aminosäure-Exports zu verstärken.
- 30

23

So kann für die Herstellung von schwefelhaltige Feinchemikalien, insbesondere L-Methionin, eines oder mehrere der folgenden Gene verstärkt sein, (d.h. z.B. in einer höheren Koplenzahl vorliegen oder ein Enzym mit höherer Aktivität oder Spezifität kodieren):

- das für eine Aspartatkinase kodierende Gen *lysC* (EP 1 108 790 A2; DNA-SEQ NO. 281),
- 5 - das für eine Aspartat-Semialdehyd Dehydrogenase kodierende Gen *asd* (EP 1 108 790 A2; DNA-SEQ NO. 282),
- das für die Glycerinaldehyd-3-Phosphat Dehydrogenase kodierende Gen *gap* (Eikmanns (1992), Journal of Bacteriology 174: 6076-6086),
- das für die 3-Phosphoglycerat Kinase kodierende Gen *pgk* (Eikmanns (1992), Journal of Bacteriology 174: 6076-6086),
- 10 - das für die Pyruvat Carboxylase kodierende Gen *pyc* (Eikmanns (1992), Journal of Bacteriology 174: 6076-6086),
- das für die Triosephosphat Isomerase kodierende Gen *tpi* (Eikmanns (1992), Journal of Bacteriology 174: 6076-6086),
- 15 - das für die Homoserin O-Acetyltransferase kodierende Gen *metA* (EP 1 108 790 A2; DNA-SEQ NO. 725),
- das für die Cystathionin-gamma-Synthase kodierende Gen *metB* (EP 1 108 790 A2; DNA-SEQ NO. 3491),
- das für die Cystathionin-gamma-Lyase kodierende Gen *metC* (EP 1 108 790 A2; DNA-SEQ NO. 3061),
- 20 - das für die Serin-Hydroxymethyltransferase kodierende Gen *glyA* (EP 1 108 790 A2; DNA-SEQ NO. 1110),
- das für die O-Acetylhomoserin-Sulfhydrylase kodierende Gen *metY* (EP 1 108 790 A2; DNA-SEQ NO. 726),
- 25 - das für die Methylentetrahydrofolat-Reduktase kodierende Gen *metF* (EP 1 108 790 A2; DNA-SEQ NO. 2379),
- das für die Phosphoserin-Aminotransferase kodierende Gen *serC* (EP 1 108 790 A2; DNA-SEQ NO. 928)
- eines für die Phosphoserin-Phosphatase kodierende Gen *serB* (EP 1 108 790 A2; DNA-SEQ NO. 334, DNA-SEQ NO. 467, DNA-SEQ NO. 2767)
- 30 - das für die Serine Acetyl-Transferase kodierende Gen *cysE* (EP 1 108 790 A2; DNA-SEQ NO. 2818)

- das für eine Homoserin-Dehydrogenase kodierende Gen *hom* (EP 1 108 790 A2; DNA-SEQ NO. 1306)

5 So kann für die Herstellung von schwefelhaltige Feinchemikalien, insbesondere L-Methionin, in coryneformen Bakterien, vorteilhaft sein, gleichzeitig wenigstens eines der nachfolgenden Gene zu mutieren, insbesondere so, dass die korrespondierenden Proteine, verglichen mit nicht mutierten Proteinen, in geringerem Maße oder nicht durch einen Stoffwechselmetaboliten in ihrer Aktivität beeinflusst werden:

- 10 - das für eine Aspartatkinase kodierende Gen *lysC* (EP 1 108 790 A2; DNA-SEQ NO. 281),
- das für die Pyruvat Carboxylase kodierende Gen *pyc* (Eikmanns (1992), Journal of Bacteriology 174: 6076-6086),
- das für die Homoserin O-Acetyltransferase kodierende Gen *metA* (EP 1 108 790 A2; DNA-SEQ NO. 725),
- 15 - das für die Cystathionin-gamma-Synthase kodierende Gen *metB* (EP 1 108 790 A2; DNA-SEQ NO. 3491),
- das für die Cystathionin-gamma-Lyase kodierende Gen *metC* (EP 1 108 790 A2; DNA-SEQ NO. 3061),
- das für die Serin-Hydroxymethyltransferase kodierende Gen *glyA* (EP 1 108 790 A2; DNA-SEQ
- 20 NO. 1110),
- das für die O-Acetylhomoserin-Sulphydrylase kodierende Gen *metY* (EP 1 108 790 A2; DNA-SEQ NO. 726),
- das für die Methylentetrahydrofolat-Reduktase kodierende Gen *metF* (EP 1 108 790 A2; DNA-SEQ NO. 2379),
- 25 - das für die Phosphoserin-Aminotransferase kodierende Gen *serC* (EP 1 108 790 A2; DNA-SEQ NO. 928)
- eines für die Phosphoserin-Phosphatase kodierende Gen *serB* (EP 1 108 790 A2; DNA-SEQ NO. 334, DNA-SEQ NO. 467, DNA-SEQ NO. 2767)
- das für die Serine Acetyl-Transferase kodierende Gen *cysE* (EP 1 108 790 A2; DNA-SEQ NO.
- 30 2818)
- das für eine Homoserin-Dehydrogenase kodierende Gen *hom* (EP 1 108 790 A2; DNA-SEQ NO. 1306)

25

Weiterhin kann es für die Produktion von schwefelhaltige Feinchemikalien, insbesondere L-Methionin, vorteilhaft sein, zusätzlich zur Expression bzw. Verstärkung eines der erfindungsgemäßen methH-Gene eines oder mehrere der folgenden Gene abzuschwächen, insbesondere deren Expression zu verringern, oder auszuschalten:

5

- das für die Homoserine-Kinase kodierende Gen thrB (EP 1 108 790 A2; DNA-SEQ NO. 3453)
- das für die Threonin Dehydratase kodierende Gen ilvA (EP 1 108 790 A2; DNA-SEQ NO. 2328)

10

- das für die Threonin Synthase kodierende Gen thrC (EP 1 108 790 A2; DNA-SEQ NO. 3486)
- das für die Meso-Diaminopimelat D-Dehydrogenase kodierende Gen ddh (EP 1 108 790 A2; DNA-SEQ NO. 3494)
- das für die Phosphoenolpyruvat-Carboxykinase kodierende Gen pck (EP 1 108 790 A2; DNA-SEQ NO. 3157)

15

- das für die Glucose-6-Phosphat-6-Isomerase kodierende Gen pgi (EP 1 108 790 A2; DNA-SEQ NO. 950)
- das für die Pyruvat-Oxidase kodierende Gen poxB (EP 1 108 790 A2; DNA-SEQ NO. 2873)
- das für die Dihydrodipicolinat Synthase kodierende Gen dapA (EP 1 108 790 A2; DNA-SEQ NO. 3476)

20

- das für die Dihydrodipicolinat Reduktase kodierende Gen dapB (EP 1 108 790 A2; DNA-SEQ NO. 3477)
- das für die Diaminopicolinat Decarboxylase kodierende Gen lysA (EP 1 108 790 A2; DNA-SEQ NO. 3451)

Weiterhin kann es für die Produktion von schwefelhaltige Feinchemikalien, insbesondere L-Methionin, vorteilhaft sein, zusätzlich zur Expression bzw. Verstärkung eines der erfindungsgemäßen methH-Gene in Coryneformen Bakterien gleichzeitig wenigstens eines der folgenden Gene so zu mutieren, dass die enzymatische Aktivität des korrespondierenden Proteins teilweise oder vollständig verringert wird:

30

- das für die Homoserine-Kinase kodierende Gen thrB (EP 1 108 790 A2; DNA-SEQ NO. 3453)
- das für die Threonin Dehydratase kodierende Gen ilvA (EP 1 108 790 A2; DNA-SEQ NO. 2328)
- das für die Threonin Synthase kodierende Gen thrC (EP 1 108 790 A2; DNA-SEQ NO. 3486)

- das für die Meso-Diaminopimelat D-Dehydrogenase kodierende Gen ddh (EP 1 108 790 A2; DNA-SEQ NO. 3494)
- das für die Phosphoenolpyruvat-Carboxykinase kodierende Gen pck (EP 1 108 790 A2; DNA-SEQ NO. 3157)
- 5 - das für die Glucose-6-Phosphat-6-Isomerase kodierende Gen pgi (EP 1 108 790 A2; DNA-SEQ NO. 950)
- das für die Pyruvat-Oxidase kodierende Gen poxB (EP 1 108 790 A2; DNA-SEQ NO. 2873)
- das für die Dihydrodipicolinat Synthase kodierende Gen dapA (EP 1 108 790 A2; DNA-SEQ NO. 3476)
- 10 - das für die Dihydrodipicolinat Reduktase kodierende Gen dapB (EP 1 108 790 A2; DNA-SEQ NO. 3477)
- das für die Diaminopicolinat Decarboxylase kodierende Gen lysA (EP 1 108 790 A2; DNA-SEQ NO. 3451)
- 15 Weiterhin kann es für die Produktion von schwefelhaltige Feinchemikalien, insbesondere L-Methionin, vorteilhaft sein, neben der Expression bzw. Verstärkung eines erfindungsgemäßen meth-Gens unerwünschte Nebenreaktionen auszuschalten, welche beispielsweise die Ausbeute an der Feinchemikalie verringern (Nakayama: "Breeding of Amino Acid Producing Microorganisms", in: Overproduction of Microbial Products, Krumphanz, Sikyta, Vanek (eds.), Academic Press, London, UK, 1982).
- 20 Die erfindungsgemäß hergestellten Mikroorganismen können kontinuierlich oder diskontinuierlich im batch-Verfahren (Satzkultivierung) oder im fed batch (Zulaufverfahren) oder repeated fed batch Verfahren (repetitives Zulaufverfahren) zur Produktion von schwefelhaltige Feinchemikalien, insbesondere L-Methionin, kultiviert werden. Eine Zusammenfassung über bekannte Kultivierungsmethoden ist im Lehrbuch von Chmiel (Bioprozeßtechnik 1. Einführung in die Bioverfahrenstechnik (Gustav Fischer Verlag, Stuttgart, 1991)) oder im Lehrbuch von Storch (Bioreaktoren und periphere Einrichtungen (Vieweg Verlag, Braunschweig/Wiesbaden, 1994)) zu finden.
- 25 Das zu verwendende Kulturmedium hat in geeigneter Weise den Ansprüchen der jeweiligen Stämme zu genügen. Beschreibungen von Kulturmedien verschiedener Mikroorganismen sind im Handbuch "Manual of Methods für General Bacteriology" der American Society für Bacteriology (Washington D. C., USA, 1981) enthalten.
- 30

Diese erfindungsgemäß einsetzbaren Medien umfassen gewöhnlich eine oder mehrere Kohlenstoffquellen, Stickstoffquellen, anorganische Salze, Vitamine und/oder Spurenelemente.

- 5 Bevorzugte Kohlenstoffquellen sind Zucker, wie Mono-, Di- oder Polysaccharide. Sehr gute Kohlenstoffquellen sind beispielsweise Glucose, Fructose, Mannose, Galactose, Ribose, Sorbose, Ribulose, Lactose, Maltose, Saccharose, Raffinose, Stärke oder Cellulose. Man kann Zucker auch über komplexe Verbindungen, wie Melassen, oder andere Nebenprodukte der Zucker-Raffinierung zu den Medien geben. Es kann auch vorteilhaft sein, Gemische verschiedener Kohlenstoffquellen zuzugeben. Andere mögliche Kohlenstoffquellen sind Öle und Fette wie z. B. Sojaöl, Sonnenblumenöl, Erdnußöl und Kokosfett, Fettsäuren wie z. B. Palmitinsäure, Stearinsäure oder Linolsäure, Alkohole wie z. B. Glycerin, Methanol oder Ethanol und organische Säuren wie z. B. Essigsäure oder Milchsäure.
- 10
- 15 Stickstoffquellen sind gewöhnlich organische oder anorganische Stickstoffverbindungen oder Materialien, die diese Verbindungen enthalten. Beispielhafte Stickstoffquellen umfassen Ammoniak-Gas oder Ammoniumsalze, wie Ammoniumsulfat, Ammoniumchlorid, Ammoniumphosphat, Ammoniumcarbonat oder Ammoniumnitrat, Nitrate, Harnstoff, Aminosäuren oder komplexe Stickstoffquellen, wie Maisquellwasser, Sojamehl, Sojaprotein, Hefeextrakt, Fleischextrakt und
- 20 andere. Die Stickstoffquellen können einzeln oder als Mischung verwendet werden.

Anorganische Salzverbindungen, die in den Medien enthalten sein können, umfassen die Chlorid-, Phosphor- oder Sulfatsalze von Calcium, Magnesium, Natrium, Kobalt, Molybdän, Kalium, Mangan, Zink, Kupfer und Eisen

- 25 Als Schwefelquelle für die Herstellung von schwefelhaltigen Feinchemikalien, insbesondere von Methionin, können anorganische schwefelhaltige Verbindungen wie beispielsweise Sulfate, Sulfite, Dithionite, Tetrathionate, Thiosulfate, Sulfide aber auch organische Schwefelverbindungen, wie Mercaptane und Thiole, verwendet werden.

- 30 Als Phosphorquelle können Phosphorsäure, Kaliumdihydrogenphosphat oder Dikaliumhydrogenphosphat oder die entsprechenden Natrium haltigen Salze verwendet werden.

Chelatbildner können zum Medium gegeben werden, um die Metallionen in Lösung zu halten. Besonders geeignete Chelatbildner umfassen Dihydroxyphenole, wie Catechol oder Protocatechuat, oder organische Säuren, wie Citronensäure.

- 5 Die erfindungsgemäß eingesetzten Fermentationsmedien enthalten üblicherweise auch andere Wachstumsfaktoren, wie Vitamine oder Wachstumsförderer, zu denen beispielsweise Biotin, Riboflavin, Thiamin, Folsäure, Nikotinsäure, Panthothenat und Pyridoxin gehören. Wachstumsfaktoren und Salze stammen häufig von komplexen Medienkomponenten, wie Hefeextrakt, Melassen, Maisquellwasser und dergleichen. Dem Kulturbedium können überdies geeignete Vorstufen zugesetzt werden. Die genaue Zusammensetzung der Medienverbindungen hängt stark vom jeweiligen Experiment ab und wird für jeden spezifischen Fall individuell entschieden. Information über die Medienoptimierung ist erhältlich aus dem Lehrbuch "Applied Microbiol. Physiology, A Practical Approach" (Hrsg. P.M. Rhodes, P.F. Stanbury, IRL Press (1997) S. 53-73, ISBN 0 19 963577 3). Wachstumsmedien lassen sich auch von kommerziellen Anbietern beziehen, wie Standard 1 (Merck) oder BHI (Brain heart infusion, DIFCO) und dergleichen.

- 20 Sämtliche Medienkomponenten werden, entweder durch Hitze (20 min bei 1,5 bar und 121°C) oder durch Sterilfiltration, sterilisiert. Die Komponenten können entweder zusammen oder nötigenfalls getrennt sterilisiert werden. Sämtliche Medienkomponenten können zu Beginn der Anzucht zugegen sein oder wahlfrei kontinuierlich oder chargenweise hinzugegeben werden.

- 25 Die Temperatur der Kultur liegt normalerweise zwischen 15°C und 45°C, vorzugsweise bei 25°C bis 40°C und kann während des Experimentes konstant gehalten oder verändert werden. Der pH-Wert des Mediums sollte im Bereich von 5 bis 8,5, vorzugsweise um 7,0 liegen. Der pH-Wert für die Anzucht läßt sich während der Anzucht durch Zugabe von basischen Verbindungen wie Natriumhydroxid, Kaliumhydroxid, Ammoniak bzw. Ammoniakwasser oder saure Verbindungen wie Phosphorsäure oder Schwefelsäure kontrollieren. Zur Kontrolle der Schaumentwicklung können Antischaummittel, wie z. B. Fettsäurepolyglykolester, eingesetzt werden. Zur Aufrechterhaltung der Stabilität von Plasmiden können dem Medium geeignete selektiv wirkende Stoffe, wie z. B. Antibiotika, hinzugefügt werden. Um aerobe Bedingungen aufrechtzuerhalten, werden Sauerstoff oder Sauerstoffhaltige Gasmischungen, wie z. B. Umgebungsluft, in die Kultur eingetragen. Die Temperatur der Kultur liegt normalerweise bei 20°C bis 45°C. Die Kultur wird solange fortgesetzt, bis sich ein Maximum des gewünschten Produktes gebildet hat. Dieses Ziel wird

normalerweise innerhalb von 10 Stunden bis 160 Stunden erreicht.

Die so erhaltenen, insbesondere L-Methionin enthaltenden, Fermentationsbrühen haben üblicherweise eine Trockenmasse von 7,5 bis 25 Gew.-%.

5

Vorteilhaft ist außerdem auch, wenn die Fermentation zumindest am Ende, insbesondere jedoch über mindestens 30% der Fermentationsdauer zuckerlimitiert gefahren wird. Das heißt, dass während dieser Zeit die Konzentration an verwertbarem Zucker im Fermentationsmedium auf ≥ 0 bis 3 g/l gehalten, beziehungsweise abgesenkt wird.

10

Die Fermentationsbrühe wird anschließend weiterverarbeitet. Je nach Anforderung kann die Biomasse ganz oder teilweise durch Separationsmethoden, wie z. B. Zentrifugation, Filtration, Dekantieren oder einer Kombination dieser Methoden aus der Fermentationsbrühe entfernt oder vollständig in ihr belassen werden.

15

Anschließend kann die Fermentationsbrühe mit bekannten Methoden, wie z. B. mit Hilfe eines Rotationsverdampfers, Dünnschichtverdampfers, Fallfilmverdampfers, durch Umkehrosmose, oder durch Nanofiltration, eingedickt beziehungsweise aufkonzentriert werden. Diese aufkonzentrierte Fermentationsbrühe kann anschließend durch Gefriertrocknung, Sprühtrocknung, Sprühgranulation oder durch anderweitige Verfahren aufgearbeitet werden.

20

Es ist aber auch möglich die schwefelhaltigen Feinchemikalien, insbesondere L-Methionin, weiter aufzureinigen. Hierzu wird die produktthaltige Brühe nach dem Abtrennen der Biomasse einer Chromatographie mit einem geeigneten Harz unterworfen, wobei das gewünschte Produkt oder die Verunreinigungen ganz oder teilweise auf dem Chromatographieharz zurückgehalten werden. Diese Chromatographieschritte können nötigenfalls wiederholt werden, wobei die gleichen oder andere Chromatographieharze verwendet werden. Der Fachmann ist in der Auswahl der geeigneten Chromatographieharze und ihrer wirksamsten Anwendung bewandert. Das gereinigte Produkt kann durch Filtration oder Ultrafiltration konzentriert und bei einer Temperatur aufbewahrt werden, bei der die Stabilität des Produktes maximal ist.

25

30

Die Identität und Reinheit der isolierten Verbindung(en) kann durch Techniken des Standes der Technik bestimmt werden. Diese umfassen Hochleistungs-Flüssigkeitschromatographie (HPLC),

spektroskopische Verfahren, Färbeverfahren, Dünnschichtchromatographie, NIRS, Enzymtest oder mikrobiologische Tests. Diese Analyseverfahren sind zusammengefaßt in: Patek et al. (1994) Appl. Environ. Microbiol. 60:133-140; Malakhova et al. (1996) Biotekhnologiya 11 27-32; und Schmidt et al. (1998) Bioprocess Engineer. 19:67-70. Ulmann's Encyclopedia of Industrial
 5 Chemistry (1996) Bd. A27, VCH: Weinheim, S. 89-90, S. 521-540, S. 540-547, S. 559-566, 575-581 und S. 581-587; Michal, G (1999) Biochemical Pathways: An Atlas of Biochemistry and Molecular Biology, John Wiley and Sons; Fallon, A. et al. (1987) Applications of HPLC in Biochemistry in: Laboratory Techniques in Biochemistry and Molecular Biology, Bd. 17.

10 Die Erfindung wird nun anhand der folgenden nicht-limitierenden Beispiele näher beschrieben:

Beispiel 1: Konstruktion von pCLIK5MCS

Zunächst wurden Ampicillinresistenz und Replikationsursprung des Vektors pBR322 mit den
 15 Oligonukleotiden p1.3 (SEQ ID NO:53) und p2.3 (SEQ ID NO:54) mit Hilfe der Polymerase-Kettenreaktion (PCR) amplifiziert.

p1.3 (SEQ ID NO:53)

5'-CCCGGGATCCGCTAGCGGCGCGCCGGCCGGCCCGGTGTGAAATACCGCACAG-3'

20

p2.3 (SEQ ID NO:54)

5'-TCTAGACTCGAGCGGCCGCGGCCGGCCTTTAAATTGAAGACGAAAGGGCCTCG-3'

Neben den zu pBR322 komplementären Sequenzen, enthält das Oligonukleotid p1.3 (SEQ ID
 25 NO:53) in 5'-3' Richtung die Schnittstellen für die Restriktionsendonukleasen SmaI, BamHI, NheI und Ascl und das Oligonukleotid p2.3 (SEQ ID NO:54) in 5'-3' Richtung die Schnittstellen für die Restriktionsendonukleasen XbaI, XhoI, NotI und DraI. Die PCR Reaktion wurde nach Standardmethode wie Innis et al. (PCR Protocols. A Guide to Methods and Applications, Academic Press (1990)) mit PfuTurbo Polymerase (Stratagene, La Jolla, USA) durchgeführt. Das erhaltene
 30 DNA Fragment mit einer Größe von ungefähr 2,1 kb wurde mit dem GFX™PCR, DNA and Gel Band Purification Kit (Amersham Pharmacia, Freiburg) nach Angaben des Herstellers gereinigt. Die stumpfen Enden des DNA-Fragmentes wurden mit dem Rapid DNA Ligation Kit (Roche

Diagnostics, Mannheim) nach Angaben des Herstellers miteinander ligiert und der Ligationsansatz nach Standardmethoden wie in Sambrook et al. (Molecular Cloning. A Laboratory Manual, Cold Spring Harbor, beschrieben (1989)), in kompetente E.coli XL-1Blue (Stratagene, La Jolla, USA) transformiert. Eine Selektion auf Plasmid tragende Zellen wurde durch das Ausplattieren auf Ampicillin (50 µg/ml) haltigen LB Agar (Lennox, 1955, Virology, 1:190) erreicht.

Die Plasmid-DNA eines individuellen Klons wurde mit dem Qiaprep Spin Miniprep Kit (Qiagen, Hilden) nach Angaben des Herstellers isoliert und über Restriktionsverdaus überprüft. Das so erhaltene Plasmid erhält den Namen pCLiK1.

Ausgehend vom Plasmid pWLT1 (Liebl et al., 1992) als Template für eine PCR Reaktion wurde mit den Oligonukleotiden neo1 (SEQ ID NO:55) und neo2 (SEQ ID NO:56) eine Kanamycin-Resistenzcassette amplifiziert.

neo1 (SEQ ID NO:55):

5'-GAGATCTAGACCCGGGGATCCGCTAGCGGGCTGCTAAAGGAAGCGGA-3'

neo2 (SEQ ID NO:56):

5'-GAGAGGCGCGCCGCTAGCGTGGGCGAAGAACTCCAGCA-3'

Neben den zu pWLT1 komplementären Sequenzen, enthält das Oligonukleotid neo1 in 5'-3' Richtung die Schnittstellen für die Restriktionsendonukleasen XbaI, SmaI, BamHI, NheI und das Oligonukleotid neo2 (SEQ ID NO:56) in 5'-3' Richtung die Schnittstellen für die Restriktionsendonukleasen AscI und NheI. Die PCR Reaktion wurde nach Standardmethode wie Innis et al. (PCR Protocols. A Guide to Methods and Applications, Academic Press (1990)) mit PfuTurbo Polymerase (Stratagene, La Jolla, USA) durchgeführt. Das erhaltene DNA Fragment mit einer Größe von ungefähr 1,3 kb wurde mit dem GFX™PCR, DNA and Gel Band Purification Kit (Amersham Pharmacia, Freiburg) nach Angaben des Herstellers gereinigt. Das DNA-Fragment wurde mit den Restriktionsendonukleasen XbaI und AscI (New England Biolabs, Beverly, USA) geschnitten und im Anschluß daran erneut mit dem GFX™PCR, DNA and Gel Band Purification Kit (Amersham Pharmacia, Freiburg) nach Angaben des Herstellers gereinigt. Der Vektor pCLiK1 wurde ebenfalls mit den Restriktionsendonukleasen XbaI und AscI geschnitten und mit alkalischer Phosphatase (Roche Diagnostics, Mannheim) nach Angaben des Herstellers

- dephosphoryliert. Nach Elektrophorese in einem 0,8%igen Agarosegel wurde der linearisierte Vektor (ca. 2,1kb) mit dem GFX™PCR, DNA and Gel Band Purification Kit (Amersham Pharmacia, Freiburg) nach Angaben des Herstellers isoliert. Dieses Vektor-Fragment wurde mit Hilfe des Rapid DNA Ligation Kit (Roche Diagnostics, Mannheim) nach Angaben des Herstellers mit dem geschnittenen PCR Fragment ligiert und der Ligationsansatz nach Standardmethoden wie in Sambrook et al. (Molecular Cloning. A Laboratory Manual, Cold Spring Harbor, beschrieben (1989)), in kompetente E.coli XL-1Blue (Stratagene, La Jolla, USA) transformiert. Eine Selektion auf Plasmid tragende Zellen wurde durch das Ausplattieren auf Ampicillin (50µg/ml) und Kanamycin (20µg/ml) haltigen LB Agar (Lennox, 1955, Virology, 1:190) erreicht.
- Die Plasmid-DNA eines individuellen Klons wurde mit dem Qiaprep Spin Miniprep Kit (Qiagen, Hilden) nach Angaben des Herstellers isoliert und über Restriktionsverdaus überprüft. Das so erhaltene Plasmid erhält den Namen pCLiK2.
- Der Vektor pCLiK2 wurde mit der Restriktionsendonuklease DraI (New England Biolabs, Beverly, USA) geschnitten. Nach Elektrophorese in einem 0,8%igen Agarosegel wurde ein ca. 2,3 kb großes Vektorfragment mit dem GFX™PCR, DNA and Gel Band Purification Kit (Amersham Pharmacia, Freiburg) nach Angaben des Herstellers isoliert. Dieses Vektor-Fragment wurde mit Hilfe des Rapid DNA Ligation Kit (Roche Diagnostics, Mannheim) nach Angaben des Herstellers religiert und der Ligationsansatz nach Standardmethoden wie in Sambrook et al. (Molecular Cloning. A Laboratory Manual, Cold Spring Harbor, beschrieben (1989)), in kompetente E.coli XL-1Blue (Stratagene, La Jolla, USA) transformiert. Eine Selektion auf Plasmid tragende Zellen wurde durch das Ausplattieren auf Kanamycin (20µg/ml) haltigen LB Agar (Lennox, 1955, Virology, 1:190) erreicht.
- Die Plasmid-DNA eines individuellen Klons wurde mit dem Qiaprep Spin Miniprep Kit (Qiagen, Hilden) nach Angaben des Herstellers isoliert und über Restriktionsverdaus überprüft. Das so erhaltene Plasmid erhält den Namen pCLiK3.
- Ausgehend vom Plasmid pWLQ2 (Liebl et al., 1992) als Template für eine PCR Reaktion wurde mit den Oligonukleotiden cg1 ((SEQ ID NO:57) und cg2 (SEQ ID NO:58) der Replikationsursprung pHM1519 amplifiziert.

cg1 (SEQ ID NO:57):

5'-GAGAGGGCGGCCGCGCAAAGTCCCGCTTCGTGAA-3'

cg2 (SEQ ID NO:58):

5 5'-GAGAGGGCGGCCGCTCAAGTCGGTCAAGCCACGC-3'

Neben den zu pWLQ2 komplementären Sequenzen, enthalten die Oligonukleotide cg1 (SEQ ID NO:57) und cg2 (SEQ ID NO:58) Schnittstellen für die Restriktionsendonuklease NotI. Die PCR Reaktion wurde nach Standardmethode wie Innis et al. (PCR Protocols. A Guide to Methods and Applications, Academic Press (1990)) mit PfuTurbo Polymerase (Stratagene, La Jolla, USA) durchgeführt. Das erhaltene DNA Fragment mit einer Größe von ungefähr 2,7 kb wurde mit dem GFX™PCR, DNA and Gel Band Purification Kit (Amersham Pharmacia, Freiburg) nach Angaben des Herstellers gereinigt. Das DNA-Fragment wurde mit der Restriktionsendonuklease NotI (New England Biolabs, Beverly, USA) geschnitten und im Anschluß daran erneut mit dem GFX™PCR, DNA and Gel Band Purification Kit (Amersham Pharmacia, Freiburg) nach Angaben des Herstellers gereinigt. Der Vektor pCLiK3 wurde ebenfalls mit der Restriktionsendonuklease NotI geschnitten und mit alkalischer Phosphatase (Roche Diagnostics, Mannheim) nach Angaben des Herstellers dephosphoryliert. Nach Elektrophorese in einem 0,8%igen Agarosegel wurde der linearisierte Vektor (ca. 2,3kb) mit dem GFX™PCR, DNA and Gel Band Purification Kit (Amersham Pharmacia, Freiburg) nach Angaben des Herstellers isoliert. Dieses Vektor-Fragment wurde mit Hilfe des Rapid DNA Ligation Kit (Roche Diagnostics, Mannheim) nach Angaben des Herstellers mit dem geschnittenen PCR Fragment ligiert und der Ligationsansatz nach Standardmethoden wie in Sambrook et al. (Molecular Cloning. A Laboratory Manual, Cold Spring Harbor, beschrieben(1989)), in kompetente E.coli XL-1Blue (Stratagene, La Jolla, USA) transformiert. Eine Selektion auf Plasmid tragende Zellen wurde durch das Ausplattieren auf Kanamycin (20µg/ml) haltigen LB Agar (Lennox, 1955, Virology, 1:190) erreicht.

Die Plasmid-DNA eines individuellen Klon wurde mit dem Qiaprep Spin Miniprep Kit (Qiagen, Hilden) nach Angaben des Herstellers isoliert und über Restriktionsverdaus überprüft. Das so erhaltene Plasmid erhält den Namen pCLiK5.

Für die Erweiterung von pCLiK5 um eine „multiple cloning site“ (MCS) wurden die beide synthetischen, weitestgehend komplementären Oligonukleotide HS445 ((SEQ ID NO:59) und HS446

(SEQ ID NO:60), die Schnittstellen für die Restriktionsendonukleasen SwaI, XhoI, AatI, ApaI, Asp718, MluI, NdeI, SpeI, EcoRV, SalI, ClaI, BamHI, XbaI und SmaI enthalten, durch gemeinsames Erhitzen auf 95°C und langsames Abkühlen zu einem doppelsträngigen DNA-Fragment vereinigt.

5

HS445 (SEQ ID NO:59):

5'-TCGAATTTAAATCTCGAGAGGCCTGACGTCGGGCCCGGTACCACGCGTCATATGACTAG
TTCGGACCTAGGGATATCGTCGACATCGATGCTCTTCTGCGTTAATTAACAATTGGGATCC
TCTAGACCCGGGATTTAAAT-3'

10

HS446 (SEQ ID NO:60):

5'-GATCATTTAAATCCCGGGTCTAGAGGATCCCAATTGTTAATTAACGCAGAAGAGCATCGA
TGTCGACGATATCCCTAGGTCCGAAGTAGTCATATGACGCGTGGTACCGGGCCCGACGTC
AGGCCTCTCGAGATTTAAAT-3'

15

Der Vektor pCLiK5 wurde mit den Restriktionsendonuklease XhoI und BamHI (New England Biolabs, Beverly, USA) geschnitten und mit alkalischer Phosphatase I (Roche Diagnostics, Mannheim) nach Angaben des Herstellers dephosphoryliert. Nach Elektrophorese in einem 0,8%igen Agarosegel wurde der linearisierte Vektor (ca. 5,0 kb) mit dem GFX™PCR, DNA and Gel Band Purification Kit (Amersham Pharmacia, Freiburg) nach Angaben des Herstellers isoliert. Dieses Vektor-Fragment wurde mit Hilfe des Rapid DNA Ligation Kit (Roche Diagnostics, Mannheim) nach Angaben des Herstellers mit dem synthetischen doppelsträngigen DNA-Fragment ligiert und der Ligationsansatz nach Standardmethoden wie in Sambrook et al. (Molecular Cloning. A Laboratory Manual, Cold Spring Harbor, beschrieben(1989)), in kompetente E.coli XL-1Blue (Stratagene, La Jolla, USA) transformiert. Eine Selektion auf Plasmid tragende Zellen wurde durch das Ausplattieren auf Kanamycin (20µg/ml) haltigen LB Agar (Lennox, 1955, Virology, 1:190) erreicht.

20

25

30

Die Plasmid-DNA eines individuellen Klon wurde mit dem Qiaprep Spin Miniprep Kit (Qiagen, Hilden) nach Angaben des Herstellers isoliert und über Restriktionsverdaus überprüft. Das so erhaltene Plasmid erhält den Namen pCLiK5MCS.

Sequenzierungsreaktionen wurden nach Sanger et al. (1977) Proceedings of the National Aca-

demy of Sciences USA 74:5463-5467 durchgeführt. Die Sequenzierreaktionen wurden mittels ABI Prism 377 (PE Applied Biosystems, Weiterstadt) aufgetrennt und ausgewertet.

Das entstandene Plasmid pCLiK5MCS ist als SEQ ID NO: 63 aufgeführt.

5

Beispiel 2: Konstruktion von pCLiK5MCS Integrativ sacB

Ausgehend vom Plasmid pK19mob (Schäfer et al., Gene 145,69-73(1994)) als Template für eine PCR Reaktion wurde mit den Oligonukleotiden BK1732 und BK1733 das *Bacillus subtilis* sacB Gen (kodierend für Levan Sucrase) amplifiziert.

10

BK1732 (SEQ ID NO:61):

5'-GAGAGCGGCCGCGATCCTTTTAAACCCATCAC-3'

15 BK1733 (SEQ ID NO:62):

5'-AGGAGCGGCCGCCATCGGCATTTTCTTTTGCG-3'

Neben den zu pEK19mobsac komplementären Sequenzen, enthalten die Oligonukleotide BK1732 und BK1733 Schnittstellen für die Restriktionsendonuklease NotI. Die PCR Reaktion wurde nach Standardmethode wie Innis et al. (PCR Protocols. A Guide to Methods and Applications, Academic Press (1990)) mit PfuTurbo Polymerase (Stratagene, La Jolla, USA) durchgeführt. Das erhaltene DNA Fragment mit einer Größe von ungefähr 1,9 kb wurde mit dem GFX™PCR, DNA and Gel Band Purification Kit (Amersham Pharmacia, Freiburg) nach Angaben des Herstellers gereinigt. Das DNA-Fragment wurde mit der Restriktionsendonuklease NotI (New England Biolabs, Beverly, USA) geschnitten und im Anschluß daran erneut mit dem GFX™PCR, DNA and Gel Band Purification Kit (Amersham Pharmacia, Freiburg) nach Angaben des Herstellers gereinigt.

20

25

Der Vektor pCLiK5MCS (hergestellt gemäß Beispiel 1) wurde ebenfalls mit der Restriktionsendonuklease NotI geschnitten und mit alkalischer Phosphatase (I (Roche Diagnostics, Mannheim)) nach Angaben des Herstellers dephosphoryliert. Nach Elektrophorese in einem 0,8%igen Agarosegel wurde ein ungefähr 2,4 kb großes Vektorfragment mit dem GFX™PCR, DNA and Gel Band Purification Kit (Amersham Pharmacia, Freiburg) nach Angaben des Herstellers iso-

30

liert. Dieses Vektor-Fragment wurde mit Hilfe des Rapid DNA Ligation Kit (Roche Diagnostics, Mannheim) nach Angaben des Herstellers mit dem geschnittenen PCR Fragment ligiert und der Ligationsansatz nach Standardmethoden wie in Sambrook et al. (Molecular Cloning. A Laboratory Manual, Cold Spring Harbor, beschrieben(1989)), in kompetente E.coli XL-1Blue (Stratagene, La Jolla, USA) transformiert. Eine Selektion auf Plasmid tragende Zellen wurde durch das Ausplattieren auf Kanamycin (20µg/ml) haltigen LB Agar (Lennox, 1955, Virology, 1:190) erreicht.

Die Plasmid-DNA eines individuellen Klons wurde mit dem Qiaprep Spin Miniprep Kit (Qiagen, Hilden) nach Angaben des Herstellers isoliert und über Restriktionsverdaus überprüft. Das so erhaltene Plasmid erhält den Namen pCLiK5MCS integrativ sacB.

Sequenzierungsreaktionen wurden nach Sanger et al. (1977) Proceedings of the National Academy of Sciences USA 74:5463-5467 durchgeführt. Die Sequenzierreaktionen wurden mittels ABI Prism 377 (PE Applied Biosystems, Weiterstadt) aufgetrennt und ausgewertet.

Das entstandene Plasmid pCLiK5MCS integrativ sacB ist als SEQ ID NO: 64 aufgeführt.

Weitere Vektoren die zur erfindungsgemäßen Expression oder Überproduktion von methH-Genen geeignet sind, können in analoger Weise hergestellt werden.

In den folgenden Beispielen 3 bis 8 wird die schrittweise Konstruktion eines verbesserten Methionin-produzierenden Stammes mit der Bezeichnung LU1479 lysC 311Ile ET-16 pC Phsdh meth_Sc beschrieben.

Beispiel 3: Isolierung des lysC gens aus dem C. glutamicum Stamm LU1479

Im ersten Schritt der Stammkonstruktion soll ein allelischer Austausch des lysC Wildtypgens, kodierend für das Enzym Aspartatkinase, in C. glutamicum ATCC13032, im folgenden LU1479 genannt, durchgeführt werden. Dabei soll im LysC Gen ein Nukleotidaustausch durchgeführt werden, so dass im resultierenden Protein die Aminosäure Thr an der Position 311 durch die Aminosäure Ile ausgetauscht ist.

Ausgehend von der chromosomalen DNA aus LU1479 als Template für eine PCR Reaktion

37

wurde mit den Oligonukleotidprimern SEQ ID NO:65 und SEQ ID NO:66 lysC mit Hilfe des Pfu-Turbo PCR Systems (Stratagene USA) nach Angaben des Herstellers amplifiziert. Chromosomale DNA aus *C. glutamicum* ATCC 13032 wurde nach Tauch et al. (1995) Plasmid 33:168-179 oder Eikmanns et al. (1994) Microbiology 140:1817-1828 präpariert. Das amplifizierte Fragment wird an seinem 5'-Ende von einem Sall Restriktionsschnitt und an seinem 3'-Ende von einem MluI Restriktionsschnitt flankiert. Vor der Klonierung wurde das amplifizierte Fragment durch diese beiden Restriktionsenzyme verdaut und mit GFX™PCR, DNA and Gel Band Purification Kit (Amersham Pharmacia, Freiburg) aufgereinigt.

10 SEQ ID NO:65

5'-GAGAGAGAGACGCGTCCCAGTGGCTGAGACGCATC-3'

SEQ ID NO:66

5'-CTCTCTCTGTGCGACGAATTCAATCTTACGGCCTG-3'

15

Das erhaltene Polynukleotid wurde über die Sall und MluI Restriktionsschnitte in pCLIK5 MCS integrativ SacB (im folgenden pCIS genannt; SEQ ID NO: 64 aus Beispiel 2) kloniert und in *E.coli* XL-1 blue transformiert. Eine Selektion auf Plasmid-tragende Zellen wurde durch das Ausplattieren auf Kanamycin (20µg/ml)-haltigen LB Agar (Lennox, 1955, Virology, 1:190) erreicht. Das Plasmid wurde isoliert und durch Sequenzierung die erwartete Nukleotidsequenz bestätigt. Die Präparation der Plasmid-DNA wurde nach Methoden und mit Materialien der Firma Qiagen durchgeführt. Sequenzierungsreaktionen wurden nach Sanger et al. (1977) Proceedings of the National Academy of Sciences USA 74:5463-5467 durchgeführt. Die Sequenzierungsreaktionen wurden mittels ABI Prism 377 (PE Applied Biosystems, Weiterstadt) aufgetrennt und ausgewertet. Das erhaltene Plasmid pCIS lysC ist als SEQ ID NO:77 aufgeführt.

20

25

Die Sequenz SEQ ID NO:77 umfasst die folgenden wesentlichen Teilbereiche:

| Position | Art der Sequenz | Beschreibung |
|-------------|-------------------|---------------------|
| 155 – 1420 | CDS ¹⁾ | lysC |
| 1974 – 2765 | CDS | Kanamycin-Resistenz |

| | | |
|---|-----|---|
| 3032 – 3892 (complement) ²⁾ | CDS | Replikationsursprung/ E.coli/Plasmid pMB |
|---|-----|---|

¹⁾ Kodierende Sequenz

²⁾ auf Komplementärstrang

Beispiel 4: Mutagenese des lysC Gens aus *C. glutamicum*

- 5 Die gerichtete Mutagenese des lysC Gens aus *C. glutamicum* (Beispiel 3) wurde mit dem QuickChange Kit (Fa. Stratagene/USA) nach Angaben des Herstellers durchgeführt. Die Mutagenese wurde im Plasmid pCIS lysC, SEQ ID NO:77 durchgeführt. Für den Austausch von thr311 nach 311ile mit Hilfe der Quickchange Methode (Stratagene) wurden folgende Oligonukleotidprimer synthetisiert

10

SEQ ID NO:67

5'-CGGCACCACCGACATCATCTTCACCTGCCCTCGTTCCG -3'

SEQ ID NO:68

- 15 5'-CGGAACGAGGGCAGGTGAAGATGATGTCGGTGGTGCCG -3'

- Der Einsatz dieser Oligonukleotidprimer in der Quickchange Reaktion führt in dem lysC Gen zu einem Austausch des Nukleotids in Position 932 (von C nach T) (vgl. SEQ ID NO:75) und im korrespondierenden Enzym zu einem Aminosäuresubstitution in Position 311 (Thr→Ile) (vgl. SEQ ID NO:76). Der resultierende Aminosäureaustausch Thr311Ile im lysC Gen wurde nach Transformation in *E.coli* XL1-blue und Plasmidpräparation durch Sequenzierung bestätigt. Das Plasmid erhielt die Bezeichnung pCIS lysC thr311ile und ist als SEQ ID NO:78 aufgeführt.

- 20 Die Sequenz SEQ ID NO:78 umfasst die folgenden wesentlichen Teilbereiche:

25

| Position | Art der Sequenz | Beschreibung |
|-------------|-------------------|---------------------|
| 155 – 1420 | CDS ¹⁾ | lysC mutiert |
| 1974 – 2765 | CDS | Kanamycin-Resistenz |

| | | |
|---|-----|---|
| 3032 – 3892 (complement) ²⁾ | CDS | Replikationsursprung/ E.coli/Plasmid pMB |
|---|-----|---|

¹⁾ Kodierende Sequenz

²⁾ auf Komplementärstrang

Das Plasmid pCIS lysC thr311ile wurde in *C. glutamicum* LU1479 mittels Elektroporation wie bei
 5 Liebl, et al. (1989) FEMS Microbiology Letters 53:299-303 beschrieben, transformiert. Modifikationen des Protokolls sind in DE-A-10046870 beschrieben. Die chromosomale Anordnung des lysC-Lokus einzelner Transformanten wurde mit Standardmethoden durch Southernblot und Hybridisierung, wie in Sambrook et al. (1989), Molecular Cloning. A Laboratory Manual, Cold Spring Harbor, beschrieben, überprüft. Dadurch wurde sichergestellt, dass es sich bei den
 10 Transformanten um solche handelt, die das transformierte Plasmid durch homologe Rekombination am lysC-Lokus integriert haben. Nach Wachstum solcher Kolonien über Nacht in Medien, die kein Antibiotikum enthielten, wurden die Zellen auf ein Saccharose-CM-Agarmedium (10% Saccharose) ausplattiert und bei 30°C für 24 Stunden inkubiert.

Da das im Vektor pCIS lysC thr311ile enthaltende sacB Gen Saccharose in ein toxisches Produkt umwandelt, können nur solche Kolonien anwachsen, die das sacB Gen durch einen zweiten homologen Rekombinationsschritt zwischen dem Wildtyp lysC Gen und dem mutierten Gen
 15 lysC thr311ile deletiert haben. Während der homologen Rekombination kann entweder das Wildtyp Gen oder das mutierte Gen zusammen mit dem sacB Gen deletiert werden. Wenn das sacB Gen zusammen mit dem Wildtyp Gen entfernt wird, resultiert eine mutierte Transformante.

20 Anwachsende Kolonien wurden gepickt, und auf eine Kanamycin-sensitiven Phänotyp hin untersucht. Klone mit deletiertem SacB Gen müssen gleichzeitig Kanamycin-sensitives Wachstumsverhalten zeigen. Solche Kan-sensitiven Klone wurde im einem Schüttelkolben auf ihre Lysin-Produktivität hin untersucht (siehe Beispiel 6). Zum Vergleich wurde der nichtbehandelte Stamm
 25 LU1479 angezogen. Klone mit einer gegenüber der Kontrolle erhöhten Lysin-Produktion wurden selektiert, chromosomale DNA wurde gewonnen und der entsprechende Bereich des lysC Gens wurde durch eine PCR-Reaktion amplifiziert und sequenziert. Ein solcher Klon mit der Eigenschaft erhöhter Lysin-Synthese und nachgewiesener Mutation in lysC an der Stelle 932 wurde mit LU1479 lysC 311ile bezeichnet).

Beispiel 5: Herstellung Ethionin-resistenter C. glutamicum Stämme

- Im zweiten Schritt der Stammkonstruktion wurde der erhaltene Stamm LU1479 lysC 311ile (Beispiel 4) behandelt, um eine Ethionin-Resistenz (Kase, H. Nakayama K.Agr. Biol. Chem. 39 153-106 1975 L-methionine production by methionine analog-resistant mutants of *Corynebacterium glutamicum*) zu induzieren: Eine Übernachtskultur in BHI-Medium (Difco) wurde in Citratpuffer (50mM pH 5,5) gewaschen und bei 30°C für 20 min mit N-Methyl-nitrosoguanidin (10mg/ml in 50mM Citrat pH5,5) behandelt. Nach der Behandlung mit dem chemischen Mutagen N-Methyl-nitrosoguanidin wurden die Zellen gewaschen (Citratpuffer 50mM pH 5,5) und auf ein Medium plattiert, das aus folgenden Komponenten, berechnet auf 500ml, zusammengesetzt war: 10g (NH₄)₂SO₄, 0.5g KH₂PO₄, 0.5g K₂HPO₄, 0.125g MgSO₄·7H₂O, 21g MOPS, 50mg CaCl₂, 15mg Proteokatechuat, 0,5mg Biotin, 1mg Thiamin, 5g/l D,L-Ethionin (Sigma Chemicals Deutschland), pH 7,0. Außerdem enthielt das Medium 0.5ml einer Spurensalzlösung aus: 10g/l FeSO₄·7H₂O, 1g/l MnSO₄·H₂O, 0.1g/l ZnSO₄·7H₂O, 0.02g/l CuSO₄, 0.002g/l NiCl₂·6H₂O. Alle Salze wurden in 0,1M HCl gelöst. Das fertig zusammengestellte Medium wurde sterilfiltriert und nach Zugabe von 40ml steriler 50% Glucoselösung, mit flüssigem sterilem Agar in einer Endkonzentration von 1,5% Agar versetzt und in Kulturschalen ausgegossen.
- Auf Platten mit dem beschriebenen Medium wurden mutagenisierte Zellen aufgebracht und 3-7 Tage bei 30°C inkubiert. Erhaltene Klone wurden isoliert, mindestens einmal auf dem Selektionsmedium vereinzelt und dann auf ihre Methionin-Produktivität in einem Schüttelkolben in Medium II untersucht (siehe Beispiel 6)
- Beispiel 6: Herstellung von Methionin mit dem Stamm LU1479 lysC 311ile ET-16.**

Die in Beispiel 5 hergestellten Stämme wurden auf einer Agar-Platte mit CM-Medium für 2 Tag bei 30°C angezogen.

CM-Agar:

- 10,0 g/l D-Glucose, 2,5 g/l NaCl, 2,0 g/l Hamstoff, 10,0 g/l Bacto Pepton (Difco), 5,0 g/l Yeast Extract (Difco), 5,0 g/l Beef Extract (Difco), 22,0 g/l Agar (Difco), autoklaviert (20 min., 121°C)

Anschließend wurden die Zellen von der Platte abgekratzt und in Saline resuspendiert. Für die Hauptkultur wurden 10 ml Medium II und 0,5 g autoklaviertes CaCO_3 (Riedel de Haen) in einem 100 ml Erlenmeyerkolben mit der Zellsuspension bis zu einer OD_{600nm} von 1,5 beimpft und für
 5 72h auf einem Orbitalschüttler mit 200 Upm bei 30°C inkubiert.

Medium II:

| | | |
|----|---------|--|
| | 40g/l | Saccharose |
| | 60g/l | Melasse (auf 100% Zuckergehalt berechnet) |
| 10 | 10g/l | $(\text{NH}_4)_2\text{SO}_4$ |
| | 0.4g/l | $\text{MgSO}_4 \cdot 7\text{H}_2\text{O}$ |
| | 0.6g/l | KH_2PO_4 |
| | 0.3mg/l | Thiamin*HCl |
| | 1mg/l | Biotin (aus einer 1 mg/ml steril filtrierten Stammlösung die mit NH_4OH auf pH |
| 15 | | 8,0 eingestellt wurde) |
| | 2mg/l | FeSO_4 |
| | 2mg/l | MnSO_4 |

mit NH_4OH auf pH 7,8 eingestellt, autoklaviert (121°C, 20 min). Zusätzlich wird Vitamin B12 (Hydroxycobalamin Sigma Chemicals) aus einer Stammlösung (200 µg/ml, steril filtriert) bis zu
 20 einer Endkonzentration von 100 µg/l zugegeben

Gebildetes Methionin, sowie andere Aminosäuren in der Kulturbrühe wurde mit Hilfe der Aminosäuresäure-Bestimmungsmethode von Agilent auf einer Agilent 1100 Series LC System HPLC. Eine Derivatisierung vor der Säulentrennung mit Ortho-Phthalaldehyd erlaubte die Quan-
 25 tifizierung der gebildeten Aminosäuren. Die Auftrennung des Aminosäuregemisch fand auf einer Hypersil AA-Säule (Agilent) statt.

Solche Klone wurden isoliert, deren Methionin-Produktivität mindestens doppelt so hoch war, wie die des Ausgangsstamm LU1479 lysC 311ile. Ein solcher Klon wurde für die weiteren Versuche
 30 eingesetzt und bekam die Bezeichnung LU1479 lysC 311ile ET-16.

Beispiel 7: Klonierung von meth aus *Streptomyces coelicolor* und Klonierung in das Plasmid pC

Phsdh meth_Sc

- a) Chromosomale DNA wurde aus *Streptomyces coelicolor* Stamm ATCC BAA-471 (von der American Type Strain Culture Collection, (ATCC) Atlanta, USA, unter der Bestellnummer BAA-471D erhältlich) isoliert. Chromosomale DNA aus *C. glutamicum* ATCC 13032 wurde nach Tauch et al. (1995) Plasmid 33:168-179 oder Eikmanns et al. (1994) Microbiology 140:1817-1828 präpariert.

- Mit den Oligonukleotidprimer SEQ ID NO:69 und SEQ ID NO:70, der chromosomalen DNA aus *C. glutamicum* als Template und Pfu Turbo Polymerase (Fa. Stratagene) wurde mit Hilfe der Polymerase-Kettenreaktion (PCR) nach Standardmethoden, wie Innis et al. (1990) PCR Protocols. A Guide to Methods and Applications, Academic Press, ein DNA Fragment von ca. 180 Basenpaaren aus dem nichtkodierenden 5'-Bereich (Promotorregion) der Homoserindehydrogenase (HsDH) amplifiziert. Das amplifizierte Fragment ist an seinem 5'-Ende von einer XhoI-Restriktionsschnittstelle und am 3'-Ende von einem über das Oligo eingeführten zu methH aus *Streptomyces coelicolor* homologen Bereich flankiert.

SEQ ID NO:69

5'-GAGACTCGAGGGAAGGTGAATCGAATTCGG-3'

und

SEQ ID NO:70

5'-GTCCCGGGGAGAACGCACGATTCTCCAAAATAATCGC-3'

- Das erhaltene DNA Fragment wurde mit dem GFX™PCR, DNA and Gel Band Purification Kit (Amersham Pharmacia, Freiburg) nach Angaben des Herstellers gereinigt.

- b) Ausgehend von der chromosomalen DNA aus *Streptomyces coelicolor* als Template für eine PCR Reaktion wurde mit den Oligonukleotidprimern SEQ ID NO:71 und SEQ ID NO:72 ein Teil von methH mit Hilfe des GC-RICH PCR Systems (Roche Diagnostics, Mannheim) nach Angaben des Herstellers amplifiziert. Das amplifizierte Fragment ist an seinem 5'-Ende von einem über das Oligo eingeführten, zur Promotorregion von HsDH aus *C. glutamicum* homologen Bereich flankiert.

SEQ ID NO:71

5'-GAATCGTGCGTTCTCCCCGGGAC -3'

und

SEQ ID NO:72

5 5'-GTAGTTGACCGAGTTGATCACC -3'

Das ca. 1,4 kb große erhaltene DNA Fragment wurde mit dem GFX™PCR, DNA and Gel Band Purification Kit (Amersham Pharmacia, Freiburg) nach Angaben des Herstellers gereinigt.

- 10 c) In einer weiteren PCR Reaktion wurden die beiden oben erhaltenen Fragmente gemeinsam als Template eingesetzt. Durch die mit dem Oligonukleotidprimern SEQ ID NO:71 und SEQ ID NO:70 eingebrachten, zu dem jeweils anderen Fragment homologen Bereichen, kommt es im Zuge der PCR-Reaktion zu einer Anlagerung beider Fragmente aneinander und einer Verlängerung zu einem durchgehenden DNA-Strang durch die eingesetzte Polymerase. Die Standardmethode wurde dahingehend modifiziert, dass die verwendeten Oligonukleotidprimer SEQ ID NO:69 und SEQ ID NO:72 erst mit Beginn des 2. Zyklus dem Reaktionsansatz zugegeben wurden.

20 Das amplifizierte DNA Fragment von ungefähr 1,6 kb wurde mit dem GFX™PCR, DNA and Gel Band Purification Kit nach Angaben des Herstellers gereinigt. Im Anschluss daran wurde es mit den Restriktionsenzymen XhoI und NotI (Roche Diagnostics, Mannheim) gespalten und gelelektrophoretisch aufgetrennt. Anschließend wurde das ca. 1,6 kb große DNA Fragment mit GFX™PCR, DNA and Gel Band Purification Kit (Amersham Pharmacia, Freiburg) aus der Agarose aufgereinigt.

25

- d) Der noch fehlende 3'-Bereich von methH wurde ausgehend von der chromosomalen DNA aus *Streptomyces coelicolor* als Template mit den Oligonukleotidprimern SEQ ID NO:73 und SEQ ID NO:74 mit Hilfe des GC-RICH PCR Systems (Roche Diagnostics, Mannheim) nach Angaben des Herstellers amplifiziert. Das amplifizierte Fragment ist an seinem 3'-Ende von einer 30 über das Oligo eingeführten EcoRV-Restriktionsschnittstelle flankiert.

SEQ ID NO:73

5'-CCGGCCTGGAGAAGCTCG-3'

und

SEQ ID NO:74

5'-GAGAGATATCCCTCAGCGGGCGTTGAAG-3'

- 5 Das erhaltene ca. 2,2 kb große DNA Fragment wurde mit dem GFX™PCR, DNA and Gel Band Purification Kit (Amersham Pharmacia, Freiburg) nach Angaben des Herstellers gereinigt. Im Anschluß daran wurde es mit den Restriktionsenzymen NotI und EcoRV (Roche Diagnostics, Mannheim) gespalten und gelelektrophoretisch aufgetrennt. Anschließend wurde das ca. 2,2 kb große DNA Fragment mit GFX™PCR, DNA and Gel Band Purification Kit (Amersham Pharmacia, Freiburg) aus der Agarose aufgereinigt.

- 10 e) Der Vektor pClik5MCS SEQ ID NO:63 (Beispiel 1) wurde mit den Restriktionsenzymen XhoI und EcoRV (Roche Diagnostics, Mannheim) geschnitten und ein 5 kb großes Fragment nach elektrophoretischer Auftrennung mit GFX™PCR, DNA and Gel Band Purification Kit isoliert.

15

- Das Vektorfragment wurde zusammen mit den beiden geschnittenen und aufgereinigten PCR-Fragmenten mit Hilfe des Rapid DNA Ligation Kit (Roche Diagnostics, Mannheim) nach Angaben des Herstellers ligiert und der Ligationsansatz nach Standardmethoden wie in Sambrook et al. (Molecular Cloning. A Laboratory Manual, Cold Spring Harbor, beschrieben(1989)), in kompetente E.coli XL-1Blue (Stratagene, La Jolla, USA) transformiert. Eine Selektion auf Plasmid-tragende Zellen wurde durch das Ausplattieren auf Kanamycin (20µg/ml) haltigen LB Agar (Lennox, 1955, Virology, 1:190) erreicht.

20

- Die Präparation der Plasmid DNA wurde nach Methoden und mit Materialien der Fa. Quiagen durchgeführt. Sequenzierungsreaktionen wurden nach Sanger et al. (1977) Proceedings of the National Academy of Sciences USA 74:5463-5467 durchgeführt. Die Sequenzierungsreaktionen wurden mittels ABI Prism 377 (PE Applied Biosystems, Weiterstadt) aufgetrennt und ausgewertet.

25

- Das entstandene Plasmid pC Phsdh meth_Sc (*Streptomyces coelicolor*) ist als SEQ ID NO:79 aufgeführt.

30

Die Sequenz SEQ ID NO:79 umfasst die folgenden wesentlichen Teilbereiche:

| Position | Art der Sequenz | Beschreibung |
|---|-------------------|---|
| 6 - 155 | Promotor | HsDH |
| 156 - 3752 | CDS ¹⁾ | Meth S. coelicolor |
| 4153 - 4944 | CDS | Kanamycin-Resistenz |
| 5211 - 6071 (complement) ²⁾ | CDS | Replikationsursprung/ E.coli/Plasmid pMB |

¹⁾ Kodierende Sequenz

²⁾ auf Komplementärstrang

5

Beispiel 8: Transformation des Stammes LU1479 lysC 311ile ET-16 mit dem Plasmid pC Phsdh meth_Sc

Der Stamm LU1479 lysC 311ile ET-16 (Beispiel 5) wurde mit dem Plasmid pC Phsdh meth_Sc (Beispiel 7) nach der beschriebenen Methode (Liebl, et al. (1989) FEMS Microbiology Letters 53:299-303) transformiert. Die Transformationsmischung wurde auf CM-Platten plattiert, die zusätzlich 20mg/l Kanamycin enthielten, um eine Selektion auf Plasmid-haltige Zellen zu erreichen. Erhaltene Kan-resistente Klone wurden gepickt und vereinzelt. Die Methionin-Produktivität der Klone wurde in einem Schüttelkolbenversuch (s. Beispiel 6) untersucht. Der Stamm LU1479 lysC 311ile ET-16 pC Phsdh meth_Sc produzierte im Vergleich zu LU1479 lysC 311ile ET-16 signifikant mehr Methionin.

Patentansprüche

1. Verfahren zur fermentativen Herstellung wenigstens einer schwefelhaltigen
5 Feinchemikalie, welches folgende Schritte umfasst:
 - a) Fermentation einer die gewünschte schwefelhaltige Feinchemikalie produzierenden coryneformen Bakterienkultur, wobei in den coryneformen Bakterien zumindest eine heterologe Nukleotidsequenz exprimiert wird, welche für ein Protein mit Methionin-Synthase (metF) –Aktivität kodiert;
 - 10 b) Anreicherung der schwefelhaltigen Feinchemikalie im Medium oder in den Zellen der Bakterien, und
 - c) Isolieren der schwefelhaltigen Feinchemikalie.
2. Verfahren nach Anspruch 1, wobei die schwefelhaltige Feinchemikalie L-Methionin
15 umfasst.
3. Verfahren nach einem der vorhergehenden Ansprüche, wobei sich die heterologe metF-kodierende Nukleotidsequenz zur metF-kodierenden Sequenz aus *Corynebacterium glutamicum* ATCC 13032 eine Sequenzhomologie vom weniger als 100% aufweist.
20
4. Verfahren nach Anspruch 3, wobei die metF-kodierende Sequenz aus einem der folgenden Organismen abgeleitet ist:

| Organismus | Stammsammlung |
|-----------------------------------|---------------|
| <i>Corynebacterium diptheriae</i> | ATCC 14779 |
| <i>Streptomyces lividans</i> | ATCC 19844 |
| <i>Streptomyces coelicolor</i> | ATCC 10147 |
| <i>Aquifex aeolicus</i> | DSM 6858 |
| <i>Burkholderia cepacia</i> | ATCC 25416 |
| <i>Nitrosomonas europaea</i> | ATCC 19718 |
| <i>Pseudomonas aeruginosa</i> | ATCC 17933 |
| <i>Xylella fastidiosa</i> | ATCC 35881 |
| <i>Pseudomonas fluorescens</i> | ATCC 13525 |
| <i>Schizosaccharomyces pombe</i> | ATCC 24969 |
| <i>Saccharomyces cerevisiae</i> | ATCC 10751 |
| <i>Erwinia carotovora</i> | ATCC 15713 |
| <i>Klebsiella pneumoniae</i> | ATCC 700721 |
| <i>Salmonella typhi</i> | ATCC 12839 |
| <i>Salmonella typhimurium</i> | ATCC 15277 |
| <i>Escherichia coli</i> K12 | ATCC55151 |

| | |
|---|------------|
| <i>Vibrio cholerae</i> | ATCC 39315 |
| <i>Haemophilus influenzae</i> | ATCC 51907 |
| <i>Caulobacter crescentus</i> | ATCC 19089 |
| <i>Actinobacillus actinomycetemcomitans</i> | ATCC 33384 |
| <i>Neisseria meningitis</i> | ATCC 6253 |
| <i>Rhodobacter capsulatus</i> | ATCC 11166 |
| <i>Campylobacter jejuni</i> | ATCC 33560 |
| <i>Lactococcus lactis</i> | ATCC 7962 |
| <i>Prochlorococcus marinus</i> | PCC7118 |
| <i>Bacillus stearothermophilus</i> | ATCC 12980 |

5. Verfahren nach einem der vorhergehenden Ansprüche, wobei die metF-kodierende Sequenz eine kodierende Sequenz gemäß SEQ ID NO:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51 und 53 oder eine dazu homologe Nukleotidsequenz, welche für ein Protein mit metF-Aktivität kodiert, umfasst.
6. Verfahren nach einem der vorhergehenden Ansprüche, wobei die metF-kodierende Sequenz für ein Protein mit metF-Aktivität kodiert, wobei das Protein eine Aminosäuresequenz gemäß SEQ ID NO:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52 und 54 oder eine dazu homologe Aminosäuresequenz, welche für ein Protein mit metF-Aktivität steht, umfasst.
7. Verfahren nach einem der vorhergehenden Ansprüche, wobei die kodierende metF-Sequenz eine in coryneformen Bakterien replizierbare oder eine stabil in das Chromosom integrierte DNA oder eine RNA ist.
8. Verfahren gemäß Anspruch 7, wobei man
 - a) einen mit einem Plasmidvektor transformierten Bakterienstamm einsetzt der wenigstens eine Kopie der kodierenden metF-Sequenz unter der Kontrolle regulativer Sequenzen trägt, oder
 - b) einen Stamm einsetzt, in dem die kodierende metF-Sequenz in das Chromosom des Bakteriums integriert wurde
9. Verfahren nach einem der vorhergehenden Ansprüche, wobei die kodierende metF-Sequenz überexprimiert wird.

- 5 10. Verfahren gemäß einem der vorhergehenden Ansprüche, wobei man Bakterien fermentiert, in denen zusätzlich wenigstens ein weiteres Gen des Biosyntheseweges der gewünschten schwefelhaltigen Feinchemikalie verstärkt ist oder derart mutiert ist, dass es durch Stoffwechselmetabolite nicht in seiner Aktivität beeinflusst wird.
- 10 11. Verfahren gemäß einem der vorhergehenden Ansprüche, wobei man Bakterien fermentiert, in denen wenigstens ein Stoffwechselweg zumindest teilweise ausgeschaltet sind, der die Bildung der gewünschten schwefelhaltigen Feinchemikalie verringert.
12. Verfahren gemäß einem der vorhergehenden Ansprüche, wobei man coryneforme Bakterien fermentiert, in denen gleichzeitig wenigstens eines der Gene, ausgewählt unter
- 15 a) dem für eine Aspartatkinase kodierenden Gen *lysC*,
b) dem für die Glycerinaldehyd-3-Phosphat Dehydrogenase kodierenden Gen *gap*,
c) dem für die 3-Phosphoglycerat Kinase kodierenden Gen *pgk*,
d) dem für die Pyruvat Carboxylase kodierenden Gen *pyc*,
e) dem für die Triosephosphat Isomerase kodierenden Gen *tpi*,
f) dem für die Homoserin O-Acetyltransferase kodierenden Gen *metA*,
20 g) dem für die Cystathionin-gamma-Synthase kodierenden Gen *metB*,
h) dem für die Cystathionin-gamma-Lyase kodierenden Gen *metC*,
i) dem für die Serin-Hydroxymethyltransferase kodierenden Gen *glyA*,
j) dem für die O-Acetylhomoserin-Sulphydrylase kodierenden Gen *metY*,
k) dem für das *metH* Gen, das für die Vitamin B12 abhängige Methionin-Synthase
25 kodiert,
l) dem für das *serC* Gen, das für die Phosphoserin-Aminotransferase kodiert,
m) dem *serB* Gen, das für die Phosphoserin-Phosphatase kodiert,
n) dem *cysE* Gen, das für die Serine Acetyl-Transferase kodiert, und
o) dem *hom* Gen, das eine Homoserin-Dehydrogenase kodiert,
30
- überexprimiert oder so mutiert ist, dass die korrespondierenden Proteine, verglichen mit nicht mutierten Proteinen, in geringerem Maße oder nicht durch Stoffwechselmetabolite in ihrer Aktivität beeinflusst werden.

13. Verfahren gemäß einem der vorhergehenden Ansprüche, wobei man coryneformen Bakterien fermentiert, in denen gleichzeitig wenigstens eines der Gene, ausgewählt unter
- a) dem für die Homoserine-Kinase kodierenden Gen *thrB*,
 - b) dem für die Threonin Dehydratase kodierenden Gen *ilvA*,
 - 5 c) dem für die Threonin Synthase kodierenden Gen *thrC*
 - d) dem für die Meso-Diaminopimelat D-Dehydrogenase kodierenden Gen *ddh*
 - e) dem für die Phosphoenolpyruvat-Carboxykinase kodierenden Gen *pck*,
 - f) dem für die Glucose-6-Phosphat-6-Isomerase kodierenden Gen *pgl*,
 - g) dem für die Pyruvat-Oxidase kodierenden Gen *poxB*,
 - 10 h) dem für die Dihydrodipicolinat Synthase kodierenden Gen *dapA*,
 - i) dem für die Dihydrodipicolinat Reduktase kodierenden Gen *dapB*; oder
 - j) dem für die Diaminopicolinat Decarboxylase kodierenden Gen
- durch Veränderung der Expressionsrate oder durch Einführung einer gezielten Mutation abschwächt ist.
- 15
14. Verfahren gemäß einem oder mehreren der vorhergehenden Ansprüche, wobei man Mikroorganismen der Art *Corynebacterium glutamicum* einsetzt.
- 20
15. Verfahren zur Herstellung eines L-Methionin haltigen Tierfuttermittel-Additivs aus Fermentationsbrühen, welches folgende Schritte umfasst
- a) Kultivierung und Fermentation eines L-Methionin produzierenden Mikroorganismus in einem Fermentationsmedium;
 - b) Entfernung von Wasser aus der L-Methionin haltigen Fermentationsbrühe;
 - 25 c) Entfernung der während der Fermentation gebildeten Biomasse in einer Menge von 0 bis 100 Gew.-%; und
 - d) Trocknung der gemäß b) und/oder c) erhaltenen Fermentationsbrühe, um das Tierfuttermittel-Additiv in der gewünschten Pulver- oder Granulatform zu erhalten.
- 30
16. Verfahren gemäß Anspruch 15, wobei man Mikroorganismen gemäß der Definition in einem der Ansprüche 1 bis 14 einsetzt.

SEQUENZPROTOKOLL

<110> BASF Aktiengesellschaft

<120> Meth

<130> M/43120

<140>

<141>

<160> 79

<210> 1

<211> 3597

<212> DNA

<213> Streptomyces coelicolor

<220>

<221> CDS

<222> (1) .. (3594)

<223> RSX14254

<400> 1

| | |
|---|-----|
| gtg cgt tct ccc cgg gac gtc cca cga cgg gcg gca ccg ggc aga ggc | 48 |
| Val Arg Ser Pro Arg Asp Val Pro Arg Arg Ala Ala Pro Gly Arg Gly | |
| 1 5 10 15 | |
| aaa gcc gac agc cgt cgc atc cta ggg agc cct ttc atg gcc tcg tcg | 96 |
| Lys Ala Asp Ser Arg Arg Ile Leu Gly Ser Pro Phe Met Ala Ser Ser | |
| 20 25 30 | |
| cca tcc acc ccg ccc gcc gac acc cgc acc cgc gtg tcc gcc ctc cga | 144 |
| Pro Ser Thr Pro Pro Ala Asp Thr Arg Thr Arg Val Ser Ala Leu Arg | |
| 35 40 45 | |
| gag gcc ctc gcc acc cgc gtg gtg gtc gcc gac ggc gcc atg ggc acc | 192 |
| Glu Ala Leu Ala Thr Arg Val Val Val Ala Asp Gly Ala Met Gly Thr | |
| 50 55 60 | |
| atg ctc cag gcc cag aac ccc acg ctg gac gac ttc cag cag ctc gaa | 240 |
| Met Leu Gln Ala Gln Asn Pro Thr Leu Asp Asp Phe Gln Gln Leu Glu | |
| 65 70 75 80 | |
| ggg tgc aac gag gtc ctg aac ctc acc cgg ccc gac atc gtc cgc tcg | 288 |
| Gly Cys Asn Glu Val Leu Asn Leu Thr Arg Pro Asp Ile Val Arg Ser | |
| 85 90 95 | |
| gtg cac gag gag tac ttc gcg gcc ggc gtc gac tgc gtc gag acc aac | 336 |
| Val His Glu Glu Tyr Phe Ala Ala Gly Val Asp Cys Val Glu Thr Asn | |
| 100 105 110 | |
| acc ttc ggc gcc aac cac tcc gcc ctg ggc gag tac gac atc ccc gag | 384 |
| Thr Phe Gly Ala Asn His Ser Ala Leu Gly Glu Tyr Asp Ile Pro Glu | |
| 115 120 125 | |
| cgc gtc cac gaa ctg tcc gag gcc ggc gcc cgc gtc gcc cgc gag gtc | 432 |
| Arg Val His Glu Leu Ser Glu Ala Gly Ala Arg Val Ala Arg Glu Val | |
| 130 135 140 | |
| gcc gac gag ttc ggc gcc cgc gac ggc cgg cag cgc tgg gtg ctg ggc | 480 |

2

| | | | | |
|---|-----|-----|-----|------|
| Ala Asp Glu Phe Gly Ala Arg Asp Gly Arg Gln Arg Trp Val Leu Gly | 145 | 150 | 155 | 160 |
| tcc atg ggc ccc ggc acc aag ctc ccc acc ctc ggc cac gcc ccg tac | | | | 528 |
| Ser Met Gly Pro Gly Thr Lys Leu Pro Thr Leu Gly His Ala Pro Tyr | | | | |
| | 165 | | 170 | 175 |
| acc gtc ctg cgc gac gcc tac cag cgc aac gcc gag gga ctg gtc gcg | | | | 576 |
| Thr Val Leu Arg Asp Ala Tyr Gln Arg Asn Ala Glu Gly Leu Val Ala | | | | |
| | 180 | | 185 | 190 |
| ggc ggc gcg gac gca ctg ctg gtg gag acc acg cag gac ctg ctc cag | | | | 624 |
| Gly Gly Ala Asp Ala Leu Leu Val Glu Thr Thr Gln Asp Leu Leu Gln | | | | |
| | 195 | | 200 | 205 |
| acc aag gcc tcg gtg ctc ggc gcc cgg cgc gcc ctg gac gtc ctc ggc | | | | 672 |
| Thr Lys Ala Ser Val Leu Gly Ala Arg Arg Ala Leu Asp Val Leu Gly | | | | |
| | 210 | | 215 | 220 |
| ctc gac ctg ccg ctc atc gtg tcc gtc acc gtc gag acc acc gcc acc | | | | 720 |
| Leu Asp Leu Pro Leu Ile Val Ser Val Thr Val Glu Thr Thr Gly Thr | | | | |
| | 225 | | 230 | 235 |
| atg ctg ctc ggc tcg gag atc ggc gcc gcg ctc acc gcg ctg gaa ccg | | | | 768 |
| Met Leu Leu Gly Ser Glu Ile Gly Ala Ala Leu Thr Ala Leu Pro | | | | |
| | 245 | | 250 | 255 |
| ctc ggc atc gac atg atc ggc ctg aac tgc gcc acc gcc ccc gcc gag | | | | 816 |
| Leu Gly Ile Asp Met Ile Gly Leu Asn Cys Ala Thr Gly Pro Ala Glu | | | | |
| | 260 | | 265 | 270 |
| atg agc gag cac ctg cgc tac ctc gcc cgg cac tcc cgc atc ccg ctg | | | | 864 |
| Met Ser Glu His Leu Arg Tyr Leu Ala Arg His Ser Arg Ile Pro Leu | | | | |
| | 275 | | 280 | 285 |
| acc tgc atg ccc aac gcc ggt ctg ccc gtc ctc ggc aag gac gcc gcc | | | | 912 |
| Thr Cys Met Pro Asn Ala Gly Leu Pro Val Leu Gly Lys Asp Gly Ala | | | | |
| | 290 | | 295 | 300 |
| cac tac ccg ctg acc gcg ccc gag ctg gcc gac gca cac gag acc ttc | | | | 960 |
| His Tyr Pro Leu Thr Ala Pro Glu Leu Ala Asp Ala His Glu Thr Phe | | | | |
| | 305 | | 310 | 315 |
| gtg cgc gag tac ggc ctg tcc ctg gtc ggc gcc tgc tgc gcc acc acg | | | | 1008 |
| Val Arg Glu Tyr Gly Leu Ser Leu Val Gly Gly Cys Cys Gly Thr Thr | | | | |
| | 325 | | 330 | 335 |
| ccc gag cac ctg cgc cag gtc gtc gag cgg gtc cgg gac acc gcc ccc | | | | 1056 |
| Pro Glu His Leu Arg Gln Val Val Glu Arg Val Arg Asp Thr Ala Pro | | | | |
| | 340 | | 345 | 350 |
| acc gca cgc gac ccg cgc ccc gag ccc ggc gcc gcc tcg ctc tac cag | | | | 1104 |
| Thr Ala Arg Asp Pro Arg Pro Glu Pro Gly Ala Ala Ser Leu Tyr Gln | | | | |
| | 355 | | 360 | 365 |
| acc gtg ccc ttc cgc cag gac acc tcc tac ctg gcc atc gcc gag cgc | | | | 1152 |
| Thr Val Pro Phe Arg Gln Asp Thr Ser Tyr Leu Ala Ile Gly Glu Arg | | | | |
| | 370 | | 375 | 380 |
| acc aac gcc aac ggg tcc aag aag ttc cgc gag gcc atg ctg gac gcc | | | | 1200 |
| Thr Asn Ala Asn Gly Ser Lys Lys Phe Arg Glu Ala Met Leu Asp Gly | | | | |
| | 385 | | 390 | 395 |
| | | | | 400 |

| | |
|---|------|
| cgc tgg gac gac tgc gtc gag atg gcc cgc gac cag atc cgc gaa ggc Arg Trp Asp Asp Cys Val Glu Met Ala Arg Asp Gln Ile Arg Glu Gly 405 410 415 | 1248 |
| gcg cac atg ctc gac ctc tgc gtc gac tac gtc ggc cgg gac ggc gtc Ala His Met Leu Asp Leu Cys Val Asp Tyr Val Gly Arg Asp Gly Val 420 425 430 | 1296 |
| gcc gac atg gag gaa ctg gcc ggc cgg ttc gcc acc gcc tcc acg ctg Ala Asp Met Glu Glu Leu Ala Gly Arg Phe Ala Thr Ala Ser Thr Leu 435 440 445 | 1344 |
| ccg atc gtc ctc gac tcc acc gag gtc gac gtc atc cgg gcc ggc ctg Pro Ile Val Leu Asp Ser Thr Glu Val Asp Val Ile Arg Ala Gly Leu 450 455 460 | 1392 |
| gag aag ctc ggc ggc cgc gcg gtg atc aac tcg gtc aac tac gag gac Glu Lys Leu Gly Gly Arg Ala Val Ile Asn Ser Val Asn Tyr Glu Asp 465 470 475 480 | 1440 |
| ggc gcc ggc ccc gag tcc cgg ttc gcc cgc gtc acg aag ctc gcc cgg Gly Ala Gly Pro Glu Ser Arg Phe Ala Arg Val Thr Lys Leu Ala Arg 485 490 495 | 1488 |
| gag cac ggc gcc gcg ctg atc gcg ctg acc atc gac gag gtg gga cag Glu His Gly Ala Ala Leu Ile Ala Leu Thr Ile Asp Glu Val Gly Gln 500 505 510 | 1536 |
| gcc cgc acc gcc gag aag aag gtc gag atc gcc gaa cgg ctc atc gac Ala Arg Thr Ala Glu Lys Lys Val Glu Ile Ala Glu Arg Leu Ile Asp 515 520 525 | 1584 |
| gac ctc acc ggc aac tgg ggc atc cac gag tcc gac atc ctc gtc gac Asp Leu Thr Gly Asn Trp Gly Ile His Glu Ser Asp Ile Leu Val Asp 530 535 540 | 1632 |
| tgc ctg acc ttc acc atc tgc acc ggc cag gag gag tcc cgc aag gac Cys Leu Thr Phe Thr Ile Cys Thr Gly Gln Glu Glu Ser Arg Lys Asp 545 550 555 560 | 1680 |
| ggc ctg gcc acc atc gag ggc atc cgg gaa ctc aag cgg cgc cac ccg Gly Leu Ala Thr Ile Glu Gly Ile Arg Glu Leu Lys Arg Arg His Pro 565 570 575 | 1728 |
| gac gtg cag acc acg ctc ggc ctg tcg aac atc tcc ttc ggc ctc aac Asp Val Gln Thr Thr Leu Gly Leu Ser Asn Ile Ser Phe Gly Leu Asn 580 585 590 | 1776 |
| ccg gcc gcc cgc atc ctg ctc aac tcc gtc ttc ctc gac gaa tgc gtc Pro Ala Ala Arg Ile Leu Leu Asn Ser Val Phe Leu Asp Glu Cys Val 595 600 605 | 1824 |
| aag gcc ggc ctg gac tcg gcc atc gtg cac gcg agc aag atc ctg ccg Lys Ala Gly Leu Asp Ser Ala Ile Val His Ala Ser Lys Ile Leu Pro 610 615 620 | 1872 |
| atc gcc cgc ttc gac gag gag cag gtc acc acc gcc ctc gac ttg atc Ile Ala Arg Phe Asp Glu Glu Gln Val Thr Thr Ala Leu Asp Leu Ile 625 630 635 640 | 1920 |
| tac gac cgc cgc cgc gag ggc tac gac ccc ctg caa aag ctc atg cag | 1968 |

4

| | |
|---|------|
| Tyr Asp Arg Arg Arg Glu Gly Tyr Asp Pro Leu Gln Lys Leu Met Gln | |
| 645 650 655 | |
| ctc ttc gag ggc gcc acc gcc aag tcg ctg aag gcc tcc aag gcc gag | 2016 |
| Leu Phe Glu Gly Ala Thr Ala Lys Ser Leu Lys Ala Ser Lys Ala Glu | |
| 660 665 670 | |
| gaa ctg gcc gcc ctc ccg ctg gag gag cgc ctc aag cgc cgc atc atc | 2064 |
| Glu Leu Ala Ala Leu Pro Leu Glu Glu Arg Leu Lys Arg Arg Ile Ile | |
| 675 680 685 | |
| gac ggc gag aag aac ggc ctc gaa cag gac ctc gac gag gcc ctc cgg | 2112 |
| Asp Gly Glu Lys Asn Gly Leu Glu Gln Asp Leu Asp Glu Ala Leu Arg | |
| 690 695 700 | |
| gag cgc ccg gcc ctc gag atc gtc aac gac acc ctg ctc gac ggt atg | 2160 |
| Glu Arg Pro Ala Leu Glu Ile Val Asn Asp Thr Leu Leu Asp Gly Met | |
| 705 710 715 720 | |
| aag gtc gtc ggc gag ctg ttc ggc tcc ggc cag atg cag ctg ccg ttc | 2208 |
| Lys Val Val Gly Glu Leu Phe Gly Ser Gly Gln Met Gln Leu Pro Phe | |
| 725 730 735 | |
| gtg ctc cag tcc gcc gag gtc atg aag acc gcg gtg gcc cac ctg gag | 2256 |
| Val Leu Gln Ser Ala Glu Val Met Lys Thr Ala Val Ala His Leu Glu | |
| 740 745 750 | |
| ccg cac atg gag aag acc gac gac gac ggc aag ggc acg atc gtg ctg | 2304 |
| Pro His Met Glu Lys Thr Asp Asp Asp Gly Lys Gly Thr Ile Val Leu | |
| 755 760 765 | |
| gcc acc gtc cgc ggc gac gtc cac gac atc ggc aag aac ctc gtc gac | 2352 |
| Ala Thr Val Arg Gly Asp Val His Asp Ile Gly Lys Asn Leu Val Asp | |
| 770 775 780 | |
| atc atc ctg tcc aac aac ggc tac aac gtc gtc aac ctc ggc atc aag | 2400 |
| Ile Ile Leu Ser Asn Asn Gly Tyr Asn Val Val Asn Leu Gly Ile Lys | |
| 785 790 795 800 | |
| cag ccc gtc tcc gcg atc ctg gaa gcg gcc gac gag cac cgg gcc gac | 2448 |
| Gln Pro Val Ser Ala Ile Leu Glu Ala Ala Asp Glu His Arg Ala Asp | |
| 805 810 815 | |
| gtc atc ggc atg tcc ggc ctc ctc gtc aag tcc acg gtg atc atg aag | 2496 |
| Val Ile Gly Met Ser Gly Leu Leu Val Lys Ser Thr Val Ile Met Lys | |
| 820 825 830 | |
| gag aac ctg gag gag ctg aac cag cgc aag ctg gcc gcc gac tac ccg | 2544 |
| Glu Asn Leu Glu Glu Leu Asn Gln Arg Lys Leu Ala Ala Asp Tyr Pro | |
| 835 840 845 | |
| gtc atc ctc ggc ggc gcc gcc ctc acc agg gcc tac gtc gaa cag gac | 2592 |
| Val Ile Leu Gly Gly Ala Ala Leu Thr Arg Ala Tyr Val Glu Gln Asp | |
| 850 855 860 | |
| ctg cac gag atc tac gac ggc gag gtc cgc tac gcc cgc gac gcc ttc | 2640 |
| Leu His Glu Ile Tyr Asp Gly Glu Val Arg Tyr Ala Arg Asp Ala Phe | |
| 865 870 875 880 | |
| gag ggc ctg cgc ctc atg gac gcc ctc atc ggc atc aag cgc ggc gtg | 2688 |
| Glu Gly Leu Arg Leu Met Asp Ala Leu Ile Gly Ile Lys Arg Gly Val | |
| 885 890 895 | |

ccc gcc gcc aag ctg ccg gag ctg aag cag cgc cgg gtg cgg gcc gcc 2736
 Pro Gly Ala Lys Leu Pro Glu Leu Lys Gln Arg Arg Val Arg Ala Ala
 900 905 910

acc gtc gag atc gac gag cgc ccc gag gaa ggc cac gtc cgc tcc gac 2784
 Thr Val Glu Ile Asp Glu Arg Pro Glu Glu Gly His Val Arg Ser Asp
 915 920 925

gtc gcc acc gac aac ccg gtc ccg acc ccg ccc ttc cgc ggc acc cgc 2832
 Val Ala Thr Asp Asn Pro Val Pro Thr Pro Phe Arg Gly Thr Arg
 930 935 940

gtc gtc aag ggc atc cag ctc aag gag tac gcc tcc tgg ctc gac gag 2880
 Val Val Lys Gly Ile Gln Leu Lys Glu Tyr Ala Ser Trp Leu Asp Glu
 945 950 955 960

ggc gcc ctc ttc aag ggc cag tgg ggc ctc aag cag gcc cgc acc ggc 2928
 Gly Ala Leu Phe Lys Gly Gln Trp Gly Leu Lys Gln Ala Arg Thr Gly
 965 970 975

gag gga ccc tcc tac gag gaa ctg gtc gag tcc gag ggc cgg ccg cgg 2976
 Glu Gly Pro Ser Tyr Glu Glu Leu Val Glu Ser Glu Gly Arg Pro Arg
 980 985 990

ctg cgc ggc ctg ctc gac cgg ctc cag acg gac aac ctt ttg gag gcg 3024
 Leu Arg Gly Leu Leu Asp Arg Leu Gln Thr Asp Asn Leu Leu Glu Ala
 995 1000 1005

gcc gtg gtc tac ggc tac ttc ccc tgc gtc tcc aag gac gac gac ctg 3072
 Ala Val Val Tyr Gly Tyr Phe Pro Cys Val Ser Lys Asp Asp Asp Leu
 1010 1015 1020

atc gtc ctc gac gac gac ggc aac gaa cgc acc cgc ttc acc ttc ccc 3120
 Ile Val Leu Asp Asp Asp Gly Asn Glu Arg Thr Arg Phe Thr Phe Pro
 1025 1030 1035 1040

cgc cag cgc cgc ggc cgg cgc ctg tgc ctg gcc gac ttc ttc cgc ccg 3168
 Arg Gln Arg Arg Gly Arg Arg Leu Cys Leu Ala Asp Phe Phe Arg Pro
 1045 1050 1055

gag gag tcc ggc gag acc gac gtg gtc ggc ttc cag gtc gtc acc gtc 3216
 Glu Glu Ser Gly Glu Thr Asp Val Val Gly Phe Gln Val Val Thr Val
 1060 1065 1070

ggc tcc cgc atc ggc gag gag acg gcc cgc atg ttc gag gcc aac gcc 3264
 Gly Ser Arg Ile Gly Glu Glu Thr Ala Arg Met Phe Glu Ala Asn Ala
 1075 1080 1085

tac cgc gac tat ctc gag ctg cac ggc ctg tcc gtg cag ctc gcc gag 3312
 Tyr Arg Asp Tyr Leu Glu Leu His Gly Leu Ser Val Gln Leu Ala Glu
 1090 1095 1100

gcc ctc gcc gag tac tgg cac gcg cgc gtg cgc tcg gaa ctc ggc ttc 3360
 Ala Leu Ala Glu Tyr Trp His Ala Arg Val Arg Ser Glu Leu Gly Phe
 1105 1110 1115 1120

gcc ggg gag gac ccg gcc gag atg gag gac atg ttc gcc ctg aag tac 3408
 Ala Gly Glu Asp Pro Ala Glu Met Glu Asp Met Phe Ala Leu Lys Tyr
 1125 1130 1135

6

cgg ggt gcc cgc ttc tcc ctc ggc tac ggc gcc tgc ccc gac ctg gag 3456
 Arg Gly Ala Arg Phe Ser Leu Gly Tyr Gly Ala Cys Pro Asp Leu Glu
 1140 1145 1150

gac cgc gcc aag atc gcc gcc ctg ctg gag ccc gag cgc atc ggc gtc 3504
 Asp Arg Ala Lys Ile Ala Ala Leu Leu Glu Pro Glu Arg Ile Gly Val
 1155 1160 1165

cac cta tcc gag gag ttc cag ctc cac ccc gag cag tcc acc gac gcc 3552
 His Leu Ser Glu Glu Phe Gln Leu His Pro Glu Gln Ser Thr Asp Ala
 1170 1175 1180

atc gtc atc cac cac ccg gag gcc aag tac ttc aac gcc cgc 3594
 Ile Val Ile His His Pro Glu Ala Lys Tyr Phe Asn Ala Arg
 1185 1190 1195

tga 3597

<210> 2

<211> 1198

<212> PRT

<213> Streptomyces coelicolor

<400> 2

Val Arg Ser Pro Arg Asp Val Pro Arg Arg Ala Ala Pro Gly Arg Gly
 1 5 10 15

Lys Ala Asp Ser Arg Arg Ile Leu Gly Ser Pro Phe Met Ala Ser Ser
 20 25 30

Pro Ser Thr Pro Pro Ala Asp Thr Arg Thr Arg Val Ser Ala Leu Arg
 35 40 45

Glu Ala Leu Ala Thr Arg Val Val Val Ala Asp Gly Ala Met Gly Thr
 50 55 60

Met Leu Gln Ala Gln Asn Pro Thr Leu Asp Asp Phe Gln Gln Leu Glu
 65 70 75 80

Gly Cys Asn Glu Val Leu Asn Leu Thr Arg Pro Asp Ile Val Arg Ser
 85 90 95

Val His Glu Glu Tyr Phe Ala Ala Gly Val Asp Cys Val Glu Thr Asn
 100 105 110

Thr Phe Gly Ala Asn His Ser Ala Leu Gly Glu Tyr Asp Ile Pro Glu
 115 120 125

Arg Val His Glu Leu Ser Glu Ala Gly Ala Arg Val Ala Arg Glu Val
 130 135 140

Ala Asp Glu Phe Gly Ala Arg Asp Gly Arg Gln Arg Trp Val Leu Gly
 145 150 155 160

Ser Met Gly Pro Gly Thr Lys Leu Pro Thr Leu Gly His Ala Pro Tyr
 165 170 175

Thr Val Leu Arg Asp Ala Tyr Gln Arg Asn Ala Glu Gly Leu Val Ala
 180 185 190

Gly Gly Ala Asp Ala Leu Leu Val Glu Thr Thr Gln Asp Leu Leu Gln

| 195 | 200 | 205 |
|--|-----|-----|
| Thr Lys Ala Ser Val Leu Gly Ala Arg Arg Ala Leu Asp Val Leu Gly 210 215 220 | | |
| Leu Asp Leu Pro Leu Ile Val Ser Val Thr Val Glu Thr Thr Gly Thr 225 230 235 240 | | |
| Met Leu Leu Gly Ser Glu Ile Gly Ala Ala Leu Thr Ala Leu Glu Pro 245 250 255 | | |
| Leu Gly Ile Asp Met Ile Gly Leu Asn Cys Ala Thr Gly Pro Ala Glu 260 265 270 | | |
| Met Ser Glu His Leu Arg Tyr Leu Ala Arg His Ser Arg Ile Pro Leu 275 280 285 | | |
| Thr Cys Met Pro Asn Ala Gly Leu Pro Val Leu Gly Lys Asp Gly Ala 290 295 300 | | |
| His Tyr Pro Leu Thr Ala Pro Glu Leu Ala Asp Ala His Glu Thr Phe 305 310 315 320 | | |
| Val Arg Glu Tyr Gly Leu Ser Leu Val Gly Gly Cys Cys Gly Thr Thr 325 330 335 | | |
| Pro Glu His Leu Arg Gln Val Val Glu Arg Val Arg Asp Thr Ala Pro 340 345 350 | | |
| Thr Ala Arg Asp Pro Arg Pro Glu Pro Gly Ala Ala Ser Leu Tyr Gln 355 360 365 | | |
| Thr Val Pro Phe Arg Gln Asp Thr Ser Tyr Leu Ala Ile Gly Glu Arg 370 375 380 | | |
| Thr Asn Ala Asn Gly Ser Lys Lys Phe Arg Glu Ala Met Leu Asp Gly 385 390 395 400 | | |
| Arg Trp Asp Asp Cys Val Glu Met Ala Arg Asp Gln Ile Arg Glu Gly 405 410 415 | | |
| Ala His Met Leu Asp Leu Cys Val Asp Tyr Val Gly Arg Asp Gly Val 420 425 430 | | |
| Ala Asp Met Glu Glu Leu Ala Gly Arg Phe Ala Thr Ala Ser Thr Leu 435 440 445 | | |
| Pro Ile Val Leu Asp Ser Thr Glu Val Asp Val Ile Arg Ala Gly Leu 450 455 460 | | |
| Glu Lys Leu Gly Gly Arg Ala Val Ile Asn Ser Val Asn Tyr Glu Asp 465 470 475 480 | | |
| Gly Ala Gly Pro Glu Ser Arg Phe Ala Arg Val Thr Lys Leu Ala Arg 485 490 495 | | |
| Glu His Gly Ala Ala Leu Ile Ala Leu Thr Ile Asp Glu Val Gly Gln 500 505 510 | | |
| Ala Arg Thr Ala Glu Lys Lys Val Glu Ile Ala Glu Arg Leu Ile Asp 515 520 525 | | |

8

Asp Leu Thr Gly Asn Trp Gly Ile His Glu Ser Asp Ile Leu Val Asp
 530 535 540

Cys Leu Thr Phe Thr Ile Cys Thr Gly Gln Glu Glu Ser Arg Lys Asp
 545 550 555 560

Gly Leu Ala Thr Ile Glu Gly Ile Arg Glu Leu Lys Arg Arg His Pro
 565 570 575

Asp Val Gln Thr Thr Leu Gly Leu Ser Asn Ile Ser Phe Gly Leu Asn
 580 585 590

Pro Ala Ala Arg Ile Leu Leu Asn Ser Val Phe Leu Asp Glu Cys Val
 595 600 605

Lys Ala Gly Leu Asp Ser Ala Ile Val His Ala Ser Lys Ile Leu Pro
 610 615 620

Ile Ala Arg Phe Asp Glu Glu Gln Val Thr Thr Ala Leu Asp Leu Ile
 625 630 635 640

Tyr Asp Arg Arg Arg Glu Gly Tyr Asp Pro Leu Gln Lys Leu Met Gln
 645 650 655

Leu Phe Glu Gly Ala Thr Ala Lys Ser Leu Lys Ala Ser Lys Ala Glu
 660 665 670

Glu Leu Ala Ala Leu Pro Leu Glu Glu Arg Leu Lys Arg Arg Ile Ile
 675 680 685

Asp Gly Glu Lys Asn Gly Leu Glu Gln Asp Leu Asp Glu Ala Leu Arg
 690 695 700

Glu Arg Pro Ala Leu Glu Ile Val Asn Asp Thr Leu Leu Asp Gly Met
 705 710 715 720

Lys Val Val Gly Glu Leu Phe Gly Ser Gly Gln Met Gln Leu Pro Phe
 725 730 735

Val Leu Gln Ser Ala Glu Val Met Lys Thr Ala Val Ala His Leu Glu
 740 745 750

Pro His Met Glu Lys Thr Asp Asp Asp Gly Lys Gly Thr Ile Val Leu
 755 760 765

Ala Thr Val Arg Gly Asp Val His Asp Ile Gly Lys Asn Leu Val Asp
 770 775 780

Ile Ile Leu Ser Asn Asn Gly Tyr Asn Val Val Asn Leu Gly Ile Lys
 785 790 795 800

Gln Pro Val Ser Ala Ile Leu Glu Ala Ala Asp Glu His Arg Ala Asp
 805 810 815

Val Ile Gly Met Ser Gly Leu Leu Val Lys Ser Thr Val Ile Met Lys
 820 825 830

Glu Asn Leu Glu Glu Leu Asn Gln Arg Lys Leu Ala Ala Asp Tyr Pro
 835 840 845

Val Ile Leu Gly Gly Ala Ala Leu Thr Arg Ala Tyr Val Glu Gln Asp
 850 855 860

Leu His Glu Ile Tyr Asp Gly Glu Val Arg Tyr Ala Arg Asp Ala Phe
 865 870 875 880
 Glu Gly Leu Arg Leu Met Asp Ala Leu Ile Gly Ile Lys Arg Gly Val
 885 890 895
 Pro Gly Ala Lys Leu Pro Glu Leu Lys Gln Arg Arg Val Arg Ala Ala
 900 905 910
 Thr Val Glu Ile Asp Glu Arg Pro Glu Glu Gly His Val Arg Ser Asp
 915 920 925
 Val Ala Thr Asp Asn Pro Val Pro Thr Pro Pro Phe Arg Gly Thr Arg
 930 935 940
 Val Val Lys Gly Ile Gln Leu Lys Glu Tyr Ala Ser Trp Leu Asp Glu
 945 950 955 960
 Gly Ala Leu Phe Lys Gly Gln Trp Gly Leu Lys Gln Ala Arg Thr Gly
 965 970 975
 Glu Gly Pro Ser Tyr Glu Glu Leu Val Glu Ser Glu Gly Arg Pro Arg
 980 985 990
 Leu Arg Gly Leu Leu Asp Arg Leu Gln Thr Asp Asn Leu Leu Glu Ala
 995 1000 1005
 Ala Val Val Tyr Gly Tyr Phe Pro Cys Val Ser Lys Asp Asp Asp Leu
 1010 1015 1020
 Ile Val Leu Asp Asp Asp Gly Asn Glu Arg Thr Arg Phe Thr Phe Pro
 1025 1030 1035 1040
 Arg Gln Arg Arg Gly Arg Arg Leu Cys Leu Ala Asp Phe Phe Arg Pro
 1045 1050 1055
 Glu Glu Ser Gly Glu Thr Asp Val Val Gly Phe Gln Val Val Thr Val
 1060 1065 1070
 Gly Ser Arg Ile Gly Glu Glu Thr Ala Arg Met Phe Glu Ala Asn Ala
 1075 1080 1085
 Tyr Arg Asp Tyr Leu Glu Leu His Gly Leu Ser Val Gln Leu Ala Glu
 1090 1095 1100
 Ala Leu Ala Glu Tyr Trp His Ala Arg Val Arg Ser Glu Leu Gly Phe
 1105 1110 1115 1120
 Ala Gly Glu Asp Pro Ala Glu Met Glu Asp Met Phe Ala Leu Lys Tyr
 1125 1130 1135
 Arg Gly Ala Arg Phe Ser Leu Gly Tyr Gly Ala Cys Pro Asp Leu Glu
 1140 1145 1150
 Asp Arg Ala Lys Ile Ala Ala Leu Leu Glu Pro Glu Arg Ile Gly Val
 1155 1160 1165
 His Leu Ser Glu Glu Phe Gln Leu His Pro Glu Gln Ser Thr Asp Ala
 1170 1175 1180
 Ile Val Ile His His Pro Glu Ala Lys Tyr Phe Asn Ala Arg

10
1195

1185

1190

<210> 3
 <211> 3537
 <212> DNA
 <213> Anabaena sp.

<220>
 <221> CDS
 <222> (1)..(3534)
 <223> RAN03790

<400> 3
 atg act cat cct ttc ctg aaa cgc ctg cac agt ccg gaa ctt ccg gtt 48
 Met Thr His Pro Phe Leu Lys Arg Leu His Ser Pro Glu Leu Pro Val
 1 5 10 15
 atc gtc ttc gac ggt gca atg gga act aac cta caa acc caa aac ctc 96
 Ile Val Phe Asp Gly Ala Met Gly Thr Asn Leu Gln Thr Gln Asn Leu
 20 25 30
 acg gct gag gat ttc ggc ggt gtg cag tat gaa ggt tgt aac gaa tac 144
 Thr Ala Glu Asp Phe Gly Gly Val Gln Tyr Glu Gly Cys Asn Glu Tyr
 35 40 45
 cta gtc cac acc aaa ccc gaa gct gtc gcc aag gtt cac cgc gac ttt 192
 Leu Val His Thr Lys Pro Glu Ala Val Ala Lys Val His Arg Asp Phe
 50 55 60
 ctc gct gtg ggt gca gat gtc atc gaa acc gac act ttc ggt gcg aca 240
 Leu Ala Val Gly Ala Asp Val Ile Glu Thr Asp Thr Phe Gly Ala Thr
 65 70 75 80
 tcc att gtt ttg gcg gaa tat gac tta gca gac caa aca tat tac ctg 288
 Ser Ile Val Leu Ala Glu Tyr Asp Leu Ala Asp Gln Thr Tyr Tyr Leu
 85 90 95
 aac aag aaa gcc gcc gaa ctg gcg aaa agt gtc gct gct gaa ttt tcc 336
 Asn Lys Lys Ala Ala Glu Leu Ala Lys Ser Val Ala Ala Glu Phe Ser
 100 105 110
 aca cca gat aaa ccc cgg ttt gtt gct ggt tcc atc ggc ccc aca acc 384
 Thr Pro Asp Lys Pro Arg Phe Val Ala Gly Ser Ile Gly Pro Thr Thr
 115 120 125
 aaa ctt ccc acc ttg gga cat atc gac ttt gac act ctc aaa act tgc 432
 Lys Leu Pro Thr Leu Gly His Ile Asp Phe Asp Thr Leu Lys Thr Cys
 130 135 140
 ttt gct gaa caa gca gaa gcg ctg tta gat ggt ggc gtg gat tta ctt 480
 Phe Ala Glu Gln Ala Glu Ala Leu Leu Asp Gly Gly Val Asp Leu Leu
 145 150 155 160
 ttg gtg gag act tgt caa gat gtg ctg caa atc aaa gcg gcg ctg aat 528
 Leu Val Glu Thr Cys Gln Asp Val Leu Gln Ile Lys Ala Ala Leu Asn
 165 170 175
 ggg ata gaa gaa gtc ttt ggc aag aga ggg gaa cgc ata ccc ttg atg 576
 Gly Ile Glu Glu Val Phe Gly Lys Arg Gly Glu Arg Ile Pro Leu Met
 180 185 190

11

| | |
|---|------|
| gtg tcc gtg aca atg gaa agc atg ggg aca atg ttg gtc ggt tcc gaa Val Ser Val Thr Met Glu Ser Met Gly Thr Met Leu Val Gly Ser Glu 195 200 205 | 624 |
| atc aac gcc gtc ctg aca att tta gaa cct ttc cca att gac att ctc Ile Asn Ala Val Leu Thr Ile Leu Glu Pro Phe Pro Ile Asp Ile Leu 210 215 220 | 672 |
| ggg ctg aac tgt gcc aca ggc cca gac ttg atg aaa cca cat att aaa Gly Leu Asn Cys Ala Thr Gly Pro Asp Leu Met Lys Pro His Ile Lys 225 230 235 240 | 720 |
| tat ttg gct gaa cat tcg ccg ttt gtg gtt tct tgt att cct aac gcg Tyr Leu Ala Glu His Ser Pro Phe Val Val Ser Cys Ile Pro Asn Ala 245 250 255 | 768 |
| ggg tta cca gaa aac gtt ggt ggt caa gca cat tat cgc tta aca cca Gly Leu Pro Glu Asn Val Gly Gly Gln Ala His Tyr Arg Leu Thr Pro 260 265 270 | 816 |
| atg gaa tta cgc atg gcg ttg atg cac ttt gtt gaa gat ttg ggt gtc Met Glu Leu Arg Met Ala Leu Met His Phe Val Glu Asp Leu Gly Val 275 280 285 | 864 |
| caa gtg atc ggg ggt tgc tgt ggg aca cgt cca gaa cac att caa caa Gln Val Ile Gly Gly Cys Cys Gly Thr Arg Pro Glu His Ile Gln Gln 290 295 300 | 912 |
| tta gca gaa att gcc aag gat tta aag cca aag gtg aga cag cca agt Leu Ala Glu Ile Ala Lys Asp Leu Lys Pro Lys Val Arg Gln Pro Ser 305 310 315 320 | 960 |
| tta gaa cct gcg gct gca tca ata tat agt act caa ccc tac gaa caa Leu Glu Pro Ala Ala Ala Ser Ile Tyr Ser Thr Gln Pro Tyr Glu Gln 325 330 335 | 1008 |
| gat aat tct ttc ttg att gtg ggt gaa cgc ctc aac gcc agt ggt tcc Asp Asn Ser Phe Leu Ile Val Gly Glu Arg Leu Asn Ala Ser Gly Ser 340 345 350 | 1056 |
| aag aaa tgc cgt gat ttg ctg aat gcg gaa gat tgg gac gga ttg gta Lys Lys Cys Arg Asp Leu Leu Asn Ala Glu Asp Trp Asp Gly Leu Val 355 360 365 | 1104 |
| tca atg gcg cga tcg caa gtc aag gaa ggc gca cat atc ctt gat gtc Ser Met Ala Arg Ser Gln Val Lys Glu Gly Ala His Ile Leu Asp Val 370 375 380 | 1152 |
| aac gtt gat tat gtg gga cgg gac ggt gtg cgg gat atg cac gaa cta Asn Val Asp Tyr Val Gly Arg Asp Gly Val Arg Asp Met His Glu Leu 385 390 395 400 | 1200 |
| gtt tcc cgc att gtg aat aat gtt aca ctc ccc tta atg ctc gac tcc Val Ser Arg Ile Val Asn Asn Val Thr Leu Pro Leu Met Leu Asp Ser 405 410 415 | 1248 |
| acc gaa tgg gaa aag atg gag gcg ggt tta aag gtg gct ggt ggt aag Thr Glu Trp Glu Lys Met Glu Ala Gly Leu Lys Val Ala Gly Gly Lys 420 425 430 | 1296 |
| tgt ttg ctg aac tcc acc aac tac gaa gat ggg gaa cca cgt ttc tta Cys Leu Leu Asn Ser Thr Asn Tyr Glu Asp Gly Glu Pro Arg Phe Leu | 1344 |

| 435 | 440 | 445 | |
|---|-----|-----|------|
| aaa gtg ttg gag ttg gcg aag aaa tat ggc gcg ggt gtt gtt att ggc Lys Val Leu Glu Leu Ala Lys Lys Tyr Gly Ala Gly Val Val Ile Gly 450 455 460 | | | 1392 |
| aca att gac gaa gaa ggg atg gcg cgg aca gcc gag aaa aag ttt caa Thr Ile Asp Glu Glu Gly Met Ala Arg Thr Ala Glu Lys Lys Phe Gln 465 470 475 480 | | | 1440 |
| att gcc cag cgt gcc tat cgt caa tcg gta gaa tat ggg att ccc ccc Ile Ala Gln Arg Ala Tyr Arg Gln Ser Val Glu Tyr Gly Ile Pro Pro 485 490 495 | | | 1488 |
| aca gaa ata ttc ttt gat acc tta gct tta cca att tct acc ggg att Thr Glu Ile Phe Phe Asp Thr Leu Ala Leu Pro Ile Ser Thr Gly Ile 500 505 510 | | | 1536 |
| gaa gaa gac cgg gaa aat ggc aag gcg aca att gaa tca att agc cgt Glu Glu Asp Arg Glu Asn Gly Lys Ala Thr Ile Glu Ser Ile Ser Arg 515 520 525 | | | 1584 |
| atc cgt aaa gaa ttg cca ggg tgt cat gtt att tta ggc gtg tca aat Ile Arg Lys Glu Leu Pro Gly Cys His Val Ile Leu Gly Val Ser Asn 530 535 540 | | | 1632 |
| ata tcc ttt ggc tta aat tca gcc tcg cgg atg gtc tta aac tcc gtg Ile Ser Phe Gly Leu Asn Ser Ala Ser Arg Met Val Leu Asn Ser Val 545 550 555 560 | | | 1680 |
| ttt ctc cat gaa gca atg act gct ggc atg gat gcg gcg atc gtc agt Phe Leu His Glu Ala Met Thr Ala Gly Met Asp Ala Ala Ile Val Ser 565 570 575 | | | 1728 |
| gct agc aag att cta cca ctg tcg aag att gaa gag cgt cat caa gaa Ala Ser Lys Ile Leu Pro Leu Ser Lys Ile Glu Glu Arg His Gln Glu 580 585 590 | | | 1776 |
| gtc tgc cgc cag tta att tat gac cag cgt aaa ttt gag ggt gat atc Val Cys Arg Gln Leu Ile Tyr Asp Gln Arg Lys Phe Glu Gly Asp Ile 595 600 605 | | | 1824 |
| tgc atc tat gac ccc tta aca gaa cta act aaa ttg ttt gag gga gtc Cys Ile Tyr Asp Pro Leu Thr Glu Leu Thr Lys Leu Phe Glu Gly Val 610 615 620 | | | 1872 |
| acc acc aaa cgt aac aaa ggc gtt gat gaa agc tta ccc atc gaa gaa Thr Thr Lys Arg Asn Lys Gly Val Asp Glu Ser Leu Pro Ile Glu Glu 625 630 635 640 | | | 1920 |
| cga ctc aag cgt cac att atc gac ggc gaa cgc att ggt tta gaa gcg Arg Leu Lys Arg His Ile Ile Asp Gly Glu Arg Ile Gly Leu Glu Ala 645 650 655 | | | 1968 |
| caa ctg aca aaa gcc tta gaa caa tat cca ccc cta gaa att atc aac Gln Leu Thr Lys Ala Leu Glu Gln Tyr Pro Pro Leu Glu Ile Ile Asn 660 665 670 | | | 2016 |
| act ttc cta cta gat ggg atg aaa gta gtc ggg gaa ttg ttc ggt tca Thr Phe Leu Leu Asp Gly Met Lys Val Val Gly Glu Leu Phe Gly Ser 675 680 685 | | | 2064 |

13

| | |
|---|------|
| gga caa atg cag cta cct ttc gtt tta cag tca gcc gaa acc atg aaa Gly Gln Met Gln Leu Pro Phe Val Leu Gln Ser Ala Glu Thr Met Lys 690 695 700 | 2112 |
| gcg gcg gta gcc tac cta gaa ccg ttc atg gaa aaa tcg gaa agt ggc Ala Ala Val Ala Tyr Leu Glu Pro Phe Met Glu Lys Ser Glu Ser Gly 705 710 715 720 | 2160 |
| aac aat gcc aaa ggt aaa gta att att gcc acc gtg aaa ggc gat gtt Asn Asn Ala Lys Gly Lys Val Ile Ile Ala Thr Val Lys Gly Asp Val 725 730 735 | 2208 |
| cac gac att ggt aaa aac cta gta gac att atc ttg tcc aac aac ggc His Asp Ile Gly Lys Asn Leu Val Asp Ile Ile Leu Ser Asn Asn Gly 740 745 750 | 2256 |
| tac aag gta att aac ctg gga att aaa cag ccg gtg gaa aat atc atc Tyr Lys Val Ile Asn Leu Gly Ile Lys Gln Pro Val Glu Asn Ile Ile 755 760 765 | 2304 |
| gag gct tac aac caa cac aaa gct gat tgt att gcc atg agt ggc ttg Glu Ala Tyr Asn Gln His Lys Ala Asp Cys Ile Ala Met Ser Gly Leu 770 775 780 | 2352 |
| ctg gta aaa tcc acc gca ttc atg aaa gaa aat ttg gag gtc ttc aac Leu Val Lys Ser Thr Ala Phe Met Lys Glu Asn Leu Glu Val Phe Asn 785 790 795 800 | 2400 |
| gaa aaa ggc att aat gtt cct gta att tta ggt ggt gcg gca tta acc Glu Lys Gly Ile Asn Val Pro Val Ile Leu Gly Gly Ala Ala Leu Thr 805 810 815 | 2448 |
| ccg aaa ttc gtg cat aaa gat tgc caa aat acc tac aaa ggt aaa gtc Pro Lys Phe Val His Lys Asp Cys Gln Asn Thr Tyr Lys Gly Lys Val 820 825 830 | 2496 |
| att tat ggc aaa gat gct ttc tca gac ctg cat ttc atg gat aaa tta Ile Tyr Gly Lys Asp Ala Phe Ser Asp Leu His Phe Met Asp Lys Leu 835 840 845 | 2544 |
| atg cca gcc aaa gcc act ggc aaa tgg gac aat tcc tta gga ttc ttg Met Pro Ala Lys Ala Thr Gly Lys Trp Asp Asn Ser Leu Gly Phe Leu 850 855 860 | 2592 |
| gat gaa gta gaa acc gag gaa aca gaa cct acc aat cac aaa tcc cca Asp Glu Val Glu Thr Glu Glu Thr Glu Pro Thr Asn His Lys Ser Pro 865 870 875 880 | 2640 |
| atc ccc agt ccc caa tcc cca gtc ccc agt ccc cag tcc cca gtc cct Ile Pro Ser Pro Gln Ser Pro Val Pro Ser Pro Gln Ser Pro Val Pro 885 890 895 | 2688 |
| ata gac acc cga cgt tcc gaa gct gta gcc ata gac att ccc cgt ccc Ile Asp Thr Arg Arg Ser Glu Ala Val Ala Ile Asp Ile Pro Arg Pro 900 905 910 | 2736 |
| aca cca cca ttc tgg gga acg caa tta tta cag cct agc gat att tcc Thr Pro Pro Phe Trp Gly Thr Gln Leu Leu Gln Pro Ser Asp Ile Ser 915 920 925 | 2784 |
| tta gag gaa ata ttc tgg cac atg gat ttg caa gcc ttg att gcg gga | 2832 |

14

| | |
|---|------|
| Leu Glu Glu Ile Phe Trp His Met Asp Leu Gln Ala Leu Ile Ala Gly | |
| 930 935 940 | |
| caa tgg caa ttc cgc aaa ccc aaa gaa caa tca aag gaa gaa tat caa | 2880 |
| Gln Trp Gln Phe Arg Lys Pro Lys Glu Gln Ser Lys Glu Glu Tyr Gln | |
| 945 950 955 960 | |
| gct ttc ttg aat gag aaa gtg tat cca gtt cta gaa act tgg aaa cag | 2928 |
| Ala Phe Leu Asn Glu Lys Val Tyr Pro Val Leu Glu Thr Trp Lys Gln | |
| 965 970 975 | |
| cgc atc att gca gaa aac ttg tta cat ccc cag gta att tat ggg tat | 2976 |
| Arg Ile Ile Ala Glu Asn Leu Leu His Pro Gln Val Ile Tyr Gly Tyr | |
| 980 985 990 | |
| ttt cct tgt caa tct gag ggt aat act tta tat gtt tac gaa aca aac | 3024 |
| Phe Pro Cys Gln Ser Glu Gly Asn Thr Leu Tyr Val Tyr Glu Thr Asn | |
| 995 1000 1005 | |
| agc cca aat gcc aca gaa atc act cag ttt gaa ttc ccc cga caa aag | 3072 |
| Ser Pro Asn Ala Thr Glu Ile Thr Gln Phe Glu Phe Pro Arg Gln Lys | |
| 1010 1015 1020 | |
| tca tca aaa cga tta tgt att gcc gat ttc ttt gca ccg aaa gat tca | 3120 |
| Ser Ser Lys Arg Leu Cys Ile Ala Asp Phe Phe Ala Pro Lys Asp Ser | |
| 1025 1030 1035 1040 | |
| gga atc att gat gtc ttc ccc atg cag gcg gtg act gta ggc gaa att | 3168 |
| Gly Ile Ile Asp Val Phe Pro Met Gln Ala Val Thr Val Gly Glu Ile | |
| 1045 1050 1055 | |
| gct aca gag ttc gcg caa aaa ttg ttt gca aac aat caa tac act gat | 3216 |
| Ala Thr Glu Phe Ala Gln Lys Leu Phe Ala Asn Asn Gln Tyr Thr Asp | |
| 1060 1065 1070 | |
| tat ctg tat ttt cac ggt ttg gcg gtg caa gta gca gaa gcc ttg gcc | 3264 |
| Tyr Leu Tyr Phe His Gly Leu Ala Val Gln Val Ala Glu Ala Leu Ala | |
| 1075 1080 1085 | |
| gag tgg aca cac gcc aga atc cgc cgt gag tta ggg ttc ggt gct gaa | 3312 |
| Glu Trp Thr His Ala Arg Ile Arg Arg Glu Leu Gly Phe Gly Ala Glu | |
| 1090 1095 1100 | |
| gaa ccg gat aat atc cgg gat att ttg gca caa cgc tat cag ggt tcc | 3360 |
| Glu Pro Asp Asn Ile Arg Asp Ile Leu Ala Gln Arg Tyr Gln Gly Ser | |
| 1105 1110 1115 1120 | |
| cgg tat agt ttt ggc tac cca gct tgt ccc aat att caa gac cag ttt | 3408 |
| Arg Tyr Ser Phe Gly Tyr Pro Ala Cys Pro Asn Ile Gln Asp Gln Phe | |
| 1125 1130 1135 | |
| aag cag ctg gat ttg ttg gag act agc aga att aac tta tac atg gat | 3456 |
| Lys Gln Leu Asp Leu Leu Glu Thr Ser Arg Ile Asn Leu Tyr Met Asp | |
| 1140 1145 1150 | |
| gaa agt gag caa ctt tat cca gaa cag tct acg acg gcg att att act | 3504 |
| Glu Ser Glu Gln Leu Tyr Pro Glu Gln Ser Thr Thr Ala Ile Ile Thr | |
| 1155 1160 1165 | |
| tat cac cca gta gct aag tac ttc acc gcg taa | 3537 |
| Tyr His Pro Val Ala Lys Tyr Phe Thr Ala | |
| 1170 1175 | |

<210> 4
 <211> 1178
 <212> PRT
 <213> Anabaena sp.

<400> 4

```

Met Thr His Pro Phe Leu Lys Arg Leu His Ser Pro Glu Leu Pro Val
  1           5           10           15

Ile Val Phe Asp Gly Ala Met Gly Thr Asn Leu Gln Thr Gln Asn Leu
      20           25           30

Thr Ala Glu Asp Phe Gly Gly Val Gln Tyr Glu Gly Cys Asn Glu Tyr
      35           40           45

Leu Val His Thr Lys Pro Glu Ala Val Ala Lys Val His Arg Asp Phe
      50           55           60

Leu Ala Val Gly Ala Asp Val Ile Glu Thr Asp Thr Phe Gly Ala Thr
      65           70           75           80

Ser Ile Val Leu Ala Glu Tyr Asp Leu Ala Asp Gln Thr Tyr Tyr Leu
      85           90           95

Asn Lys Lys Ala Ala Glu Leu Ala Lys Ser Val Ala Ala Glu Phe Ser
      100          105          110

Thr Pro Asp Lys Pro Arg Phe Val Ala Gly Ser Ile Gly Pro Thr Thr
      115          120          125

Lys Leu Pro Thr Leu Gly His Ile Asp Phe Asp Thr Leu Lys Thr Cys
      130          135          140

Phe Ala Glu Gln Ala Glu Ala Leu Leu Asp Gly Gly Val Asp Leu Leu
      145          150          155          160

Leu Val Glu Thr Cys Gln Asp Val Leu Gln Ile Lys Ala Ala Leu Asn
      165          170          175

Gly Ile Glu Glu Val Phe Gly Lys Arg Gly Glu Arg Ile Pro Leu Met
      180          185          190

Val Ser Val Thr Met Glu Ser Met Gly Thr Met Leu Val Gly Ser Glu
      195          200          205

Ile Asn Ala Val Leu Thr Ile Leu Glu Pro Phe Pro Ile Asp Ile Leu
      210          215          220

Gly Leu Asn Cys Ala Thr Gly Pro Asp Leu Met Lys Pro His Ile Lys
      225          230          235          240

Tyr Leu Ala Glu His Ser Pro Phe Val Val Ser Cys Ile Pro Asn Ala
      245          250          255

Gly Leu Pro Glu Asn Val Gly Gly Gln Ala His Tyr Arg Leu Thr Pro
      260          265          270

Met Glu Leu Arg Met Ala Leu Met His Phe Val Glu Asp Leu Gly Val
      275          280          285

```

Gln Val Ile Gly Gly Cys Cys Gly Thr Arg Pro Glu His Ile Gln Gln
 290 295 300
 Leu Ala Glu Ile Ala Lys Asp Leu Lys Pro Lys Val Arg Gln Pro Ser
 305 310 315 320
 Leu Glu Pro Ala Ala Ala Ser Ile Tyr Ser Thr Gln Pro Tyr Glu Gln
 325 330 335
 Asp Asn Ser Phe Leu Ile Val Gly Glu Arg Leu Asn Ala Ser Gly Ser
 340 345 350
 Lys Lys Cys Arg Asp Leu Leu Asn Ala Glu Asp Trp Asp Gly Leu Val
 355 360 365
 Ser Met Ala Arg Ser Gln Val Lys Glu Gly Ala His Ile Leu Asp Val
 370 375 380
 Asn Val Asp Tyr Val Gly Arg Asp Gly Val Arg Asp Met His Glu Leu
 385 390 395 400
 Val Ser Arg Ile Val Asn Asn Val Thr Leu Pro Leu Met Leu Asp Ser
 405 410 415
 Thr Glu Trp Glu Lys Met Glu Ala Gly Leu Lys Val Ala Gly Gly Lys
 420 425 430
 Cys Leu Leu Asn Ser Thr Asn Tyr Glu Asp Gly Glu Pro Arg Phe Leu
 435 440 445
 Lys Val Leu Glu Leu Ala Lys Lys Tyr Gly Ala Gly Val Val Ile Gly
 450 455 460
 Thr Ile Asp Glu Glu Gly Met Ala Arg Thr Ala Glu Lys Lys Phe Gln
 465 470 475 480
 Ile Ala Gln Arg Ala Tyr Arg Gln Ser Val Glu Tyr Gly Ile Pro Pro
 485 490 495
 Thr Glu Ile Phe Phe Asp Thr Leu Ala Leu Pro Ile Ser Thr Gly Ile
 500 505 510
 Glu Glu Asp Arg Glu Asn Gly Lys Ala Thr Ile Glu Ser Ile Ser Arg
 515 520 525
 Ile Arg Lys Glu Leu Pro Gly Cys His Val Ile Leu Gly Val Ser Asn
 530 535 540
 Ile Ser Phe Gly Leu Asn Ser Ala Ser Arg Met Val Leu Asn Ser Val
 545 550 555 560
 Phe Leu His Glu Ala Met Thr Ala Gly Met Asp Ala Ala Ile Val Ser
 565 570 575
 Ala Ser Lys Ile Leu Pro Leu Ser Lys Ile Glu Glu Arg His Gln Glu
 580 585 590
 Val Cys Arg Gln Leu Ile Tyr Asp Gln Arg Lys Phe Glu Gly Asp Ile
 595 600 605
 Cys Ile Tyr Asp Pro Leu Thr Glu Leu Thr Lys Leu Phe Glu Gly Val

| | | |
|---|-----|-------------|
| 610 | 615 | 620 |
| Thr Thr Lys Arg Asn Lys Gly Val Asp Glu Ser Leu Pro Ile Glu Glu | | |
| 625 | 630 | 635 640 |
| Arg Leu Lys Arg His Ile Ile Asp Gly Glu Arg Ile Gly Leu Glu Ala | | |
| | 645 | 650 655 |
| Gln Leu Thr Lys Ala Leu Glu Gln Tyr Pro Pro Leu Glu Ile Ile Asn | | |
| | 660 | 665 670 |
| Thr Phe Leu Leu Asp Gly Met Lys Val Val Gly Glu Leu Phe Gly Ser | | |
| | 675 | 680 685 |
| Gly Gln Met Gln Leu Pro Phe Val Leu Gln Ser Ala Glu Thr Met Lys | | |
| | 690 | 695 700 |
| Ala Ala Val Ala Tyr Leu Glu Pro Phe Met Glu Lys Ser Glu Ser Gly | | |
| | 705 | 710 715 720 |
| Asn Asn Ala Lys Gly Lys Val Ile Ile Ala Thr Val Lys Gly Asp Val | | |
| | 725 | 730 735 |
| His Asp Ile Gly Lys Asn Leu Val Asp Ile Ile Leu Ser Asn Asn Gly | | |
| | 740 | 745 750 |
| Tyr Lys Val Ile Asn Leu Gly Ile Lys Gln Pro Val Glu Asn Ile Ile | | |
| | 755 | 760 765 |
| Glu Ala Tyr Asn Gln His Lys Ala Asp Cys Ile Ala Met Ser Gly Leu | | |
| | 770 | 775 780 |
| Leu Val Lys Ser Thr Ala Phe Met Lys Glu Asn Leu Glu Val Phe Asn | | |
| | 785 | 790 795 800 |
| Glu Lys Gly Ile Asn Val Pro Val Ile Leu Gly Gly Ala Ala Leu Thr | | |
| | 805 | 810 815 |
| Pro Lys Phe Val His Lys Asp Cys Gln Asn Thr Tyr Lys Gly Lys Val | | |
| | 820 | 825 830 |
| Ile Tyr Gly Lys Asp Ala Phe Ser Asp Leu His Phe Met Asp Lys Leu | | |
| | 835 | 840 845 |
| Met Pro Ala Lys Ala Thr Gly Lys Trp Asp Asn Ser Leu Gly Phe Leu | | |
| | 850 | 855 860 |
| Asp Glu Val Glu Thr Glu Glu Thr Glu Pro Thr Asn His Lys Ser Pro | | |
| | 865 | 870 875 880 |
| Ile Pro Ser Pro Gln Ser Pro Val Pro Ser Pro Gln Ser Pro Val Pro | | |
| | 885 | 890 895 |
| Ile Asp Thr Arg Arg Ser Glu Ala Val Ala Ile Asp Ile Pro Arg Pro | | |
| | 900 | 905 910 |
| Thr Pro Pro Phe Trp Gly Thr Gln Leu Leu Gln Pro Ser Asp Ile Ser | | |
| | 915 | 920 925 |
| Leu Glu Glu Ile Phe Trp His Met Asp Leu Gln Ala Leu Ile Ala Gly | | |
| | 930 | 935 940 |

18

Gln Trp Gln Phe Arg Lys Pro Lys Glu Gln Ser Lys Glu Glu Tyr Gln
 945 950 955 960
 Ala Phe Leu Asn Glu Lys Val Tyr Pro Val Leu Glu Thr Trp Lys Gln
 965 970 975
 Arg Ile Ile Ala Glu Asn Leu Leu His Pro Gln Val Ile Tyr Gly Tyr
 980 985 990
 Phe Pro Cys Gln Ser Glu Gly Asn Thr Leu Tyr Val Tyr Glu Thr Asn
 995 1000 1005
 Ser Pro Asn Ala Thr Glu Ile Thr Gln Phe Glu Phe Pro Arg Gln Lys
 1010 1015 1020
 Ser Ser Lys Arg Leu Cys Ile Ala Asp Phe Phe Ala Pro Lys Asp Ser
 1025 1030 1035 1040
 Gly Ile Ile Asp Val Phe Pro Met Gln Ala Val Thr Val Gly Glu Ile
 1045 1050 1055
 Ala Thr Glu Phe Ala Gln Lys Leu Phe Ala Asn Asn Gln Tyr Thr Asp
 1060 1065 1070
 Tyr Leu Tyr Phe His Gly Leu Ala Val Gln Val Ala Glu Ala Leu Ala
 1075 1080 1085
 Glu Trp Thr His Ala Arg Ile Arg Arg Glu Leu Gly Phe Gly Ala Glu
 1090 1095 1100
 Glu Pro Asp Asn Ile Arg Asp Ile Leu Ala Gln Arg Tyr Gln Gly Ser
 1105 1110 1115 1120
 Arg Tyr Ser Phe Gly Tyr Pro Ala Cys Pro Asn Ile Gln Asp Gln Phe
 1125 1130 1135
 Lys Gln Leu Asp Leu Leu Glu Thr Ser Arg Ile Asn Leu Tyr Met Asp
 1140 1145 1150
 Glu Ser Glu Gln Leu Tyr Pro Glu Gln Ser Thr Thr Ala Ile Ile Thr
 1155 1160 1165
 Tyr His Pro Val Ala Lys Tyr Phe Thr Ala
 1170 1175

<210> 5

<211> 3588

<212> DNA

<213> Synechocystis sp.

<220>

<221> CDS

<222> (1) .. (3585)

<223> RCY35965

<400> 5

atg aaa agt gct ttt tta gac cgt atc cac agt ccc gat cgc ccg gta 48
 Met Lys Ser Ala Phe Leu Asp Arg Ile His Ser Pro Asp Arg Pro Val
 1 5 10 15
 tta gtc ttt gac ggg gct atg ggt aca aac ctg cag gta cag aac cta 96

19

| | |
|---|-----|
| Leu Val Phe Asp Gly Ala Met Gly Thr Asn Leu Gln Val Gln Asn Leu | |
| 20 25 30 | |
| acg gcg gcg gat ttt ggt ggg gcg gaa tac gaa ggt tgc aat gaa tat | 144 |
| Thr Ala Ala Asp Phe Gly Gly Ala Glu Tyr Glu Gly Cys Asn Glu Tyr | |
| 35 40 45 | |
| tta gtc cat acc aag cca gag gcc gtg gct acg gtg cat cgt gct ttt | 192 |
| Leu Val His Thr Lys Pro Glu Ala Val Ala Thr Val His Arg Ala Phe | |
| 50 55 60 | |
| tac gaa gcg ggg gcc gat gtc gtg gaa acg gat act ttt ggg gga acg | 240 |
| Tyr Glu Ala Gly Ala Asp Val Val Glu Thr Asp Thr Phe Gly Gly Thr | |
| 65 70 75 80 | |
| ccc ctg gtg ctg gcg gag tac gat tta gca gac caa agt tat tac tta | 288 |
| Pro Leu Val Leu Ala Glu Tyr Asp Leu Ala Asp Gln Ser Tyr Tyr Leu | |
| 85 90 95 | |
| aat aaa gca gcg gcg gag ttg gcc aag gcg gta gca gcg gaa ttt tct | 336 |
| Asn Lys Ala Ala Ala Glu Leu Ala Lys Ala Val Ala Ala Glu Phe Ser | |
| 100 105 110 | |
| acc cca gaa aag cct cga ttc gtg gcc ggc tcc atg gga cca ggc acc | 384 |
| Thr Pro Glu Lys Pro Arg Phe Val Ala Gly Ser Met Gly Pro Gly Thr | |
| 115 120 125 | |
| aag cta ccc acc cta ggt cat gtg gac tac gat agt ctc aag gat gcc | 432 |
| Lys Leu Pro Thr Leu Gly His Val Asp Tyr Asp Ser Leu Lys Asp Ala | |
| 130 135 140 | |
| tat gtg gtt cag gtg cgg ggt tta tac gat ggc gga gtg gat tta ttg | 480 |
| Tyr Val Val Gln Val Arg Gly Leu Tyr Asp Gly Gly Val Asp Leu Leu | |
| 145 150 155 160 | |
| cta gtg gaa acc tgc cag gat gtg ctg caa att aaa gcg gcc ttg aac | 528 |
| Leu Val Glu Thr Cys Gln Asp Val Leu Gln Ile Lys Ala Ala Leu Asn | |
| 165 170 175 | |
| gcc att gaa cag gtc ttt gcc gaa aaa ggc gat cgc cta ccg ttg atg | 576 |
| Ala Ile Glu Gln Val Phe Ala Glu Lys Gly Asp Arg Leu Pro Leu Met | |
| 180 185 190 | |
| gtg tca gta acc atg gaa acc atg ggg acc atg ctg gtg ggt acg gag | 624 |
| Val Ser Val Thr Met Glu Thr Met Gly Thr Met Leu Val Gly Thr Glu | |
| 195 200 205 | |
| atg gcg gcg gcc ctg gcc att ttg gag ccc tat ccc atc gat att ttg | 672 |
| Met Ala Ala Ala Leu Ala Ile Leu Glu Pro Tyr Pro Ile Asp Ile Leu | |
| 210 215 220 | |
| ggg cta aac tgc gcc acc ggg cca gat ttg atg aag gaa cac gtt aaa | 720 |
| Gly Leu Asn Cys Ala Thr Gly Pro Asp Leu Met Lys Glu His Val Lys | |
| 225 230 235 240 | |
| tat ctt tcc gaa cat tcc ccc ttt gtg gtg tcc tgt att ccc aat gct | 768 |
| Tyr Leu Ser Glu His Ser Pro Phe Val Val Ser Cys Ile Pro Asn Ala | |
| 245 250 255 | |
| ggt ttg cca gaa aac gtt ggc ggt caa gct ttt tat cgc ctc acc ccg | 816 |
| Gly Leu Pro Glu Asn Val Gly Gly Gln Ala Phe Tyr Arg Leu Thr Pro | |
| 260 265 270 | |

| | |
|---|------|
| atg gaa ctg caa atg tcc ctg atg cac ttc atc gaa gac ctg gga gta Met Glu Leu Gln Met Ser Leu Met His Phe Ile Glu Asp Leu Gly Val 275 280 285 | 864 |
| cag gta att ggt ggt tgt tgt ggc act aga ccc gat cac atc aag gcc Gln Val Ile Gly Gly Cys Cys Gly Thr Arg Pro Asp His Ile Lys Ala 290 295 300 | 912 |
| ctg gcg gat att gcc aag gat ctc cag ccc aaa caa cgc caa cct cac Leu Ala Asp Ile Ala Lys Asp Leu Gln Pro Lys Gln Arg Gln Pro His 305 310 315 320 | 960 |
| tac gaa ccc agc gcc gct tcc att tat tcc acc caa acc tac gcc caa Tyr Glu Pro Ser Ala Ala Ser Ile Tyr Ser Thr Gln Thr Tyr Ala Gln 325 330 335 | 1008 |
| gaa aat tct ttt tta atc att ggc gaa cgg ctc aat gcc agt ggc tcg Glu Asn Ser Phe Leu Ile Ile Gly Glu Arg Leu Asn Ala Ser Gly Ser 340 345 350 | 1056 |
| aaa aaa tgt cga gat ctg ctc aat gct gaa gat tgg gac agc cta gtt Lys Lys Cys Arg Asp Leu Leu Asn Ala Glu Asp Trp Asp Ser Leu Val 355 360 365 | 1104 |
| tcc ctg gct aaa tcc caa gtc aag gaa gga gcc caa atc ctt gac gtc Ser Leu Ala Lys Ser Gln Val Lys Glu Gly Ala Gln Ile Leu Asp Val 370 375 380 | 1152 |
| aac gtg gat tac gtt ggt cga gat ggg gta agg gac atg aaa gaa tta Asn Val Asp Tyr Val Gly Arg Asp Gly Val Arg Asp Met Lys Glu Leu 385 390 395 400 | 1200 |
| gct tcc cga cta gtc aat aat gtc acc ctg ccg ttg atg ttg gac tcc Ala Ser Arg Leu Val Asn Asn Val Thr Leu Pro Leu Met Leu Asp Ser 405 410 415 | 1248 |
| acc gaa tgg caa aaa atg gag gcg ggt tta aaa gtt gca ggg gga aaa Thr Glu Trp Gln Lys Met Glu Ala Gly Leu Lys Val Ala Gly Gly Lys 420 425 430 | 1296 |
| tgt att ctc aat tcc acc aac tac gaa gac ggg gaa gaa cgg ttt tat Cys Ile Leu Asn Ser Thr Asn Tyr Glu Asp Gly Glu Glu Arg Phe Tyr 435 440 445 | 1344 |
| aaa gtg tta gaa att gcc aaa gaa tat gga gct ggt att gtc att ggc Lys Val Leu Glu Ile Ala Lys Glu Tyr Gly Ala Gly Ile Val Ile Gly 450 455 460 | 1392 |
| acc atc gat gaa gat ggc atg gga cgc act gca gat aaa aaa ttt gag Thr Ile Asp Glu Asp Gly Met Gly Arg Thr Ala Asp Lys Lys Phe Glu 465 470 475 480 | 1440 |
| att gcc aaa cgg gcc tac gaa gcg gcg atc gcc ttt ggc att ccg gcc Ile Ala Lys Arg Ala Tyr Glu Ala Ala Ile Ala Phe Gly Ile Pro Ala 485 490 495 | 1488 |
| aca gaa att ttc ttt gat cct tta gct ctg cct att tcc acc ggc att Thr Glu Ile Phe Phe Asp Pro Leu Ala Leu Pro Ile Ser Thr Gly Ile 500 505 510 | 1536 |
| gaa gaa gac agg gag aac ggt aaa gcc acc gtg gat gct atc cgc aga | 1584 |

21

| | |
|---|------|
| Glu Glu Asp Arg Glu Asn Gly Lys Ala Thr Val Asp Ala Ile Arg Arg 515 520 525 | |
| att cgc cag gaa ttg ccc gat tgt cat att ttg ttg ggg gtt tct aac Ile Arg Gln Glu Leu Pro Asp Cys His Ile Leu Leu Gly Val Ser Asn 530 535 540 | 1632 |
| gtt tcc ttt ggc ttg aat ccc gcc gct cgc cag gta ctc aat tcc atc Val Ser Phe Gly Leu Asn Pro Ala Ala Arg Gln Val Leu Asn Ser Ile 545 550 555 560 | 1680 |
| ttt ctc cac gaa tgt atg cag gtg ggc atg gat gcg gcc att gtc agt Phe Leu His Glu Cys Met Gln Val Gly Met Asp Ala Ala Ile Val Ser 565 570 575 | 1728 |
| gcc aat aag att tta ccc ctg gca aaa att gac cca gaa caa caa caa Ala Asn Lys Ile Leu Pro Leu Ala Lys Ile Asp Pro Glu Gln Gln Gln 580 585 590 | 1776 |
| gtc tgt cta gat tta atc tat gac cgc cgg gaa ttt gaa gga gag cgc Val Cys Leu Asp Leu Ile Tyr Asp Arg Arg Glu Phe Glu Gly Glu Arg 595 600 605 | 1824 |
| tgt aca tat gac ccg tta acc aaa ctc acc act tta ttt gaa ggt aaa Cys Thr Tyr Asp Pro Leu Thr Lys Leu Thr Thr Leu Phe Glu Gly Lys 610 615 620 | 1872 |
| acc acc aaa cgg gat aaa tcc ggt gat gcc aat tta ccg gtg gaa gaa Thr Thr Lys Arg Asp Lys Ser Gly Asp Ala Asn Leu Pro Val Glu Glu 625 630 635 640 | 1920 |
| aga tta aaa cgc cac atc att gat ggg gaa aga ttg ggc tta gaa gag Arg Leu Lys Arg His Ile Ile Asp Gly Glu Arg Leu Gly Leu Glu Glu 645 650 655 | 1968 |
| gcc ctc aat gaa gct tta aaa ctt tac gct ccc tta gat atc att aac Ala Leu Asn Glu Ala Leu Lys Leu Tyr Ala Pro Leu Asp Ile Ile Asn 660 665 670 | 2016 |
| atc tat ttg ttg gat ggc atg aaa gtg gtg ggg gaa cta ttt ggt tcc Ile Tyr Leu Leu Asp Gly Met Lys Val Val Gly Glu Leu Phe Gly Ser 675 680 685 | 2064 |
| ggg caa atg cag ttg ccc ttt gtg ttg cag tcg gcc caa acc atg aaa Gly Gln Met Gln Leu Pro Phe Val Leu Gln Ser Ala Gln Thr Met Lys 690 695 700 | 2112 |
| gcg gcg gtg gct ttt tta gaa ccc cat atg gat aag gat gat tcc gcc Ala Ala Val Ala Phe Leu Glu Pro His Met Asp Lys Asp Asp Ser Ala 705 710 715 720 | 2160 |
| gac aat gct aag ggt act ttt tta att gcc act gtt aag ggg gat gtc Asp Asn Ala Lys Gly Thr Phe Leu Ile Ala Thr Val Lys Gly Asp Val 725 730 735 | 2208 |
| cat gat att ggc aaa aac tta gtg gat att atc ctt tcc aac aat ggc His Asp Ile Gly Lys Asn Leu Val Asp Ile Ile Leu Ser Asn Asn Gly 740 745 750 | 2256 |
| tat cga gtg gtc aac cta ggc att aaa cag cca gtg gaa aat att atc Tyr Arg Val Val Asn Leu Gly Ile Lys Gln Pro Val Glu Asn Ile Ile 755 760 765 | 2304 |

| | |
|---|------|
| gaa gcc tac aaa aaa cac agg ccc gat tgc att gcc atg agt ggt ttg | 2352 |
| Glu Ala Tyr Lys Lys His Arg Pro Asp Cys Ile Ala Met Ser Gly Leu | |
| 770 775 780 | |
| ttg gtc aaa tca act gct ttt atg aag gaa aat tta gaa gtt ttc aac | 2400 |
| Leu Val Lys Ser Thr Ala Phe Met Lys Glu Asn Leu Glu Val Phe Asn | |
| 785 790 795 800 | |
| caa gag ggc att act gtt ccc gtc att ctt ggt ggt gct gct tta acg | 2448 |
| Gln Glu Gly Ile Thr Val Pro Val Ile Leu Gly Gly Ala Ala Leu Thr | |
| 805 810 815 | |
| cct aaa ttt gtt cac cag gac tgc caa aat acc tac aaa ggc caa gta | 2496 |
| Pro Lys Phe Val His Gln Asp Cys Gln Asn Thr Tyr Lys Gly Gln Val | |
| 820 825 830 | |
| att tac ggc aaa gat gcg ttc gcc gat tta cat ttc atg gat aag cta | 2544 |
| Ile Tyr Gly Lys Asp Ala Phe Ala Asp Leu His Phe Met Asp Lys Leu | |
| 835 840 845 | |
| atg ccc gct aaa aat agc cac aat tgg gat gat ttc cag ggc ttt tta | 2592 |
| Met Pro Ala Lys Asn Ser His Asn Trp Asp Asp Phe Gln Gly Phe Leu | |
| 850 855 860 | |
| ggg gaa tat gca acg gaa aat ggc cat aat gtg acc act gat gat ggt | 2640 |
| Gly Glu Tyr Ala Thr Glu Asn Gly His Asn Val Thr Thr Asp Asp Gly | |
| 865 870 875 880 | |
| gct aaa act aat ttt ggc att gaa gaa gaa aaa tta att gac gct agt | 2688 |
| Ala Lys Thr Asn Phe Gly Ile Glu Glu Glu Lys Leu Ile Asp Ala Ser | |
| 885 890 895 | |
| gag cag tct agg gag ccg gag gta att gat act gtt cgt tct gaa gcg | 2736 |
| Glu Gln Ser Arg Glu Pro Glu Val Ile Asp Thr Val Arg Ser Glu Ala | |
| 900 905 910 | |
| gtg gac cct gat cta gaa aga cct gtg cca cct ttt tgg ggc act aaa | 2784 |
| Val Asp Pro Asp Leu Glu Arg Pro Val Pro Pro Phe Trp Gly Thr Lys | |
| 915 920 925 | |
| att ttg caa tcc agt gat att tcc ctc gat gaa gtc ttc cct tta ctg | 2832 |
| Ile Leu Gln Ser Ser Asp Ile Ser Leu Asp Glu Val Phe Pro Leu Leu | |
| 930 935 940 | |
| gat tta caa gca tta ttt gtt ggt cag tgg cag ttt cgc aaa cct agg | 2880 |
| Asp Leu Gln Ala Leu Phe Val Gly Gln Trp Gln Phe Arg Lys Pro Arg | |
| 945 950 955 960 | |
| gag caa tcc agg gaa gaa tac gag caa ttc cta gcg gaa aaa gtt cat | 2928 |
| Glu Gln Ser Arg Glu Glu Tyr Glu Gln Phe Leu Ala Glu Lys Val His | |
| 965 970 975 | |
| ccc att ttg gct gag tgg aaa ggt aag gtc atg gca gaa aat tta ctc | 2976 |
| Pro Ile Leu Ala Glu Trp Lys Gly Lys Val Met Ala Glu Asn Leu Leu | |
| 980 985 990 | |
| cat cct acg gtg gtt tat ggt tat ttt ccc tgt caa tcc cag ggc aat | 3024 |
| His Pro Thr Val Val Tyr Gly Tyr Phe Pro Cys Gln Ser Gln Gly Asn | |
| 995 1000 1005 | |
| acc ttg tta att tat gac cca gaa ttg gtc agc caa aat aat ggc caa | 3072 |

23

Thr Leu Leu Ile Tyr Asp Pro Glu Leu Val Ser Gln Asn Asn Gly Gln
 1010 1015 1020
 att ccc cca gac gca acg gcg atc gcc aaa ttt gag ttt ccc cgg caa 3120
 Ile Pro Pro Asp Ala Thr Ala Ile Ala Lys Phe Glu Phe Pro Arg Gln
 1025 1030 1035 1040
 aaa tca ggg cgg cgg ctc tgt att gcg gac ttt ttt gct tca aaa gaa 3168
 Lys Ser Gly Arg Arg Leu Cys Ile Ala Asp Phe Phe Ala Ser Lys Glu
 1045 1050 1055
 tcg ggg att act gat gtt ttt cct ttg caa gcg gtt aca gtg ggg gaa 3216
 Ser Gly Ile Thr Asp Val Phe Pro Leu Gln Ala Val Thr Val Gly Glu
 1060 1065 1070
 atc gcg acg gaa tat gca agg aaa ctt ttt gct ggc gat aat tac acc 3264
 Ile Ala Thr Glu Tyr Ala Arg Lys Leu Phe Ala Gly Asp Asn Tyr Thr
 1075 1080 1085
 gat tac ctc tac ttc cac ggc atg gcg gtg cag atg gcg gaa gct tta 3312
 Asp Tyr Leu Tyr Phe His Gly Met Ala Val Gln Met Ala Glu Ala Leu
 1090 1095 1100
 gcg gag tgg act cac caa cgg ata cgt cag gaa ttg ggc ttt ggc cat 3360
 Ala Glu Trp Thr His Gln Arg Ile Arg Gln Glu Leu Gly Phe Gly His
 1105 1110 1115 1120
 tta gat cca gat aac atc cgt gat ctt ctc cag caa cgt tac caa ggt 3408
 Leu Asp Pro Asp Asn Ile Arg Asp Leu Leu Gln Gln Arg Tyr Gln Gly
 1125 1130 1135
 tcc cgc tac agt ttt ggt tat ccc gct tgt ccc aac atg cag gat caa 3456
 Ser Arg Tyr Ser Phe Gly Tyr Pro Ala Cys Pro Asn Met Gln Asp Gln
 1140 1145 1150
 tac aca caa tta gaa ttg tta caa acc gaa cga att ggc ttg tat atg 3504
 Tyr Thr Gln Leu Glu Leu Leu Gln Thr Glu Arg Ile Gly Leu Tyr Met
 1155 1160 1165
 gat gaa agt gaa cag gtt tat cca gaa caa tcc acc acg gcg att att 3552
 Asp Glu Ser Glu Gln Val Tyr Pro Glu Gln Ser Thr Thr Ala Ile Ile
 1170 1175 1180
 tcc tat cat cct gcg gct aaa tat ttc agc gct taa 3588
 Ser Tyr His Pro Ala Ala Lys Tyr Phe Ser Ala
 1185 1190 1195

<210> 6

<211> 1195

<212> PRT

<213> Synechocystis sp.

<400> 6

Met Lys Ser Ala Phe Leu Asp Arg Ile His Ser Pro Asp Arg Pro Val
 1 5 10 15

Leu Val Phe Asp Gly Ala Met Gly Thr Asn Leu Gln Val Gln Asn Leu
 20 25 30

Thr Ala Ala Asp Phe Gly Gly Ala Glu Tyr Glu Gly Cys Asn Glu Tyr

24

35 40 45
 Leu Val His Thr Lys Pro Glu Ala Val Ala Thr Val His Arg Ala Phe
 50 55 60
 Tyr Glu Ala Gly Ala Asp Val Val Glu Thr Asp Thr Phe Gly Gly Thr
 65 70 75 80
 Pro Leu Val Leu Ala Glu Tyr Asp Leu Ala Asp Gln Ser Tyr Tyr Leu
 85 90 95
 Asn Lys Ala Ala Ala Glu Leu Ala Lys Ala Val Ala Ala Glu Phe Ser
 100 105 110
 Thr Pro Glu Lys Pro Arg Phe Val Ala Gly Ser Met Gly Pro Gly Thr
 115 120 125
 Lys Leu Pro Thr Leu Gly His Val Asp Tyr Asp Ser Leu Lys Asp Ala
 130 135 140
 Tyr Val Val Gln Val Arg Gly Leu Tyr Asp Gly Gly Val Asp Leu Leu
 145 150 155 160
 Leu Val Glu Thr Cys Gln Asp Val Leu Gln Ile Lys Ala Ala Leu Asn
 165 170 175
 Ala Ile Glu Gln Val Phe Ala Glu Lys Gly Asp Arg Leu Pro Leu Met
 180 185 190
 Val Ser Val Thr Met Glu Thr Met Gly Thr Met Leu Val Gly Thr Glu
 195 200 205
 Met Ala Ala Ala Leu Ala Ile Leu Glu Pro Tyr Pro Ile Asp Ile Leu
 210 215 220
 Gly Leu Asn Cys Ala Thr Gly Pro Asp Leu Met Lys Glu His Val Lys
 225 230 235 240
 Tyr Leu Ser Glu His Ser Pro Phe Val Val Ser Cys Ile Pro Asn Ala
 245 250 255
 Gly Leu Pro Glu Asn Val Gly Gly Gln Ala Phe Tyr Arg Leu Thr Pro
 260 265 270
 Met Glu Leu Gln Met Ser Leu Met His Phe Ile Glu Asp Leu Gly Val
 275 280 285
 Gln Val Ile Gly Gly Cys Cys Gly Thr Arg Pro Asp His Ile Lys Ala
 290 295 300
 Leu Ala Asp Ile Ala Lys Asp Leu Gln Pro Lys Gln Arg Gln Pro His
 305 310 315 320
 Tyr Glu Pro Ser Ala Ala Ser Ile Tyr Ser Thr Gln Thr Tyr Ala Gln
 325 330 335
 Glu Asn Ser Phe Leu Ile Ile Gly Glu Arg Leu Asn Ala Ser Gly Ser
 340 345 350
 Lys Lys Cys Arg Asp Leu Leu Asn Ala Glu Asp Trp Asp Ser Leu Val
 355 360 365

25

Ser Leu Ala Lys Ser Gln Val Lys Glu Gly Ala Gln Ile Leu Asp Val
 370 375 380
 Asn Val Asp Tyr Val Gly Arg Asp Gly Val Arg Asp Met Lys Glu Leu
 385 390 395 400
 Ala Ser Arg Leu Val Asn Asn Val Thr Leu Pro Leu Met Leu Asp Ser
 405 410 415
 Thr Glu Trp Gln Lys Met Glu Ala Gly Leu Lys Val Ala Gly Gly Lys
 420 425 430
 Cys Ile Leu Asn Ser Thr Asn Tyr Glu Asp Gly Glu Glu Arg Phe Tyr
 435 440 445
 Lys Val Leu Glu Ile Ala Lys Glu Tyr Gly Ala Gly Ile Val Ile Gly
 450 455 460
 Thr Ile Asp Glu Asp Gly Met Gly Arg Thr Ala Asp Lys Lys Phe Glu
 465 470 475 480
 Ile Ala Lys Arg Ala Tyr Glu Ala Ala Ile Ala Phe Gly Ile Pro Ala
 485 490 495
 Thr Glu Ile Phe Phe Asp Pro Leu Ala Leu Pro Ile Ser Thr Gly Ile
 500 505 510
 Glu Glu Asp Arg Glu Asn Gly Lys Ala Thr Val Asp Ala Ile Arg Arg
 515 520 525
 Ile Arg Gln Glu Leu Pro Asp Cys His Ile Leu Leu Gly Val Ser Asn
 530 535 540
 Val Ser Phe Gly Leu Asn Pro Ala Ala Arg Gln Val Leu Asn Ser Ile
 545 550 555 560
 Phe Leu His Glu Cys Met Gln Val Gly Met Asp Ala Ala Ile Val Ser
 565 570 575
 Ala Asn Lys Ile Leu Pro Leu Ala Lys Ile Asp Pro Glu Gln Gln Gln
 580 585 590
 Val Cys Leu Asp Leu Ile Tyr Asp Arg Arg Glu Phe Glu Gly Glu Arg
 595 600 605
 Cys Thr Tyr Asp Pro Leu Thr Lys Leu Thr Thr Leu Phe Glu Gly Lys
 610 615 620
 Thr Thr Lys Arg Asp Lys Ser Gly Asp Ala Asn Leu Pro Val Glu Glu
 625 630 635 640
 Arg Leu Lys Arg His Ile Ile Asp Gly Glu Arg Leu Gly Leu Glu Glu
 645 650 655
 Ala Leu Asn Glu Ala Leu Lys Leu Tyr Ala Pro Leu Asp Ile Ile Asn
 660 665 670
 Ile Tyr Leu Leu Asp Gly Met Lys Val Val Gly Glu Leu Phe Gly Ser
 675 680 685
 Gly Gln Met Gln Leu Pro Phe Val Leu Gln Ser Ala Gln Thr Met Lys
 690 695 700

Ala Ala Val Ala Phe Leu Glu Pro His Met Asp Lys Asp Asp Ser Ala
 705 710 715 720
 Asp Asn Ala Lys Gly Thr Phe Leu Ile Ala Thr Val Lys Gly Asp Val
 725 730 735
 His Asp Ile Gly Lys Asn Leu Val Asp Ile Ile Leu Ser Asn Asn Gly
 740 745 750
 Tyr Arg Val Val Asn Leu Gly Ile Lys Gln Pro Val Glu Asn Ile Ile
 755 760 765
 Glu Ala Tyr Lys Lys His Arg Pro Asp Cys Ile Ala Met Ser Gly Leu
 770 775 780
 Leu Val Lys Ser Thr Ala Phe Met Lys Glu Asn Leu Glu Val Phe Asn
 785 790 795 800
 Gln Glu Gly Ile Thr Val Pro Val Ile Leu Gly Gly Ala Ala Leu Thr
 805 810 815
 Pro Lys Phe Val His Gln Asp Cys Gln Asn Thr Tyr Lys Gly Gln Val
 820 825 830
 Ile Tyr Gly Lys Asp Ala Phe Ala Asp Leu His Phe Met Asp Lys Leu
 835 840 845
 Met Pro Ala Lys Asn Ser His Asn Trp Asp Asp Phe Gln Gly Phe Leu
 850 855 860
 Gly Glu Tyr Ala Thr Glu Asn Gly His Asn Val Thr Thr Asp Asp Gly
 865 870 875 880
 Ala Lys Thr Asn Phe Gly Ile Glu Glu Glu Lys Leu Ile Asp Ala Ser
 885 890 895
 Glu Gln Ser Arg Glu Pro Glu Val Ile Asp Thr Val Arg Ser Glu Ala
 900 905 910
 Val Asp Pro Asp Leu Glu Arg Pro Val Pro Pro Phe Trp Gly Thr Lys
 915 920 925
 Ile Leu Gln Ser Ser Asp Ile Ser Leu Asp Glu Val Phe Pro Leu Leu
 930 935 940
 Asp Leu Gln Ala Leu Phe Val Gly Gln Trp Gln Phe Arg Lys Pro Arg
 945 950 955 960
 Glu Gln Ser Arg Glu Glu Tyr Glu Gln Phe Leu Ala Glu Lys Val His
 965 970 975
 Pro Ile Leu Ala Glu Trp Lys Gly Lys Val Met Ala Glu Asn Leu Leu
 980 985 990
 His Pro Thr Val Val Tyr Gly Tyr Phe Pro Cys Gln Ser Gln Gly Asn
 995 1000 1005
 Thr Leu Leu Ile Tyr Asp Pro Glu Leu Val Ser Gln Asn Asn Gly Gln
 1010 1015 1020
 Ile Pro Pro Asp Ala Thr Ala Ile Ala Lys Phe Glu Phe Pro Arg Gln

27

1025 1030 1035 1040
 Lys Ser Gly Arg Arg Leu Cys Ile Ala Asp Phe Phe Ala Ser Lys Glu
 1045 1050 1055
 Ser Gly Ile Thr Asp Val Phe Pro Leu Gln Ala Val Thr Val Gly Glu
 1060 1065 1070
 Ile Ala Thr Glu Tyr Ala Arg Lys Leu Phe Ala Gly Asp Asn Tyr Thr
 1075 1080 1085
 Asp Tyr Leu Tyr Phe His Gly Met Ala Val Gln Met Ala Glu Ala Leu
 1090 1095 1100
 Ala Glu Trp Thr His Gln Arg Ile Arg Gln Glu Leu Gly Phe Gly His
 1105 1110 1115 1120
 Leu Asp Pro Asp Asn Ile Arg Asp Leu Leu Gln Gln Arg Tyr Gln Gly
 1125 1130 1135
 Ser Arg Tyr Ser Phe Gly Tyr Pro Ala Cys Pro Asn Met Gln Asp Gln
 1140 1145 1150
 Tyr Thr Gln Leu Glu Leu Leu Gln Thr Glu Arg Ile Gly Leu Tyr Met
 1155 1160 1165
 Asp Glu Ser Glu Gln Val Tyr Pro Glu Gln Ser Thr Thr Ala Ile Ile
 1170 1175 1180
 Ser Tyr His Pro Ala Ala Lys Tyr Phe Ser Ala
 1185 1190 1195

<210> 7
 <211> 3561
 <212> DNA
 <213> Prochlorococcus marinus

<220>
 <221> CDS
 <222> (1) .. (3558)
 <223> RCK00830

<400> 7
 atg gtt tca ttt aga aat tat tta aat aga gat gat aaa cca att att 48
 Met Val Ser Phe Arg Asn Tyr Leu Asn Arg Asp Asp Lys Pro Ile Ile
 1 5 10 15
 att ttc gat ggt ggg aca ggt act tct ttt caa aat tta aat tta tca 96
 Ile Phe Asp Gly Gly Thr Gly Thr Ser Phe Gln Asn Leu Asn Leu Ser
 20 25 30
 tca cat gat ttt ggt gga gat gat tta gag ggt tgc aat gaa aac tta 144
 Ser His Asp Phe Gly Gly Asp Asp Leu Glu Gly Cys Asn Glu Asn Leu
 35 40 45
 gtt cta tcc tct cct aat act gtt gaa caa gta cat aat tca ttt ctt 192
 Val Leu Ser Ser Pro Asn Thr Val Glu Gln Val His Asn Ser Phe Leu
 50 55 60
 gaa gca ggt tgt cat gta att gaa acc aat aca ttt ggt gct tca tct 240
 Glu Ala Gly Cys His Val Ile Glu Thr Asn Thr Phe Gly Ala Ser Ser

| | | | | | | | | | | 28 | | | | | | | | | | |
|---|--|--|--|--|-----|--|--|--|--|-----|-----|--|--|--|----|--|--|--|--|--|
| 65 | | | | | 70 | | | | | 75 | | | | | 80 | | | | | |
| att gtt tta gac gaa tat agt att tct aat aaa gct tat gaa atc aat | | | | | | | | | | | 288 | | | | | | | | | |
| Ile Val Leu Asp Glu Tyr Ser Ile Ser Asn Lys Ala Tyr Glu Ile Asn | | | | | | | | | | | | | | | | | | | | |
| | | | | | 85 | | | | | | 90 | | | | | | | | | |
| aaa aaa gca gct cag ata gct aaa aaa tgt gca aat tta ttt tca tct | | | | | | | | | | | 336 | | | | | | | | | |
| Lys Lys Ala Ala Gln Ile Ala Lys Lys Cys Ala Asn Leu Phe Ser Ser | | | | | | | | | | | | | | | | | | | | |
| | | | | | 100 | | | | | | 105 | | | | | | | | | |
| att aat act cct aga ttt gtc gct gga tca att ggg cca act aca aaa | | | | | | | | | | | 384 | | | | | | | | | |
| Ile Asn Thr Pro Arg Phe Val Ala Gly Ser Ile Gly Pro Thr Thr Lys | | | | | | | | | | | | | | | | | | | | |
| | | | | | 115 | | | | | | 120 | | | | | | | | | |
| tta cca aca tta ggt cat att agt ttt gat aag ctt aaa gat tca tat | | | | | | | | | | | 432 | | | | | | | | | |
| Leu Pro Thr Leu Gly His Ile Ser Phe Asp Lys Leu Lys Asp Ser Tyr | | | | | | | | | | | | | | | | | | | | |
| | | | | | 130 | | | | | | 135 | | | | | | | | | |
| gaa gaa caa ata aat ggt cta att gac gga ggt att gac ctt cta ttg | | | | | | | | | | | 480 | | | | | | | | | |
| Glu Glu Gln Ile Asn Gly Leu Ile Asp Gly Gly Ile Asp Leu Leu Leu | | | | | | | | | | | | | | | | | | | | |
| | | | | | 145 | | | | | | 150 | | | | | | | | | |
| att gaa aca tgc caa gat gtt tta caa ata aaa tca gca tta tct gct | | | | | | | | | | | 528 | | | | | | | | | |
| Ile Glu Thr Cys Gln Asp Val Leu Gln Ile Lys Ser Ala Leu Ser Ala | | | | | | | | | | | | | | | | | | | | |
| | | | | | 165 | | | | | | 170 | | | | | | | | | |
| tct caa gaa gtt att aaa aac agg aat att gaa tta cca ata atg ata | | | | | | | | | | | 576 | | | | | | | | | |
| Ser Gln Glu Val Ile Lys Asn Arg Asn Ile Glu Leu Pro Ile Met Ile | | | | | | | | | | | | | | | | | | | | |
| | | | | | 180 | | | | | | 185 | | | | | | | | | |
| tcc ata act atg gaa acc aca gga acg atg ctt gtc ggg tca gat ata | | | | | | | | | | | 624 | | | | | | | | | |
| Ser Ile Thr Met Glu Thr Thr Gly Thr Met Leu Val Gly Ser Asp Ile | | | | | | | | | | | | | | | | | | | | |
| | | | | | 195 | | | | | | 200 | | | | | | | | | |
| gct tct gca tta aca ata tta gag cca tac aat att gat att ctg gga | | | | | | | | | | | 672 | | | | | | | | | |
| Ala Ser Ala Leu Thr Ile Leu Glu Pro Tyr Asn Ile Asp Ile Leu Gly | | | | | | | | | | | | | | | | | | | | |
| | | | | | 210 | | | | | | 215 | | | | | | | | | |
| ctg aat tgt gca act ggt cca gtt caa atg aaa gaa cat att aag tat | | | | | | | | | | | 720 | | | | | | | | | |
| Leu Asn Cys Ala Thr Gly Pro Val Gln Met Lys Glu His Ile Lys Tyr | | | | | | | | | | | | | | | | | | | | |
| | | | | | 225 | | | | | | 230 | | | | | | | | | |
| tta gct gaa aat tca cct ttt gca att agt tgt ata cct aat gca gga | | | | | | | | | | | 768 | | | | | | | | | |
| Leu Ala Glu Asn Ser Pro Phe Ala Ile Ser Cys Ile Pro Asn Ala Gly | | | | | | | | | | | | | | | | | | | | |
| | | | | | 245 | | | | | | 250 | | | | | | | | | |
| tta cct gaa aat ata gga ggt gtt gct cac tat aaa tta act cca ttg | | | | | | | | | | | 816 | | | | | | | | | |
| Leu Pro Glu Asn Ile Gly Gly Val Ala His Tyr Lys Leu Thr Pro Leu | | | | | | | | | | | | | | | | | | | | |
| | | | | | 260 | | | | | | 265 | | | | | | | | | |
| gag ttg aaa atg cag tta atg aac ttt att tat gat ttt aac gta caa | | | | | | | | | | | 864 | | | | | | | | | |
| Glu Leu Lys Met Gln Leu Met Asn Phe Ile Tyr Asp Phe Asn Val Gln | | | | | | | | | | | | | | | | | | | | |
| | | | | | 275 | | | | | | 280 | | | | | | | | | |
| ctt att ggc gga tgt tgt ggt act act cct gaa cat atc aag cat tta | | | | | | | | | | | 912 | | | | | | | | | |
| Leu Ile Gly Gly Cys Cys Gly Thr Thr Pro Glu His Ile Lys His Leu | | | | | | | | | | | | | | | | | | | | |
| | | | | | 290 | | | | | | 295 | | | | | | | | | |
| tca tca atc att gag gaa ata gtt gat aaa aaa ata aat aaa aga ctt | | | | | | | | | | | 960 | | | | | | | | | |
| Ser Ser Ile Ile Glu Glu Ile Val Asp Lys Lys Ile Asn Lys Arg Leu | | | | | | | | | | | | | | | | | | | | |
| | | | | | 305 | | | | | | 310 | | | | | | | | | |
| | | | | | | | | | | 315 | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | |

29

| | |
|---|------|
| cct act gta aaa aca aat ttt gtt cct tca gca gct tct ata tat aac | 1008 |
| Pro Thr Val Lys Thr Asn Phe Val Pro Ser Ala Ala Ser Ile Tyr Asn | |
| 325 330 335 | |
| gca gtt cca tat aaa caa gat aac tca ata tta ata gtt gga gaa cgt | 1056 |
| Ala Val Pro Tyr Lys Gln Asp Asn Ser Ile Leu Ile Val Gly Glu Arg | |
| 340 345 350 | |
| tta aat gct agt gga tca aaa aaa gta agg gaa tta cta aat gaa gat | 1104 |
| Leu Asn Ala Ser Gly Ser Lys Lys Val Arg Glu Leu Leu Asn Glu Asp | |
| 355 360 365 | |
| gat tgg gac ggc ctg cta tca att gct aaa caa cag caa aaa gaa aat | 1152 |
| Asp Trp Asp Gly Leu Leu Ser Ile Ala Lys Gln Gln Gln Lys Glu Asn | |
| 370 375 380 | |
| gct cac ata cta gat gtc aat gtt gat tat gta gga aga gat gga gtt | 1200 |
| Ala His Ile Leu Asp Val Asn Val Asp Tyr Val Gly Arg Asp Gly Val | |
| 385 390 395 400 | |
| aaa gat atg aaa gaa att acc tca aga tta gtt aca aat ata aat ctt | 1248 |
| Lys Asp Met Lys Glu Ile Thr Ser Arg Leu Val Thr Asn Ile Asn Leu | |
| 405 410 415 | |
| cca tta atg ata gat tca aca gaa gca gat aaa atg gaa agt gga tta | 1296 |
| Pro Leu Met Ile Asp Ser Thr Glu Ala Asp Lys Met Glu Ser Gly Leu | |
| 420 425 430 | |
| aag act gta gga gga aaa tgc att ata aat tca aca aac tac gaa gat | 1344 |
| Lys Thr Val Gly Gly Lys Cys Ile Ile Asn Ser Thr Asn Tyr Glu Asp | |
| 435 440 445 | |
| gga gat gac aga ttt aat cag gtc tta aga ctt gca tta gat tat ggt | 1392 |
| Gly Asp Asp Arg Phe Asn Gln Val Leu Arg Leu Ala Leu Asp Tyr Gly | |
| 450 455 460 | |
| gct gga ata gta att gga act att gat gaa gat gga atg gca aga aca | 1440 |
| Ala Gly Ile Val Ile Gly Thr Ile Asp Glu Asp Gly Met Ala Arg Thr | |
| 465 470 475 480 | |
| tca cag aaa aaa tat gac att gca aaa aga gca tta att aaa act aga | 1488 |
| Ser Gln Lys Lys Tyr Asp Ile Ala Lys Arg Ala Leu Ile Lys Thr Arg | |
| 485 490 495 | |
| tca agt ggc ctc gct gat tat gag ata ttt ttt gat cct cta gca ttg | 1536 |
| Ser Ser Gly Leu Ala Asp Tyr Glu Ile Phe Phe Asp Pro Leu Ala Leu | |
| 500 505 510 | |
| cca ata tct act gga att gaa gaa gat aga tta aat gct aaa gca act | 1584 |
| Pro Ile Ser Thr Gly Ile Glu Glu Asp Arg Leu Asn Ala Lys Ala Thr | |
| 515 520 525 | |
| att gaa gct ata tca aaa ata aga aaa agc ttt cca gat att cat att | 1632 |
| Ile Glu Ala Ile Ser Lys Ile Arg Lys Ser Phe Pro Asp Ile His Ile | |
| 530 535 540 | |
| att tta ggg ata tct aat att agt ttc ggg ctt tca cca tta tca aga | 1680 |
| Ile Leu Gly Ile Ser Asn Ile Ser Phe Gly Leu Ser Pro Leu Ser Arg | |
| 545 550 555 560 | |
| att aat cta aat tca ata ttt ctc gat gaa tgt ata aag gca gga tta | 1728 |
| Ile Asn Leu Asn Ser Ile Phe Leu Asp Glu Cys Ile Lys Ala Gly Leu | |

30

| | | | |
|---|-----|-----|------|
| 565 | 570 | 575 | |
| gat tca gcg att att gca cca aat aaa ata ttg cct ctt tca aaa ata | | | 1776 |
| Asp Ser Ala Ile Ile Ala Pro Asn Lys Ile Leu Pro Leu Ser Lys Ile | | | |
| 580 | 585 | 590 | |
| tct gcg gaa aca aaa aaa tta tgt tta gat tta att tat gac aga aga | | | 1824 |
| Ser Ala Glu Thr Lys Lys Leu Cys Leu Asp Leu Ile Tyr Asp Arg Arg | | | |
| 595 | 600 | 605 | |
| aat ttc gaa aat gaa ata tgt ata tat gat cca tta gtt gaa cta aca | | | 1872 |
| Asn Phe Glu Asn Glu Ile Cys Ile Tyr Asp Pro Leu Val Glu Leu Thr | | | |
| 610 | 615 | 620 | |
| aaa gca ttc caa gat ata aca atc agt gac ttt aaa aaa gga tct act | | | 1920 |
| Lys Ala Phe Gln Asp Ile Thr Ile Ser Asp Phe Lys Lys Gly Ser Thr | | | |
| 625 | 630 | 635 | 640 |
| tca aac aaa aac ctc acc tta gaa gaa aaa ctt aaa aac cat att gta | | | 1968 |
| Ser Asn Lys Asn Leu Thr Leu Glu Glu Lys Leu Lys Asn His Ile Val | | | |
| 645 | 650 | 655 | |
| gat ggg gaa aaa ata ggt tta gaa gaa caa tta aat aat gcg ctt aaa | | | 2016 |
| Asp Gly Glu Lys Ile Gly Leu Glu Glu Gln Leu Asn Asn Ala Leu Lys | | | |
| 660 | 665 | 670 | |
| aag tac aaa cca ctt gaa ata att aat act tat tta tta gat gga atg | | | 2064 |
| Lys Tyr Lys Pro Leu Glu Ile Ile Asn Thr Tyr Leu Leu Asp Gly Met | | | |
| 675 | 680 | 685 | |
| aaa gta gtc ggt gaa cta ttt gga tcc ggc caa atg caa tta cct ttt | | | 2112 |
| Lys Val Val Gly Glu Leu Phe Gly Ser Gly Gln Met Gln Leu Pro Phe | | | |
| 690 | 695 | 700 | |
| gta ttg caa tca gcg gaa aca atg aaa ttt gct gtt tca gtg ctt gaa | | | 2160 |
| Val Leu Gln Ser Ala Glu Thr Met Lys Phe Ala Val Ser Val Leu Glu | | | |
| 705 | 710 | 715 | 720 |
| cct cat atg gaa aca gta gat gaa aaa ata tct aac gga aaa tta cta | | | 2208 |
| Pro His Met Glu Thr Val Asp Glu Lys Ile Ser Asn Gly Lys Leu Leu | | | |
| 725 | 730 | 735 | |
| ata gca act gtt aaa gga gat gtt cat gat ata ggt aaa aat tta gtt | | | 2256 |
| Ile Ala Thr Val Lys Gly Asp Val His Asp Ile Gly Lys Asn Leu Val | | | |
| 740 | 745 | 750 | |
| gat ata att ctc tca aat aat ggt ttt gat gta atc aac ctt gga att | | | 2304 |
| Asp Ile Ile Leu Ser Asn Asn Gly Phe Asp Val Ile Asn Leu Gly Ile | | | |
| 755 | 760 | 765 | |
| aag caa gat gtt tca gcg att att gat gca caa aaa aaa cat aaa gca | | | 2352 |
| Lys Gln Asp Val Ser Ala Ile Ile Asp Ala Gln Lys Lys His Lys Ala | | | |
| 770 | 775 | 780 | |
| gac tgt att gct atg agt ggt tta ctt gtt aaa tct aca gca ttt atg | | | 2400 |
| Asp Cys Ile Ala Met Ser Gly Leu Leu Val Lys Ser Thr Ala Phe Met | | | |
| 785 | 790 | 795 | 800 |
| aag gat aat tta gaa gca ttt aac aat gct gaa att aat gtt cca gtt | | | 2448 |
| Lys Asp Asn Leu Glu Ala Phe Asn Asn Ala Glu Ile Asn Val Pro Val | | | |
| 805 | 810 | 815 | |

31

| | |
|---|------|
| att ctt gga ggt gca gca tta act cca aaa ttt gtg aat gaa gat tgt Ile Leu Gly Gly Ala Ala Leu Thr Pro Lys Phe Val Asn Glu Asp Cys 820 825 830 | 2496 |
| agt cag ata tat aaa ggt aaa att ttg tat ggg aaa gat gct ttt aca Ser Gln Ile Tyr Lys Gly Lys Ile Leu Tyr Gly Lys Asp Ala Phe Thr 835 840 845 | 2544 |
| gat tta caa ttt atg aat gac tat atg gat agt aaa aag aag ggc aat Asp Leu Gln Phe Met Asn Asp Tyr Met Asp Ser Lys Lys Lys Gly Asn 850 855 860 | 2592 |
| tgg tct aat gaa aat ggt ttt act aat act gat gat att caa att aaa Trp Ser Asn Glu Asn Gly Phe Thr Asn Thr Asp Asp Ile Gln Ile Lys 865 870 875 880 | 2640 |
| tta gct tcc cca agg tct tcc gct aaa gat aaa aat tta aat aaa aat Leu Ala Ser Pro Arg Ser Ser Ala Lys Asp Lys Asn Leu Asn Lys Asn 885 890 895 | 2688 |
| ttt gaa aaa acc aaa agt att caa tta att gag aat ttt aat aga tct Phe Glu Lys Thr Lys Ser Ile Gln Leu Ile Glu Asn Phe Asn Arg Ser 900 905 910 | 2736 |
| aat ttt gta gag gaa gag gaa cct ata aag gct cca ttt ttg gga act Asn Phe Val Glu Glu Glu Glu Pro Ile Lys Ala Pro Phe Leu Gly Thr 915 920 925 | 2784 |
| aga gtt ctt caa gat att gaa ata gac ttt gac aaa cta att ttt tat Arg Val Leu Gln Asp Ile Glu Ile Asp Phe Asp Lys Leu Ile Phe Tyr 930 935 940 | 2832 |
| cta gat aaa aaa gca tta ttt agt ggt caa tgg caa att aaa aaa aat Leu Asp Lys Lys Ala Leu Phe Ser Gly Gln Trp Gln Ile Lys Lys Asn 945 950 955 960 | 2880 |
| aaa ggt caa tca gta gaa gaa tac aat aat tat tta gat tca tat gca Lys Gly Gln Ser Val Glu Glu Tyr Asn Asn Tyr Leu Asp Ser Tyr Ala 965 970 975 | 2928 |
| aat cca tta ctt gaa aaa tgg att aat att att tta gat aaa ggc tta Asn Pro Leu Leu Glu Lys Trp Ile Asn Ile Ile Leu Asp Lys Gly Leu 980 985 990 | 2976 |
| att tca cca aaa gta gtc tat ggc tac ttc cgt tgc ggg agg aat gat Ile Ser Pro Lys Val Val Tyr Gly Tyr Phe Arg Cys Gly Arg Asn Asp 995 1000 1005 | 3024 |
| aat agt att tat ctc ttt gat aat gta tca aat aaa aga att tct gaa Asn Ser Ile Tyr Leu Phe Asp Asn Val Ser Asn Lys Arg Ile Ser Glu 1010 1015 1020 | 3072 |
| ttt aac ttt cct aga caa aaa tcg gga aat aat ctt tgt att gca gat Phe Asn Phe Pro Arg Gln Lys Ser Gly Asn Asn Leu Cys Ile Ala Asp 1025 1030 1035 1040 | 3120 |
| ttt tac tgt gat ctt aaa aat aat gat cca gta gat ata ttt cca atg Phe Tyr Cys Asp Leu Lys Asn Asn Asp Pro Val Asp Ile Phe Pro Met 1045 1050 1055 | 3168 |
| caa gca gta aca atg ggg gaa ata gct agc gaa tat tcc caa gaa tta Gln Ala Val Thr Met Gly Glu Ile Ala Ser Glu Tyr Ser Gln Glu Leu | 3216 |

32

| 1060 | 1065 | 1070 | |
|---|------|------|------|
| ttt aaa gct gat aaa tat agt gat tat tta ata ttt cat ggt tta acc | | | 3264 |
| Phe Lys Ala Asp Lys Tyr Ser Asp Tyr Leu Ile Phe His Gly Leu Thr | | | |
| 1075 | 1080 | 1085 | |
| ggt caa tta gca gaa gct ctt gca gaa tat ggt cat tca ata gta aga | | | 3312 |
| Val Gln Leu Ala Glu Ala Leu Ala Glu Tyr Val His Ser Ile Val Arg | | | |
| 1090 | 1095 | 1100 | |
| att gaa tgc gga ttt aaa tca tat gag cca aac aat aac cgt gat ata | | | 3360 |
| Ile Glu Cys Gly Phe Lys Ser Tyr Glu Pro Asn Asn Asn Arg Asp Ile | | | |
| 1105 | 1110 | 1115 | 1120 |
| tta gct caa aaa tat aga gga gct aga tac tca ttt ggt tat cca gct | | | 3408 |
| Leu Ala Gln Lys Tyr Arg Gly Ala Arg Tyr Ser Phe Gly Tyr Pro Ala | | | |
| 1125 | 1130 | 1135 | |
| tgt cct aaa gtt tct gat tca aat ata cag tta tca tta ttg gat aca | | | 3456 |
| Cys Pro Lys Val Ser Asp Ser Asn Ile Gln Leu Ser Leu Leu Asp Thr | | | |
| 1140 | 1145 | 1150 | |
| aaa agg att aat tta aca atg gat gaa tca gag caa tta cat cct gaa | | | 3504 |
| Lys Arg Ile Asn Leu Thr Met Asp Glu Ser Glu Gln Leu His Pro Glu | | | |
| 1155 | 1160 | 1165 | |
| caa agt act act gct ata att tca ctt cat tca aaa gca aaa tat ttt | | | 3552 |
| Gln Ser Thr Thr Ala Ile Ile Ser Leu His Ser Lys Ala Lys Tyr Phe | | | |
| 1170 | 1175 | 1180 | |
| agt gcc taa | | | 3561 |
| Ser Ala | | | |
| 1185 | | | |
| <210> 8 | | | |
| <211> 1186 | | | |
| <212> PRT | | | |
| <213> Prochlorococcus marinus | | | |
| <400> 8 | | | |
| Met Val Ser Phe Arg Asn Tyr Leu Asn Arg Asp Asp Lys Pro Ile Ile | | | |
| 1 | 5 | 10 | 15 |
| Ile Phe Asp Gly Gly Thr Gly Thr Ser Phe Gln Asn Leu Asn Leu Ser | | | |
| 20 | 25 | 30 | |
| Ser His Asp Phe Gly Gly Asp Asp Leu Glu Gly Cys Asn Glu Asn Leu | | | |
| 35 | 40 | 45 | |
| Val Leu Ser Ser Pro Asn Thr Val Glu Gln Val His Asn Ser Phe Leu | | | |
| 50 | 55 | 60 | |
| Glu Ala Gly Cys His Val Ile Glu Thr Asn Thr Phe Gly Ala Ser Ser | | | |
| 65 | 70 | 75 | 80 |
| Ile Val Leu Asp Glu Tyr Ser Ile Ser Asn Lys Ala Tyr Glu Ile Asn | | | |
| 85 | 90 | 95 | |
| Lys Lys Ala Ala Gln Ile Ala Lys Lys Cys Ala Asn Leu Phe Ser Ser | | | |
| 100 | 105 | 110 | |

33

Ile Asn Thr Pro Arg Phe Val Ala Gly Ser Ile Gly Pro Thr Thr Lys
 115 120 125
 Leu Pro Thr Leu Gly His Ile Ser Phe Asp Lys Leu Lys Asp Ser Tyr
 130 135 140
 Glu Glu Gln Ile Asn Gly Leu Ile Asp Gly Gly Ile Asp Leu Leu Leu
 145 150 155 160
 Ile Glu Thr Cys Gln Asp Val Leu Gln Ile Lys Ser Ala Leu Ser Ala
 165 170 175
 Ser Gln Glu Val Ile Lys Asn Arg Asn Ile Glu Leu Pro Ile Met Ile
 180 185 190
 Ser Ile Thr Met Glu Thr Thr Gly Thr Met Leu Val Gly Ser Asp Ile
 195 200 205
 Ala Ser Ala Leu Thr Ile Leu Glu Pro Tyr Asn Ile Asp Ile Leu Gly
 210 215 220
 Leu Asn Cys Ala Thr Gly Pro Val Gln Met Lys Glu His Ile Lys Tyr
 225 230 235 240
 Leu Ala Glu Asn Ser Pro Phe Ala Ile Ser Cys Ile Pro Asn Ala Gly
 245 250 255
 Leu Pro Glu Asn Ile Gly Gly Val Ala His Tyr Lys Leu Thr Pro Leu
 260 265 270
 Glu Leu Lys Met Gln Leu Met Asn Phe Ile Tyr Asp Phe Asn Val Gln
 275 280 285
 Leu Ile Gly Gly Cys Cys Gly Thr Thr Pro Glu His Ile Lys His Leu
 290 295 300
 Ser Ser Ile Ile Glu Glu Ile Val Asp Lys Lys Ile Asn Lys Arg Leu
 305 310 315 320
 Pro Thr Val Lys Thr Asn Phe Val Pro Ser Ala Ala Ser Ile Tyr Asn
 325 330 335
 Ala Val Pro Tyr Lys Gln Asp Asn Ser Ile Leu Ile Val Gly Glu Arg
 340 345 350
 Leu Asn Ala Ser Gly Ser Lys Lys Val Arg Glu Leu Leu Asn Glu Asp
 355 360 365
 Asp Trp Asp Gly Leu Leu Ser Ile Ala Lys Gln Gln Gln Lys Glu Asn
 370 375 380
 Ala His Ile Leu Asp Val Asn Val Asp Tyr Val Gly Arg Asp Gly Val
 385 390 395 400
 Lys Asp Met Lys Glu Ile Thr Ser Arg Leu Val Thr Asn Ile Asn Leu
 405 410 415
 Pro Leu Met Ile Asp Ser Thr Glu Ala Asp Lys Met Glu Ser Gly Leu
 420 425 430
 Lys Thr Val Gly Gly Lys Cys Ile Ile Asn Ser Thr Asn Tyr Glu Asp
 435 440 445

Gly Asp Asp Arg Phe Asn Gln Val Leu Arg Leu Ala Leu Asp Tyr Gly
 450 455 460
 Ala Gly Ile Val Ile Gly Thr Ile Asp Glu Asp Gly Met Ala Arg Thr
 465 470 475 480
 Ser Gln Lys Lys Tyr Asp Ile Ala Lys Arg Ala Leu Ile Lys Thr Arg
 485 490 495
 Ser Ser Gly Leu Ala Asp Tyr Glu Ile Phe Phe Asp Pro Leu Ala Leu
 500 505 510
 Pro Ile Ser Thr Gly Ile Glu Glu Asp Arg Leu Asn Ala Lys Ala Thr
 515 520 525
 Ile Glu Ala Ile Ser Lys Ile Arg Lys Ser Phe Pro Asp Ile His Ile
 530 535 540
 Ile Leu Gly Ile Ser Asn Ile Ser Phe Gly Leu Ser Pro Leu Ser Arg
 545 550 555 560
 Ile Asn Leu Asn Ser Ile Phe Leu Asp Glu Cys Ile Lys Ala Gly Leu
 565 570 575
 Asp Ser Ala Ile Ile Ala Pro Asn Lys Ile Leu Pro Leu Ser Lys Ile
 580 585 590
 Ser Ala Glu Thr Lys Lys Leu Cys Leu Asp Leu Ile Tyr Asp Arg Arg
 595 600 605
 Asn Phe Glu Asn Glu Ile Cys Ile Tyr Asp Pro Leu Val Glu Leu Thr
 610 615 620
 Lys Ala Phe Gln Asp Ile Thr Ile Ser Asp Phe Lys Lys Gly Ser Thr
 625 630 635 640
 Ser Asn Lys Asn Leu Thr Leu Glu Glu Lys Leu Lys Asn His Ile Val
 645 650 655
 Asp Gly Glu Lys Ile Gly Leu Glu Glu Gln Leu Asn Asn Ala Leu Lys
 660 665 670
 Lys Tyr Lys Pro Leu Glu Ile Ile Asn Thr Tyr Leu Leu Asp Gly Met
 675 680 685
 Lys Val Val Gly Glu Leu Phe Gly Ser Gly Gln Met Gln Leu Pro Phe
 690 695 700
 Val Leu Gln Ser Ala Glu Thr Met Lys Phe Ala Val Ser Val Leu Glu
 705 710 715 720
 Pro His Met Glu Thr Val Asp Glu Lys Ile Ser Asn Gly Lys Leu Leu
 725 730 735
 Ile Ala Thr Val Lys Gly Asp Val His Asp Ile Gly Lys Asn Leu Val
 740 745 750
 Asp Ile Ile Leu Ser Asn Asn Gly Phe Asp Val Ile Asn Leu Gly Ile
 755 760 765
 Lys Gln Asp Val Ser Ala Ile Ile Asp Ala Gln Lys Lys His Lys Ala

35

| | | |
|---|------|-----------|
| 770 | 775 | 780 |
| Asp Cys Ile Ala Met Ser Gly Leu Leu Val Lys Ser Thr Ala Phe Met | | |
| 785 | 790 | 795 800 |
| Lys Asp Asn Leu Glu Ala Phe Asn Asn Ala Glu Ile Asn Val Pro Val | | |
| 805 | 810 | 815 |
| Ile Leu Gly Gly Ala Ala Leu Thr Pro Lys Phe Val Asn Glu Asp Cys | | |
| 820 | 825 | 830 |
| Ser Gln Ile Tyr Lys Gly Lys Ile Leu Tyr Gly Lys Asp Ala Phe Thr | | |
| 835 | 840 | 845 |
| Asp Leu Gln Phe Met Asn Asp Tyr Met Asp Ser Lys Lys Lys Gly Asn | | |
| 850 | 855 | 860 |
| Trp Ser Asn Glu Asn Gly Phe Thr Asn Thr Asp Asp Ile Gln Ile Lys | | |
| 865 | 870 | 875 880 |
| Leu Ala Ser Pro Arg Ser Ser Ala Lys Asp Lys Asn Leu Asn Lys Asn | | |
| 885 | 890 | 895 |
| Phe Glu Lys Thr Lys Ser Ile Gln Leu Ile Glu Asn Phe Asn Arg Ser | | |
| 900 | 905 | 910 |
| Asn Phe Val Glu Glu Glu Glu Pro Ile Lys Ala Pro Phe Leu Gly Thr | | |
| 915 | 920 | 925 |
| Arg Val Leu Gln Asp Ile Glu Ile Asp Phe Asp Lys Leu Ile Phe Tyr | | |
| 930 | 935 | 940 |
| Leu Asp Lys Lys Ala Leu Phe Ser Gly Gln Trp Gln Ile Lys Lys Asn | | |
| 945 | 950 | 955 960 |
| Lys Gly Gln Ser Val Glu Glu Tyr Asn Asn Tyr Leu Asp Ser Tyr Ala | | |
| 965 | 970 | 975 |
| Asn Pro Leu Leu Glu Lys Trp Ile Asn Ile Ile Leu Asp Lys Gly Leu | | |
| 980 | 985 | 990 |
| Ile Ser Pro Lys Val Val Tyr Gly Tyr Phe Arg Cys Gly Arg Asn Asp | | |
| 995 | 1000 | 1005 |
| Asn Ser Ile Tyr Leu Phe Asp Asn Val Ser Asn Lys Arg Ile Ser Glu | | |
| 1010 | 1015 | 1020 |
| Phe Asn Phe Pro Arg Gln Lys Ser Gly Asn Asn Leu Cys Ile Ala Asp | | |
| 1025 | 1030 | 1035 1040 |
| Phe Tyr Cys Asp Leu Lys Asn Asn Asp Pro Val Asp Ile Phe Pro Met | | |
| 1045 | 1050 | 1055 |
| Gln Ala Val Thr Met Gly Glu Ile Ala Ser Glu Tyr Ser Gln Glu Leu | | |
| 1060 | 1065 | 1070 |
| Phe Lys Ala Asp Lys Tyr Ser Asp Tyr Leu Ile Phe His Gly Leu Thr | | |
| 1075 | 1080 | 1085 |
| Val Gln Leu Ala Glu Ala Leu Ala Glu Tyr Val His Ser Ile Val Arg | | |
| 1090 | 1095 | 1100 |

36

Ile Glu Cys Gly Phe Lys Ser Tyr Glu Pro Asn Asn Asn Arg Asp Ile
 1105 1110 1115 1120

Leu Ala Gln Lys Tyr Arg Gly Ala Arg Tyr Ser Phe Gly Tyr Pro Ala
 1125 1130 1135

Cys Pro Lys Val Ser Asp Ser Asn Ile Gln Leu Ser Leu Leu Asp Thr
 1140 1145 1150

Lys Arg Ile Asn Leu Thr Met Asp Glu Ser Glu Gln Leu His Pro Glu
 1155 1160 1165

Gln Ser Thr Thr Ala Ile Ile Ser Leu His Ser Lys Ala Lys Tyr Phe
 1170 1175 1180

Ser Ala
 1185

<210> 9

<211> 3048

<212> DNA

<213> Thermus thermophilus

<220>

<221> CDS

<222> (1)..(3045)

<223> RTT00266

<400> 9

atg cgg gcc tac aag gag gcg gca cgg ggg ctt ctt aag ggc ggg gtg 48
 Met Arg Ala Tyr Lys Glu Ala Ala Arg Gly Leu Leu Lys Gly Gly Val
 1 5 10 15

gac ctc atc ctc ttg gag acc gcc cag gac atc ctc cag gtg cgc tgc 96
 Asp Leu Ile Leu Leu Glu Thr Ala Gln Asp Ile Leu Gln Val Arg Cys
 20 25 30

gcc gtc ttg gcg gtg cgg gag gcc atg gcc gag gtg ggc cgg gag gtg 144
 Ala Val Leu Ala Val Arg Glu Ala Met Ala Glu Val Gly Arg Glu Val
 35 40 45

ccc ctc cag gtc cag gtg acc ttt gag gcc acg ggg acg atg ctc gtg 192
 Pro Leu Gln Val Gln Val Thr Phe Glu Ala Thr Gly Thr Met Leu Val
 50 55 60

ggc acg gac gag cag gcg gcc ctg gcc gct ctg gag agc ctc ccc gtg 240
 Gly Thr Asp Glu Gln Ala Ala Leu Ala Ala Leu Glu Ser Leu Pro Val
 65 70 75 80

gac gtg gtg ggg atg aac tgc gcc acg ggc ccc gac ctc atg gac agc 288
 Asp Val Val Gly Met Asn Cys Ala Thr Gly Pro Asp Leu Met Asp Ser
 85 90 95

aag gtg cgc tac ttc gcc gag cac agc acc cgc ttc gtc tcc tgc ctc 336
 Lys Val Arg Tyr Phe Ala Glu His Ser Thr Arg Phe Val Ser Cys Leu
 100 105 110

ccg aac gcg ggc ctg ccc cgg aac gag ggg ggg agg gtg gtc tac gac 384
 Pro Asn Ala Gly Leu Pro Arg Asn Glu Gly Gly Arg Val Val Tyr Asp
 115 120 125

37

| | |
|---|------|
| ctc acc ccc gag gag ctc gcc aag tgg cac ctc aag ttc gtg gcc gag | 432 |
| Leu Thr Pro Glu Glu Leu Ala Lys Trp His Leu Lys Phe Val Ala Glu | |
| 130 135 140 | |
| tac ggg gtg aac gcc gtg ggg gga tgc tgc ggc acg ggg ccc gag cac | 480 |
| Tyr Gly Val Asn Ala Val Gly Gly Cys Cys Gly Thr Gly Pro Glu His | |
| 145 150 155 160 | |
| ata agg aag gtg gcc gag gcg gtg aag ggg ctc gcc ccg aag cca agg | 528 |
| Ile Arg Lys Val Ala Glu Ala Val Lys Gly Leu Ala Pro Lys Pro Arg | |
| 165 170 175 | |
| ccc gaa agc ttc cct ccc cag gtg gcc tcc ttg tac cag gcg gtg tcc | 576 |
| Pro Glu Ser Phe Pro Pro Gln Val Ala Ser Leu Tyr Gln Ala Val Ser | |
| 180 185 190 | |
| ctc aag cag gag gcg agc ctt ttc ctc gtg ggg gag agg ctc aac gcc | 624 |
| Leu Lys Gln Glu Ala Ser Leu Phe Leu Val Gly Glu Arg Leu Asn Ala | |
| 195 200 205 | |
| acg ggg agc aag cgc ttc cgg gag atg ctc ttc gcg aga gac ctc gag | 672 |
| Thr Gly Ser Lys Arg Phe Arg Glu Met Leu Phe Ala Arg Asp Leu Glu | |
| 210 215 220 | |
| ggc atc ctc gcc ctc gcc cgg gag cag gtg gag gag ggg gcc cac gcc | 720 |
| Gly Ile Leu Ala Leu Ala Arg Glu Gln Val Glu Glu Gly Ala His Ala | |
| 225 230 235 240 | |
| ctg gac ctc tcc gtg gcc tgg acg ggg cgg gac gag ctt gag gac ctc | 768 |
| Leu Asp Leu Ser Val Ala Trp Thr Gly Arg Asp Glu Leu Glu Asp Leu | |
| 245 250 255 | |
| cgg tgg ctc ctt ccc cat ctc gcc acc gcc ctt acc gtc ccc gtc atg | 816 |
| Arg Trp Leu Leu Pro His Leu Ala Thr Ala Leu Thr Val Pro Val Met | |
| 260 265 270 | |
| gtg gac tcc acc tcc cct gag gcc atg gag ctc gcc ctc aaa tac ctc | 864 |
| Val Asp Ser Thr Ser Pro Glu Ala Met Glu Leu Ala Leu Lys Tyr Leu | |
| 275 280 285 | |
| ccg ggc cgg gtc ctc ctg aac tcc gcc aac ctc gag gat ggc tta gag | 912 |
| Pro Gly Arg Val Leu Leu Asn Ser Ala Asn Leu Glu Asp Gly Leu Glu | |
| 290 295 300 | |
| cgc ttt gac cgg gtg gcc tcc ctg gcc aag gcc cac ggg gcg gcc ctc | 960 |
| Arg Phe Asp Arg Val Ala Ser Leu Ala Lys Ala His Gly Ala Ala Leu | |
| 305 310 315 320 | |
| gtg gtc ctc gcc att gag gag aag ggg atg gcc aag acc cgg gag gag | 1008 |
| Val Val Leu Ala Ile Asp Glu Lys Gly Met Ala Lys Thr Arg Glu Glu | |
| 325 330 335 | |
| aag gtg cgg gtg gcc ctg agg atg tac gag cgc ctc acg gag cac cac | 1056 |
| Lys Val Arg Val Ala Leu Arg Met Tyr Glu Arg Leu Thr Glu His His | |
| 340 345 350 | |
| ggc ctc cgc ccc gag gac ctc ctc ttt gac ctc ctt acc ttc ccc atc | 1104 |
| Gly Leu Arg Pro Glu Asp Leu Leu Phe Asp Leu Leu Thr Phe Pro Ile | |
| 355 360 365 | |
| acc caa ggg gac gag gag agc cgc cct ctg gcc aag gag acc ctc ctc | 1152 |
| Thr Gln Gly Asp Glu Glu Ser Arg Pro Leu Ala Lys Glu Thr Leu Leu | |

38

| 370 | 375 | 380 | |
|---|-----|-----|------|
| gcc ata gag gag cta cgg gag agg ctt ccc ggg gtg ggc ttc gtc ctt Ala Ile Glu Glu Leu Arg Glu Arg Leu Pro Gly Val Gly Phe Val Leu 385 390 395 400 | | | 1200 |
| cgg gtc tcc aac gtc tcc ttc ggg ctc aag ccc cgg gcg agg cgc gtc Arg Val Ser Asn Val Ser Phe Gly Leu Lys Pro Arg Ala Arg Arg Val 405 410 415 | | | 1248 |
| ctg aac tcc gtc ttc ctg gac gag gcg agg aaa cgg ggc ctc acc gcg Leu Asn Ser Val Phe Leu Asp Glu Ala Arg Lys Arg Gly Leu Thr Ala 420 425 430 | | | 1296 |
| gcc atc gtg gac gcg ggg aag atc ctc ccc ata agc cag atc ccc gag Ala Ile Val Asp Ala Gly Lys Ile Leu Pro Ile Ser Gln Ile Pro Glu 435 440 445 | | | 1344 |
| gag gcc tac gcc ctc gcc tta gac ctc atc tac gac cgc cgc aag gag Glu Ala Tyr Ala Leu Ala Leu Asp Leu Ile Tyr Asp Arg Arg Lys Glu 450 455 460 | | | 1392 |
| ggc ttt gac ccc ctc ctc gcc ttc atg gcc tac ttt gag gcc cac aag Gly Phe Asp Pro Leu Leu Ala Phe Met Ala Tyr Phe Glu Ala His Lys 465 470 475 480 | | | 1440 |
| gag gac ccg ggg aag agg gag gac gcc ttc ctg gcc ctt ccc ctt ctg Glu Asp Pro Gly Lys Arg Glu Asp Ala Phe Leu Ala Leu Pro Leu Leu 485 490 495 | | | 1488 |
| gag agg ctc aag cgc cgc gtg gtg gag ggg agg aag cag ggc ctc gag Glu Arg Leu Lys Arg Arg Val Val Glu Gly Arg Lys Gln Gly Leu Glu 500 505 510 | | | 1536 |
| gcc gac ctg gag gag gcc ctg aag gcg ggg cac aag ccc ttg gac ctc Ala Asp Leu Glu Glu Ala Leu Lys Ala Gly His Lys Pro Leu Asp Leu 515 520 525 | | | 1584 |
| atc aac ggc ccc ctc ctc gcg ggg atg aag gag gtg ggg gac ctc ttc Ile Asn Gly Pro Leu Leu Ala Gly Met Lys Glu Val Gly Asp Leu Phe 530 535 540 | | | 1632 |
| ggg gcg ggg aag atg cag ctc ccc ttc gtc ctc cag gcc gcc gag gtg Gly Ala Gly Lys Met Gln Leu Pro Phe Val Leu Gln Ala Ala Glu Val 545 550 555 560 | | | 1680 |
| atg aag cgg gcg gtg gcc tac ctc gag ccc cac atg gag aag aag ggg Met Lys Arg Ala Val Ala Tyr Leu Glu Pro His Met Glu Lys Lys Gly 565 570 575 | | | 1728 |
| gag ggc aag ggt acc ctg gtc ctc gcc acc gtc aag ggg gac gtg cac Glu Gly Lys Gly Thr Leu Val Leu Ala Thr Val Lys Gly Asp Val His 580 585 590 | | | 1776 |
| gac atc ggc aag aac ctg gtg gac atc atc ctc agc aac aac ggc tac Asp Ile Gly Lys Asn Leu Val Asp Ile Ile Leu Ser Asn Asn Gly Tyr 595 600 605 | | | 1824 |
| cgg gtg gtg aac ctg ggg atc aag gtg ccc att gag gag atc ctg aag Arg Val Val Asn Leu Gly Ile Lys Val Pro Ile Glu Glu Ile Leu Lys 610 615 620 | | | 1872 |

39

| | |
|---|------|
| gcc gtg gag gcg cac aag ccc cac gcc gtg ggc atg tcg ggc ctc ctg Ala Val Glu Ala His Lys Pro His Ala Val Gly Met Ser Gly Leu Leu 625 630 635 640 | 1920 |
| gtg aag agc acc ctg gtg atg aag gag aac ctg gag tac atg cgg gat Val Lys Ser Thr Leu Val Met Lys Glu Asn Leu Glu Tyr Met Arg Asp 645 650 655 | 1968 |
| agg ggc tac acc ctc ccc gtg atc ctg ggc ggg gcc gcc ctc acc cgg Arg Gly Tyr Thr Leu Pro Val Ile Leu Gly Gly Ala Ala Leu Thr Arg 660 665 670 | 2016 |
| agc tac gtg gag gag ctt aag gcc atc tac ccc aac gtc tac tac gcc Ser Tyr Val Glu Glu Leu Lys Ala Ile Tyr Pro Asn Val Tyr Tyr Ala 675 680 685 | 2064 |
| gag gac gcc ttt gag ggc tta agg ctc atg gag gag ctc acg ggc cac Glu Asp Ala Phe Glu Gly Leu Arg Leu Met Glu Glu Leu Thr Gly His 690 695 700 | 2112 |
| gcc cct ccc gag ctc acc cgg aag gcc cca gct agg ccc aag cgg gag Ala Pro Pro Glu Leu Thr Arg Lys Ala Pro Ala Arg Pro Lys Arg Glu 705 710 715 720 | 2160 |
| gcc ccc aag gtg gcg ccc cgc gct cgg ccc gtg ggg gag gcc ccc gcc Ala Pro Lys Val Ala Pro Arg Ala Arg Pro Val Gly Glu Ala Pro Ala 725 730 735 | 2208 |
| gtc ccc cgg ccc ccc ttc ttc ggc gtg cgg gtg gag gaa ggc ttg gac Val Pro Arg Pro Pro Phe Phe Gly Val Arg Val Glu Glu Gly Leu Asp 740 745 750 | 2256 |
| ctc gcc acc atc gcc cac tac gtc aac aag ctc gcc ctc tac cgg ggc Leu Ala Thr Ile Ala His Tyr Val Asn Lys Leu Ala Leu Tyr Arg Gly 755 760 765 | 2304 |
| cag tgg ggc tac agc cgc aag ggc ttt ccc ggg agg cgt ggc agg ccc Gln Trp Gly Tyr Ser Arg Lys Gly Phe Pro Gly Arg Arg Gly Arg Pro 770 775 780 | 2352 |
| tgg tgg agc ggg agg cgg agc ctg tct tcc aga ggc tcc tca agg agg Trp Trp Ser Gly Arg Arg Ser Leu Ser Ser Arg Gly Ser Ser Arg Arg 785 790 795 800 | 2400 |
| cga tgg cgg aag ggt ggc ttg aac cca agg tcc tct acg gct tct tcc Arg Trp Arg Lys Gly Gly Leu Asn Pro Arg Ser Ser Thr Ala Ser Ser 805 810 815 | 2448 |
| ccg tgg ccc ggg agg gga gga gct tct cgt ctt ctc ccc aga gac ggg Pro Trp Pro Gly Arg Gly Gly Ala Ser Arg Leu Leu Pro Arg Asp Gly 820 825 830 | 2496 |
| gga ggt gct gga gcg ctt ccg ctt ccc ccg gca aag ggg cgg ggg cct Gly Gly Ala Gly Ala Leu Pro Leu Pro Pro Ala Lys Gly Arg Gly Pro 835 840 845 | 2544 |
| gag cct cgt gga cta ctt ccg ccc ccg gtt tgc cgc gcc ttt ggg gga Glu Pro Arg Gly Leu Leu Pro Pro Val Cys Arg Ala Phe Gly Gly 850 855 860 | 2592 |
| cga ggc gga ctg gat gcc caa gga ggc ctt ccg ggc ggg ggc cgg gac Arg Gly Gly Leu Asp Ala Gln Gly Gly Leu Pro Gly Gly Gly Arg Asp 860 | 2640 |

40

| | | | | |
|---|------|------|------|------|
| 865 | 870 | 875 | 880 | |
| gtc ctc ggg gtc cag ctc gtc acc atg ggg gag gcc cct tcc cga aag | | | | 2688 |
| Val Leu Gly Val Gln Leu Val Thr Met Gly Glu Ala Pro Ser Arg Lys | | | | |
| | 885 | 890 | 895 | |
| gcc cag gcc ctc ttt gcg tcc ggg gcc tac cag gac tac ctc ttc gtc | | | | 2736 |
| Ala Gln Ala Leu Phe Ala Ser Gly Ala Tyr Gln Asp Tyr Leu Phe Val | | | | |
| | 900 | 905 | 910 | |
| cac ggc ttc agc gtg gag atg acc gag gcc ttg gcg gag tac tgg cac | | | | 2784 |
| His Gly Phe Ser Val Glu Met Thr Glu Ala Leu Ala Glu Tyr Trp His | | | | |
| | 915 | 920 | 925 | |
| aag agg atg cgg cag atg tgg ggc atc gcc cac aag gac gcc acc gag | | | | 2832 |
| Lys Arg Met Arg Gln Met Trp Gly Ile Ala His Lys Asp Ala Thr Glu | | | | |
| | 930 | 935 | 940 | |
| atc cag aag ctc ttc cag cag ggc tac cag ggg gcc cgc tac tcc ttc | | | | 2880 |
| Ile Gln Lys Leu Phe Gln Gln Gly Tyr Gln Gly Ala Arg Tyr Ser Phe | | | | |
| | 945 | 950 | 955 | 960 |
| ggc tac ccc gcc tgc ccg gac ctc gcc gac cag gcc aag ctg gac cgg | | | | 2928 |
| Gly Tyr Pro Ala Cys Pro Asp Leu Ala Asp Gln Ala Lys Leu Asp Arg | | | | |
| | 965 | 970 | 975 | |
| ctc atg ggc ttc cac cgg gtg ggg gtg cac ctc acg gag aac ttc cag | | | | 2976 |
| Leu Met Gly Phe His Arg Val Gly Val His Leu Thr Glu Asn Phe Gln | | | | |
| | 980 | 985 | 990 | |
| ctg gag ccg gag cac gcc acc agc gcc ctc gtg gtc cac cac ccc gag | | | | 3024 |
| Leu Glu Pro Glu His Ala Thr Ser Ala Leu Val Val His His Pro Glu | | | | |
| | 995 | 1000 | 1005 | |
| gcc cgc tac ttc agc gtg gac tag | | | | 3048 |
| Ala Arg Tyr Phe Ser Val Asp | | | | |
| | 1010 | 1015 | | |

<210> 10
 <211> 1015
 <212> PRT
 <213> Thermus thermophilus

<400> 10
 Met Arg Ala Tyr Lys Glu Ala Ala Arg Gly Leu Leu Lys Gly Gly Val
 1 5 10 15
 Asp Leu Ile Leu Leu Glu Thr Ala Gln Asp Ile Leu Gln Val Arg Cys
 20 25 30
 Ala Val Leu Ala Val Arg Glu Ala Met Ala Glu Val Gly Arg Glu Val
 35 40 45
 Pro Leu Gln Val Gln Val Thr Phe Glu Ala Thr Gly Thr Met Leu Val
 50 55 60
 Gly Thr Asp Glu Gln Ala Ala Leu Ala Ala Leu Glu Ser Leu Pro Val
 65 70 75 80
 Asp Val Val Gly Met Asn Cys Ala Thr Gly Pro Asp Leu Met Asp Ser
 85 90 95

Lys Val Arg Tyr Phe Ala Glu His Ser Thr Arg Phe Val Ser Cys Leu
 100 105 110
 Pro Asn Ala Gly Leu Pro Arg Asn Glu Gly Gly Arg Val Val Tyr Asp
 115 120 125
 Leu Thr Pro Glu Glu Leu Ala Lys Trp His Leu Lys Phe Val Ala Glu
 130 135 140
 Tyr Gly Val Asn Ala Val Gly Gly Cys Cys Gly Thr Gly Pro Glu His
 145 150 155 160
 Ile Arg Lys Val Ala Glu Ala Val Lys Gly Leu Ala Pro Lys Pro Arg
 165 170 175
 Pro Glu Ser Phe Pro Pro Gln Val Ala Ser Leu Tyr Gln Ala Val Ser
 180 185 190
 Leu Lys Gln Glu Ala Ser Leu Phe Leu Val Gly Glu Arg Leu Asn Ala
 195 200 205
 Thr Gly Ser Lys Arg Phe Arg Glu Met Leu Phe Ala Arg Asp Leu Glu
 210 215 220
 Gly Ile Leu Ala Leu Ala Arg Glu Gln Val Glu Glu Gly Ala His Ala
 225 230 235 240
 Leu Asp Leu Ser Val Ala Trp Thr Gly Arg Asp Glu Leu Glu Asp Leu
 245 250 255
 Arg Trp Leu Leu Pro His Leu Ala Thr Ala Leu Thr Val Pro Val Met
 260 265 270
 Val Asp Ser Thr Ser Pro Glu Ala Met Glu Leu Ala Leu Lys Tyr Leu
 275 280 285
 Pro Gly Arg Val Leu Leu Asn Ser Ala Asn Leu Glu Asp Gly Leu Glu
 290 295 300
 Arg Phe Asp Arg Val Ala Ser Leu Ala Lys Ala His Gly Ala Ala Leu
 305 310 315 320
 Val Val Leu Ala Ile Asp Glu Lys Gly Met Ala Lys Thr Arg Glu Glu
 325 330 335
 Lys Val Arg Val Ala Leu Arg Met Tyr Glu Arg Leu Thr Glu His His
 340 345 350
 Gly Leu Arg Pro Glu Asp Leu Leu Phe Asp Leu Leu Thr Phe Pro Ile
 355 360 365
 Thr Gln Gly Asp Glu Glu Ser Arg Pro Leu Ala Lys Glu Thr Leu Leu
 370 375 380
 Ala Ile Glu Glu Leu Arg Glu Arg Leu Pro Gly Val Gly Phe Val Leu
 385 390 395 400
 Arg Val Ser Asn Val Ser Phe Gly Leu Lys Pro Arg Ala Arg Arg Val
 405 410 415
 Leu Asn Ser Val Phe Leu Asp Glu Ala Arg Lys Arg Gly Leu Thr Ala

42

| | | |
|---|-------------------------------------|---------|
| 420 | 425 | 430 |
| Ala Ile Val Asp Ala Gly Lys | Ile Leu Pro Ile Ser Gln Ile Pro Glu | |
| 435 | 440 | 445 |
| Glu Ala Tyr Ala Leu Ala Leu Asp Leu Ile Tyr Asp Arg Arg Lys Glu | | |
| 450 | 455 | 460 |
| Gly Phe Asp Pro Leu Leu Ala Phe Met Ala Tyr Phe Glu Ala His Lys | | |
| 465 | 470 | 475 480 |
| Glu Asp Pro Gly Lys Arg Glu Asp Ala Phe Leu Ala Leu Pro Leu Leu | | |
| | 485 | 490 495 |
| Glu Arg Leu Lys Arg Arg Val Val Glu Gly Arg Lys Gln Gly Leu Glu | | |
| | 500 | 505 510 |
| Ala Asp Leu Glu Glu Ala Leu Lys Ala Gly His Lys Pro Leu Asp Leu | | |
| | 515 | 520 525 |
| Ile Asn Gly Pro Leu Leu Ala Gly Met Lys Glu Val Gly Asp Leu Phe | | |
| | 530 | 535 540 |
| Gly Ala Gly Lys Met Gln Leu Pro Phe Val Leu Gln Ala Ala Glu Val | | |
| 545 | 550 | 555 560 |
| Met Lys Arg Ala Val Ala Tyr Leu Glu Pro His Met Glu Lys Lys Gly | | |
| | 565 | 570 575 |
| Glu Gly Lys Gly Thr Leu Val Leu Ala Thr Val Lys Gly Asp Val His | | |
| | 580 | 585 590 |
| Asp Ile Gly Lys Asn Leu Val Asp Ile Ile Leu Ser Asn Asn Gly Tyr | | |
| | 595 | 600 605 |
| Arg Val Val Asn Leu Gly Ile Lys Val Pro Ile Glu Glu Ile Leu Lys | | |
| | 610 | 615 620 |
| Ala Val Glu Ala His Lys Pro His Ala Val Gly Met Ser Gly Leu Leu | | |
| 625 | 630 | 635 640 |
| Val Lys Ser Thr Leu Val Met Lys Glu Asn Leu Glu Tyr Met Arg Asp | | |
| | 645 | 650 655 |
| Arg Gly Tyr Thr Leu Pro Val Ile Leu Gly Gly Ala Ala Leu Thr Arg | | |
| | 660 | 665 670 |
| Ser Tyr Val Glu Glu Leu Lys Ala Ile Tyr Pro Asn Val Tyr Tyr Ala | | |
| | 675 | 680 685 |
| Glu Asp Ala Phe Glu Gly Leu Arg Leu Met Glu Glu Leu Thr Gly His | | |
| | 690 | 695 700 |
| Ala Pro Pro Glu Leu Thr Arg Lys Ala Pro Ala Arg Pro Lys Arg Glu | | |
| 705 | 710 | 715 720 |
| Ala Pro Lys Val Ala Pro Arg Ala Arg Pro Val Gly Glu Ala Pro Ala | | |
| | 725 | 730 735 |
| Val Pro Arg Pro Pro Phe Phe Gly Val Arg Val Glu Glu Gly Leu Asp | | |
| | 740 | 745 750 |

43

Leu Ala Thr Ile Ala His Tyr Val Asn Lys Leu Ala Leu Tyr Arg Gly
 755 760 765
 Gln Trp Gly Tyr Ser Arg Lys Gly Phe Pro Gly Arg Arg Gly Arg Pro
 770 775 780
 Trp Trp Ser Gly Arg Arg Ser Leu Ser Ser Arg Gly Ser Ser Arg Arg
 785 790 795 800
 Arg Trp Arg Lys Gly Gly Leu Asn Pro Arg Ser Ser Thr Ala Ser Ser
 805 810 815
 Pro Trp Pro Gly Arg Gly Gly Ala Ser Arg Leu Leu Pro Arg Asp Gly
 820 825 830
 Gly Gly Ala Gly Ala Leu Pro Leu Pro Pro Ala Lys Gly Arg Gly Pro
 835 840 845
 Glu Pro Arg Gly Leu Leu Pro Pro Pro Val Cys Arg Ala Phe Gly Gly
 850 855 860
 Arg Gly Gly Leu Asp Ala Gln Gly Gly Leu Pro Gly Gly Gly Arg Asp
 865 870 875 880
 Val Leu Gly Val Gln Leu Val Thr Met Gly Glu Ala Pro Ser Arg Lys
 885 890 895
 Ala Gln Ala Leu Phe Ala Ser Gly Ala Tyr Gln Asp Tyr Leu Phe Val
 900 905 910
 His Gly Phe Ser Val Glu Met Thr Glu Ala Leu Ala Glu Tyr Trp His
 915 920 925
 Lys Arg Met Arg Gln Met Trp Gly Ile Ala His Lys Asp Ala Thr Glu
 930 935 940
 Ile Gln Lys Leu Phe Gln Gln Gly Tyr Gln Gly Ala Arg Tyr Ser Phe
 945 950 955 960
 Gly Tyr Pro Ala Cys Pro Asp Leu Ala Asp Gln Ala Lys Leu Asp Arg
 965 970 975
 Leu Met Gly Phe His Arg Val Gly Val His Leu Thr Glu Asn Phe Gln
 980 985 990
 Leu Glu Pro Glu His Ala Thr Ser Ala Leu Val Val His His Pro Glu
 995 1000 1005
 Ala Arg Tyr Phe Ser Val Asp
 1010 1015

<210> 11

<211> 3441

<212> DNA

<213> Bacillus halodurans

<220>

<221> CDS

<222> (1) .. (3438)

<223> RHD05550

44

<400> 11

| | |
|---|-----|
| atg act aaa tcg ttg ttt gaa caa cag tta gag cga aaa atc gtc atc | 48 |
| Met Thr Lys Ser Leu Phe Glu Gln Gln Leu Glu Arg Lys Ile Val Ile | |
| 1 5 10 15 | |
| ctt gat ggg gcg atg ggg acc atg tta caa gcc gcg aat cta acc gct | 96 |
| Leu Asp Gly Ala Met Gly Thr Met Leu Gln Ala Ala Asn Leu Thr Ala | |
| 20 25 30 | |
| gat gac ttt ggc gga gaa gag tat gaa ggg tgt aat gaa tat tta aat | 144 |
| Asp Asp Phe Gly Gly Glu Glu Tyr Glu Gly Cys Asn Glu Tyr Leu Asn | |
| 35 40 45 | |
| gag acg gcc ccc cat gtc gtt gag gac att cat cgc gca tac tta gag | 192 |
| Glu Thr Ala Pro His Val Val Glu Asp Ile His Arg Ala Tyr Leu Glu | |
| 50 55 60 | |
| gca gga gca gac gtc att gcg acg aac acg ttc ggg gca aca gat atc | 240 |
| Ala Gly Ala Asp Val Ile Ala Thr Asn Thr Phe Gly Ala Thr Asp Ile | |
| 65 70 75 80 | |
| gtt ctt gac gat tat gat ctc gga tac aaa gca gag gag tta aac ata | 288 |
| Val Leu Asp Asp Tyr Asp Leu Gly Tyr Lys Ala Glu Glu Leu Asn Ile | |
| 85 90 95 | |
| tgc gcg gtg aaa atc gct aaa cgt gta gct gaa gag ttt tcc act cca | 336 |
| Cys Ala Val Lys Ile Ala Lys Arg Val Ala Glu Glu Phe Ser Thr Pro | |
| 100 105 110 | |
| gat tgg cct cga ttc gtt gca ggg gcg atg ggg ccg acg acg aaa tct | 384 |
| Asp Trp Pro Arg Phe Val Ala Gly Ala Met Gly Pro Thr Thr Lys Ser | |
| 115 120 125 | |
| ctt tcc gtc aca ggg ggc gcg aca ttc gaa caa ctt atc gag tct tat | 432 |
| Leu Ser Val Thr Gly Gly Ala Thr Phe Glu Gln Leu Ile Glu Ser Tyr | |
| 130 135 140 | |
| cgc cag caa gct aca ggt cta att aaa ggc ggg gcg gat att tta tta | 480 |
| Arg Gln Gln Ala Thr Gly Leu Ile Lys Gly Gly Ala Asp Ile Leu Leu | |
| 145 150 155 160 | |
| ctc gaa acg agc cag gat atg cga aac gtg aag gcg gct tat tta gga | 528 |
| Leu Glu Thr Ser Gln Asp Met Arg Asn Val Lys Ala Ala Tyr Leu Gly | |
| 165 170 175 | |
| ctg agc caa gcg caa aaa gag cta gag gtg aaa ctg cct ctc att att | 576 |
| Leu Ser Gln Ala Gln Lys Glu Leu Glu Val Lys Leu Pro Leu Ile Ile | |
| 180 185 190 | |
| tct gga acg att gaa ccg atg gga aca acg ctc gcc ggc caa aac atc | 624 |
| Ser Gly Thr Ile Glu Pro Met Gly Thr Thr Leu Ala Gly Gln Asn Ile | |
| 195 200 205 | |
| gag gcg ttc tat ttg tca tta gag cat atg aat ccc gtc gtt gtc ggt | 672 |
| Glu Ala Phe Tyr Leu Ser Leu Glu His Met Asn Pro Val Val Val Gly | |
| 210 215 220 | |
| ctc aac tgc gct aca gga cca gaa ttt atg cgc gat cac ctc cgt tct | 720 |
| Leu Asn Cys Ala Thr Gly Pro Glu Phe Met Arg Asp His Leu Arg Ser | |
| 225 230 235 240 | |
| ctt tca gac ctt gcg acc tgc tct gta agc tgt tat ccg aat gct ggg | 768 |

45

| | |
|---|-------------|
| Leu Ser Asp Leu Ala Thr Cys Ser Val Ser Cys Tyr Pro Asn Ala Gly | |
| 245 | 250 255 |
| tta cct gat gaa gag ggg aac tat cac gaa tcc cca gaa tca tta gca | 816 |
| Leu Pro Asp Glu Glu Gly Asn Tyr His Glu Ser Pro Glu Ser Leu Ala | |
| 260 | 265 270 |
| gcc aag ctc gca ggt ttt gcg gaa aag ggc tgg ttg aat atg gtt ggt | 864 |
| Ala Lys Leu Ala Gly Phe Ala Glu Lys Gly Trp Leu Asn Met Val Gly | |
| 275 | 280 285 |
| ggc tgt tgc ggg acg act cca gac cac att cgt gct ctt ttg gac gtt | 912 |
| Gly Cys Cys Gly Thr Thr Pro Asp His Ile Arg Ala Leu Leu Asp Val | |
| 290 | 295 300 |
| atg aag caa ttt gag ccg aga caa cca aaa ggg gat cac ccc cac tcg | 960 |
| Met Lys Gln Phe Glu Pro Arg Gln Pro Lys Gly Asp His Pro His Ser | |
| 305 | 310 315 320 |
| gtc tca gga att gag cca ctg tta tac gat gac agc atg cgt cca cta | 1008 |
| Val Ser Gly Ile Glu Pro Leu Leu Tyr Asp Asp Ser Met Arg Pro Leu | |
| 325 | 330 335 |
| ttt gtc ggt gaa cgg aca aac gtc atc ggg tct cgt aaa ttt aaa cgg | 1056 |
| Phe Val Gly Glu Arg Thr Asn Val Ile Gly Ser Arg Lys Phe Lys Arg | |
| 340 | 345 350 |
| ttg atc gaa gaa gaa aaa tat gaa gaa gcc tca gaa att gca aga tcc | 1104 |
| Leu Ile Glu Glu Glu Lys Tyr Glu Glu Ala Ser Glu Ile Ala Arg Ser | |
| 355 | 360 365 |
| caa gtg aag aaa ggg gcc cac gtt atc gat gtt tgt ctt gct gat ccg | 1152 |
| Gln Val Lys Lys Gly Ala His Val Ile Asp Val Cys Leu Ala Asp Pro | |
| 370 | 375 380 |
| gat cgc gat gaa atg gag gac atg gag gaa ttt tta aaa ttc gtg atc | 1200 |
| Asp Arg Asp Glu Met Glu Asp Met Glu Glu Phe Leu Lys Phe Val Ile | |
| 385 | 390 395 400 |
| aac aaa gtg aag gta ccg ctc atg att gac tcc acc gac gaa aag gta | 1248 |
| Asn Lys Val Lys Val Pro Leu Met Ile Asp Ser Thr Asp Glu Lys Val | |
| 405 | 410 415 |
| att gaa caa gcg ctt acg tat tca caa ggg aaa gcg atc att aat tcg | 1296 |
| Ile Glu Gln Ala Leu Thr Tyr Ser Gln Gly Lys Ala Ile Ile Asn Ser | |
| 420 | 425 430 |
| atc aac tta gag gac ggc gaa gaa cgt ttt gaa aaa gtg gtc ccg ctc | 1344 |
| Ile Asn Leu Glu Asp Gly Glu Glu Arg Phe Glu Lys Val Val Pro Leu | |
| 435 | 440 445 |
| gtc cat aag tat gga gcc gcg gtt gtc gtt ggt acg atc gac gaa gaa | 1392 |
| Val His Lys Tyr Gly Ala Ala Val Val Val Gly Thr Ile Asp Glu Glu | |
| 450 | 455 460 |
| gga atg gcg att acg gca gaa aaa aaa tta gcg gtt gcg aaa cga tca | 1440 |
| Gly Met Ala Ile Thr Ala Glu Lys Lys Leu Ala Val Ala Lys Arg Ser | |
| 465 | 470 475 480 |
| tac gac ctg ctc gta aac aaa tac aac att cgt ccg agc gat att att | 1488 |
| Tyr Asp Leu Leu Val Asn Lys Tyr Asn Ile Arg Pro Ser Asp Ile Ile | |
| 485 | 490 495 |

| | |
|---|------|
| ttt gat ccg ctc gtg ttc cca gta gga aca ggc gat gag caa tac att | 1536 |
| Phe Asp Pro Leu Val Phe Pro Val Gly Thr Gly Asp Glu Gln Tyr Ile | |
| 500 505 510 | |
| ggc tcg gcg aat gag acg gtg gaa gga att agg agg atc aaa gaa gag | 1584 |
| Gly Ser Ala Asn Glu Thr Val Glu Gly Ile Arg Arg Ile Lys Glu Glu | |
| 515 520 525 | |
| ctc cct gaa tgt tta acg att ctt gga gtt agt aac gtg tcg ttc ggt | 1632 |
| Leu Pro Glu Cys Leu Thr Ile Leu Gly Val Ser Asn Val Ser Phe Gly | |
| 530 535 540 | |
| ctt ccg cct gtc gga aga gag gtg ctg aac gcg gcg tac tta tac cat | 1680 |
| Leu Pro Pro Val Gly Arg Glu Val Leu Asn Ala Ala Tyr Leu Tyr His | |
| 545 550 555 560 | |
| tgt aca caa gct ggc ctt gat tac gct atc gtg aac aca gaa aag ctt | 1728 |
| Cys Thr Gln Ala Gly Leu Asp Tyr Ala Ile Val Asn Thr Glu Lys Leu | |
| 565 570 575 | |
| gag cgt tat gcc tcg att tct gat gaa gaa aaa gaa ttg tca agg aag | 1776 |
| Glu Arg Tyr Ala Ser Ile Ser Asp Glu Glu Lys Glu Leu Ser Arg Lys | |
| 580 585 590 | |
| ctc tta ttt gaa acg aca gat gaa acg ctc gct gag ttc acc gcc ttt | 1824 |
| Leu Leu Phe Glu Thr Thr Asp Glu Thr Leu Ala Glu Phe Thr Ala Phe | |
| 595 600 605 | |
| tat cga ggg aaa aaa gca gag aaa aaa gtg gag act tct aat tta act | 1872 |
| Tyr Arg Gly Lys Lys Ala Glu Lys Lys Val Glu Thr Ser Asn Leu Thr | |
| 610 615 620 | |
| ttg gaa gag cgg ttg gca aac tac att gtt gaa ggg tca aag gac gga | 1920 |
| Leu Glu Glu Arg Leu Ala Asn Tyr Ile Val Glu Gly Ser Lys Asp Gly | |
| 625 630 635 640 | |
| ctg aca gaa gat tta gat aaa gcg ctc gcg aaa tat gat gat ccg ctt | 1968 |
| Leu Thr Glu Asp Leu Asp Lys Ala Leu Ala Lys Tyr Asp Asp Pro Leu | |
| 645 650 655 | |
| gat atc att aac ggc ccg ctc atg aat gga atg gac gaa gtc ggt cgt | 2016 |
| Asp Ile Ile Asn Gly Pro Leu Met Asn Gly Met Asp Glu Val Gly Arg | |
| 660 665 670 | |
| ttg ttt aac aat aac gag ctt att gtc gct gaa gta ttg caa agc gct | 2064 |
| Leu Phe Asn Asn Asn Glu Leu Ile Val Ala Glu Val Leu Gln Ser Ala | |
| 675 680 685 | |
| gag gtt atg aag gct tcc gtc gcc cac ctt gag cca cat atg gaa aag | 2112 |
| Glu Val Met Lys Ala Ser Val Ala His Leu Glu Pro His Met Glu Lys | |
| 690 695 700 | |
| aaa gca gac gat cat gga aaa gga aaa atc att ctt gcc acg gtc aag | 2160 |
| Lys Ala Asp Asp His Gly Lys Gly Lys Ile Ile Leu Ala Thr Val Lys | |
| 705 710 715 720 | |
| ggc gat gtt cac gat atc ggg aaa aat cta gtg gaa att att ttg agc | 2208 |
| Gly Asp Val His Asp Ile Gly Lys Asn Leu Val Glu Ile Ile Leu Ser | |
| 725 730 735 | |
| aat aat ggt ttc cgc atc gtg aac cta gga att aaa gtt acc tct aat | 2256 |

47

| | |
|---|------|
| Asn Asn Gly Phe Arg Ile Val Asn Leu Gly Ile Lys Val Thr Ser Asn | |
| 740 745 750 | |
| gag ctg att gaa gcg gtg gcg aga gaa aat cca gat gcg att ggc ttg | 2304 |
| Glu Leu Ile Glu Ala Val Ala Arg Glu Asn Pro Asp Ala Ile Gly Leu | |
| 755 760 765 | |
| tca ggg ttg ctc gtc aaa tca gca caa caa atg gta ctt acc gcc caa | 2352 |
| Ser Gly Leu Leu Val Lys Ser Ala Gln Gln Met Val Leu Thr Ala Gln | |
| 770 775 780 | |
| gat ttg aag caa caa caa att tcc att ccg att tta gtc gga ggc gca | 2400 |
| Asp Leu Lys Gln Gln Ile Ser Ile Pro Ile Leu Val Gly Gly Ala | |
| 785 790 795 800 | |
| gcc ctt acg cgg aaa ttt acg aat aca aaa atc gct cca gag tat gat | 2448 |
| Ala Leu Thr Arg Lys Phe Thr Asn Thr Lys Ile Ala Pro Glu Tyr Asp | |
| 805 810 815 | |
| ggt ctc gtc gtc tac gcg aag gat gcg atg aac ggg tta gag ctt gcc | 2496 |
| Gly Leu Val Val Tyr Ala Lys Asp Ala Met Asn Gly Leu Glu Leu Ala | |
| 820 825 830 | |
| aat aaa tta atg aaa cct gat gaa cga gaa aag cta gcg gtc tcc ctc | 2544 |
| Asn Lys Leu Met Lys Pro Asp Glu Arg Glu Lys Leu Ala Val Ser Leu | |
| 835 840 845 | |
| cat gaa gcg aag gag cag gcg aac tcg agg aca caa atg gga gga ggc | 2592 |
| His Glu Ala Lys Glu Gln Ala Asn Ser Arg Thr Gln Met Gly Gly Gly | |
| 850 855 860 | |
| gga act gca gtt gcg gta aag ccg act cga tcc cat gtt tcg aca acg | 2640 |
| Gly Thr Ala Val Ala Val Lys Pro Thr Arg Ser His Val Ser Thr Thr | |
| 865 870 875 880 | |
| gtg cct gta gcg gtc cca cct gat gtg aag ccg cac att ttg cgc cac | 2688 |
| Val Pro Val Ala Val Pro Pro Asp Val Lys Pro His Ile Leu Arg His | |
| 885 890 895 | |
| cat agc att gcc cat tta gag ccg tat att aac atg cag atg ttg tta | 2736 |
| His Ser Ile Ala His Leu Glu Pro Tyr Ile Asn Met Gln Met Leu Leu | |
| 900 905 910 | |
| gga cgt cac tta ggc tta caa ggg aaa gtg agc cgc ctg ctt gca gaa | 2784 |
| Gly Arg His Leu Gly Leu Gln Gly Lys Val Ser Arg Leu Leu Ala Glu | |
| 915 920 925 | |
| aaa gac gag aag gct ctt gaa tta aaa gaa aaa gtt gat gcg cta ctc | 2832 |
| Lys Asp Glu Lys Ala Leu Glu Leu Lys Glu Lys Val Asp Ala Leu Leu | |
| 930 935 940 | |
| acc agg gtg aaa gag gag cag ctc atg gaa gcc cat ggc atg tat cag | 2880 |
| Thr Arg Val Lys Glu Glu Gln Leu Met Glu Ala His Gly Met Tyr Gln | |
| 945 950 955 960 | |
| ttt ttt cct gcc cag tcg gat ggg gac gat att gtc att tat gat caa | 2928 |
| Phe Phe Pro Ala Gln Ser Asp Gly Asp Asp Ile Val Ile Tyr Asp Gln | |
| 965 970 975 | |
| acg gga aca aat gaa atc gag cga ttc cat ttt ccg cgt cag aat aag | 2976 |
| Thr Gly Thr Asn Glu Ile Glu Arg Phe His Phe Pro Arg Gln Asn Lys | |
| 980 985 990 | |

gag cct tat ctg tgt ctt gcc gat ttc ctt cgc cca gtt tcc agt ggg 3024
 Glu Pro Tyr Leu Cys Leu Ala Asp Phe Leu Arg Pro Val Ser Ser Gly
 995 1000 1005

gaa atg gac tat gtt ggc ttc ctt gct gta acc gca gga aaa ggc att 3072
 Glu Met Asp Tyr Val Gly Phe Leu Ala Val Thr Ala Gly Lys Gly Ile
 1010 1015 1020

cgt gaa tta ggg gag cag gcg aaa gag gct gga gac tat tta ttc agt 3120
 Arg Glu Leu Gly Glu Gln Ala Lys Glu Ala Gly Asp Tyr Leu Phe Ser
 1025 1030 1035 1040

cac tta atc caa gca aca gcc tta gag atg gcg gaa ggg ttt gcc gag 3168
 His Leu Ile Gln Ala Thr Ala Leu Glu Met Ala Glu Gly Phe Ala Glu
 1045 1050 1055

cgt gtc cat cag ctc atg cgt gat aag tgg ggg ttt cct gat tcg gct 3216
 Arg Val His Gln Leu Met Arg Asp Lys Trp Gly Phe Pro Asp Ser Ala
 1060 1065 1070

gac ttt aca atg gaa gag cgt ttc gct gca aaa tac cgt ggc atc cgt 3264
 Asp Phe Thr Met Glu Glu Arg Phe Ala Ala Lys Tyr Arg Gly Ile Arg
 1075 1080 1085

gta tcg ttt ggc tac cct gca tgc cct gac ttg gat gac caa gca aag 3312
 Val Ser Phe Gly Tyr Pro Ala Cys Pro Asp Leu Asp Asp Gln Ala Lys
 1090 1095 1100

ttg ttt aag ctg ttg aag cct gga aag atc gga att gag ttg acg gaa 3360
 Leu Phe Lys Leu Leu Lys Pro Gly Lys Ile Gly Ile Glu Leu Thr Glu
 1105 1110 1115 1120

ggg ttt atg atg gag cca gaa gcc tcc gtc acc gcg atg gtg ttt gcc 3408
 Gly Phe Met Met Glu Pro Glu Ala Ser Val Thr Ala Met Val Phe Ala
 1125 1130 1135

cat cct gag gct cgc tat ttt aat gtt tta tag 3441
 His Pro Glu Ala Arg Tyr Phe Asn Val Leu
 1140 1145

<210> 12
 <211> 1146
 <212> PRT
 <213> Bacillus halodurans

<400> 12
 Met Thr Lys Ser Leu Phe Glu Gln Gln Leu Glu Arg Lys Ile Val Ile
 1 5 10 15
 Leu Asp Gly Ala Met Gly Thr Met Leu Gln Ala Ala Asn Leu Thr Ala
 20 25 30
 Asp Asp Phe Gly Gly Glu Glu Tyr Glu Gly Cys Asn Glu Tyr Leu Asn
 35 40 45
 Glu Thr Ala Pro His Val Val Glu Asp Ile His Arg Ala Tyr Leu Glu
 50 55 60
 Ala Gly Ala Asp Val Ile Ala Thr Asn Thr Phe Gly Ala Thr Asp Ile
 65 70 75 80

Val Leu Asp Asp Tyr Asp Leu Gly Tyr Lys Ala Glu Glu Leu Asn Ile
 85 90 95
 Cys Ala Val Lys Ile Ala Lys Arg Val Ala Glu Glu Phe Ser Thr Pro
 100 105 110
 Asp Trp Pro Arg Phe Val Ala Gly Ala Met Gly Pro Thr Thr Lys Ser
 115 120 125
 Leu Ser Val Thr Gly Gly Ala Thr Phe Glu Gln Leu Ile Glu Ser Tyr
 130 135 140
 Arg Gln Gln Ala Thr Gly Leu Ile Lys Gly Gly Ala Asp Ile Leu Leu
 145 150 155 160
 Leu Glu Thr Ser Gln Asp Met Arg Asn Val Lys Ala Ala Tyr Leu Gly
 165 170 175
 Leu Ser Gln Ala Gln Lys Glu Leu Glu Val Lys Leu Pro Leu Ile Ile
 180 185 190
 Ser Gly Thr Ile Glu Pro Met Gly Thr Thr Leu Ala Gly Gln Asn Ile
 195 200 205
 Glu Ala Phe Tyr Leu Ser Leu Glu His Met Asn Pro Val Val Val Gly
 210 215 220
 Leu Asn Cys Ala Thr Gly Pro Glu Phe Met Arg Asp His Leu Arg Ser
 225 230 235 240
 Leu Ser Asp Leu Ala Thr Cys Ser Val Ser Cys Tyr Pro Asn Ala Gly
 245 250 255
 Leu Pro Asp Glu Glu Gly Asn Tyr His Glu Ser Pro Glu Ser Leu Ala
 260 265 270
 Ala Lys Leu Ala Gly Phe Ala Glu Lys Gly Trp Leu Asn Met Val Gly
 275 280 285
 Gly Cys Cys Gly Thr Thr Pro Asp His Ile Arg Ala Leu Leu Asp Val
 290 295 300
 Met Lys Gln Phe Glu Pro Arg Gln Pro Lys Gly Asp His Pro His Ser
 305 310 315 320
 Val Ser Gly Ile Glu Pro Leu Leu Tyr Asp Asp Ser Met Arg Pro Leu
 325 330 335
 Phe Val Gly Glu Arg Thr Asn Val Ile Gly Ser Arg Lys Phe Lys Arg
 340 345 350
 Leu Ile Glu Glu Glu Lys Tyr Glu Glu Ala Ser Glu Ile Ala Arg Ser
 355 360 365
 Gln Val Lys Lys Gly Ala His Val Ile Asp Val Cys Leu Ala Asp Pro
 370 375 380
 Asp Arg Asp Glu Met Glu Asp Met Glu Glu Phe Leu Lys Phe Val Ile
 385 390 395 400
 Asn Lys Val Lys Val Pro Leu Met Ile Asp Ser Thr Asp Glu Lys Val

50

| | | |
|---|-----|-----|
| 405 | 410 | 415 |
| Ile Glu Gln Ala Leu Thr Tyr Ser Gln Gly Lys Ala Ile Ile Asn Ser | | |
| 420 | 425 | 430 |
| Ile Asn Leu Glu Asp Gly Glu Glu Arg Phe Glu Lys Val Val Pro Leu | | |
| 435 | 440 | 445 |
| Val His Lys Tyr Gly Ala Ala Val Val Val Gly Thr Ile Asp Glu Glu | | |
| 450 | 455 | 460 |
| Gly Met Ala Ile Thr Ala Glu Lys Lys Leu Ala Val Ala Lys Arg Ser | | |
| 465 | 470 | 475 |
| Tyr Asp Leu Leu Val Asn Lys Tyr Asn Ile Arg Pro Ser Asp Ile Ile | | |
| 485 | 490 | 495 |
| Phe Asp Pro Leu Val Phe Pro Val Gly Thr Gly Asp Glu Gln Tyr Ile | | |
| 500 | 505 | 510 |
| Gly Ser Ala Asn Glu Thr Val Glu Gly Ile Arg Arg Ile Lys Glu Glu | | |
| 515 | 520 | 525 |
| Leu Pro Glu Cys Leu Thr Ile Leu Gly Val Ser Asn Val Ser Phe Gly | | |
| 530 | 535 | 540 |
| Leu Pro Pro Val Gly Arg Glu Val Leu Asn Ala Ala Tyr Leu Tyr His | | |
| 545 | 550 | 555 |
| Cys Thr Gln Ala Gly Leu Asp Tyr Ala Ile Val Asn Thr Glu Lys Leu | | |
| 565 | 570 | 575 |
| Glu Arg Tyr Ala Ser Ile Ser Asp Glu Glu Lys Glu Leu Ser Arg Lys | | |
| 580 | 585 | 590 |
| Leu Leu Phe Glu Thr Thr Asp Glu Thr Leu Ala Glu Phe Thr Ala Phe | | |
| 595 | 600 | 605 |
| Tyr Arg Gly Lys Lys Ala Glu Lys Lys Val Glu Thr Ser Asn Leu Thr | | |
| 610 | 615 | 620 |
| Leu Glu Glu Arg Leu Ala Asn Tyr Ile Val Glu Gly Ser Lys Asp Gly | | |
| 625 | 630 | 635 |
| Leu Thr Glu Asp Leu Asp Lys Ala Leu Ala Lys Tyr Asp Asp Pro Leu | | |
| 645 | 650 | 655 |
| Asp Ile Ile Asn Gly Pro Leu Met Asn Gly Met Asp Glu Val Gly Arg | | |
| 660 | 665 | 670 |
| Leu Phe Asn Asn Asn Glu Leu Ile Val Ala Glu Val Leu Gln Ser Ala | | |
| 675 | 680 | 685 |
| Glu Val Met Lys Ala Ser Val Ala His Leu Glu Pro His Met Glu Lys | | |
| 690 | 695 | 700 |
| Lys Ala Asp Asp His Gly Lys Gly Lys Ile Ile Leu Ala Thr Val Lys | | |
| 705 | 710 | 715 |
| Gly Asp Val His Asp Ile Gly Lys Asn Leu Val Glu Ile Ile Leu Ser | | |
| 725 | 730 | 735 |

51

Asn Asn Gly Phe Arg Ile Val Asn Leu Gly Ile Lys Val Thr Ser Asn
 740 745 750
 Glu Leu Ile Glu Ala Val Ala Arg Glu Asn Pro Asp Ala Ile Gly Leu
 755 760 765
 Ser Gly Leu Leu Val Lys Ser Ala Gln Gln Met Val Leu Thr Ala Gln
 770 775 780
 Asp Leu Lys Gln Gln Gln Ile Ser Ile Pro Ile Leu Val Gly Gly Ala
 785 790 795 800
 Ala Leu Thr Arg Lys Phe Thr Asn Thr Lys Ile Ala Pro Glu Tyr Asp
 805 810 815
 Gly Leu Val Val Tyr Ala Lys Asp Ala Met Asn Gly Leu Glu Leu Ala
 820 825 830
 Asn Lys Leu Met Lys Pro Asp Glu Arg Glu Lys Leu Ala Val Ser Leu
 835 840 845
 His Glu Ala Lys Glu Gln Ala Asn Ser Arg Thr Gln Met Gly Gly Gly
 850 855 860
 Gly Thr Ala Val Ala Val Lys Pro Thr Arg Ser His Val Ser Thr Thr
 865 870 875 880
 Val Pro Val Ala Val Pro Pro Asp Val Lys Pro His Ile Leu Arg His
 885 890 895
 His Ser Ile Ala His Leu Glu Pro Tyr Ile Asn Met Gln Met Leu Leu
 900 905 910
 Gly Arg His Leu Gly Leu Gln Gly Lys Val Ser Arg Leu Leu Ala Glu
 915 920 925
 Lys Asp Glu Lys Ala Leu Glu Leu Lys Glu Lys Val Asp Ala Leu Leu
 930 935 940
 Thr Arg Val Lys Glu Glu Gln Leu Met Glu Ala His Gly Met Tyr Gln
 945 950 955 960
 Phe Phe Pro Ala Gln Ser Asp Gly Asp Asp Ile Val Ile Tyr Asp Gln
 965 970 975
 Thr Gly Thr Asn Glu Ile Glu Arg Phe His Phe Pro Arg Gln Asn Lys
 980 985 990
 Glu Pro Tyr Leu Cys Leu Ala Asp Phe Leu Arg Pro Val Ser Ser Gly
 995 1000 1005
 Glu Met Asp Tyr Val Gly Phe Leu Ala Val Thr Ala Gly Lys Gly Ile
 1010 1015 1020
 Arg Glu Leu Gly Glu Gln Ala Lys Glu Ala Gly Asp Tyr Leu Phe Ser
 1025 1030 1035 1040
 His Leu Ile Gln Ala Thr Ala Leu Glu Met Ala Glu Gly Phe Ala Glu
 1045 1050 1055
 Arg Val His Gln Leu Met Arg Asp Lys Trp Gly Phe Pro Asp Ser Ala
 1060 1065 1070

52

Asp Phe Thr Met Glu Glu Arg Phe Ala Ala Lys Tyr Arg Gly Ile Arg
 1075 1080 1085

Val Ser Phe Gly Tyr Pro Ala Cys Pro Asp Leu Asp Asp Gln Ala Lys
 1090 1095 1100

Leu Phe Lys Leu Leu Lys Pro Gly Lys Ile Gly Ile Glu Leu Thr Glu
 1105 1110 1115 1120

Gly Phe Met Met Glu Pro Glu Ala Ser Val Thr Ala Met Val Phe Ala
 1125 1130 1135

His Pro Glu Ala Arg Tyr Phe Asn Val Leu
 1140 1145

<210> 13

<211> 3411

<212> DNA

<213> Bacillus stearothermophilus

<220>

<221> CDS

<222> (1) .. (3408)

<223> RBE02044

<400> 13

| | |
|---|-----|
| atg gct aac gtc acc tta gaa cag caa ctg caa aga aaa att ctt gtc | 48 |
| Met Ala Asn Val Thr Leu Glu Gln Gln Leu Gln Arg Lys Ile Leu Val | |
| 1 5 10 15 | |
| atc gat ggc gcc atg ggc acg atg atc caa agc gcc aac cta tcg gcc | 96 |
| Ile Asp Gly Ala Met Gly Thr Met Ile Gln Ser Ala Asn Leu Ser Ala | |
| 20 25 30 | |
| gcc gac ttt ggc ggc gag gcg tat gaa ggg tgc aac gaa tat ttg acc | 144 |
| Ala Asp Phe Gly Gly Glu Ala Tyr Glu Gly Cys Asn Glu Tyr Leu Thr | |
| 35 40 45 | |
| ctc acc gcc ccg cat gtc atc cgc cgc att cat gaa gcg tac cta gaa | 192 |
| Leu Thr Ala Pro His Val Ile Arg Arg Ile His Glu Ala Tyr Leu Glu | |
| 50 55 60 | |
| gcc ggt gct gat atc att gaa acg aac acg ttc gga gcg aca cgc atc | 240 |
| Ala Gly Ala Asp Ile Ile Glu Thr Asn Thr Phe Gly Ala Thr Arg Ile | |
| 65 70 75 80 | |
| gtg ctt gac gaa tat ggc ctc ggt cat ttg gcg ctt gag ctg aac atc | 288 |
| Val Leu Asp Glu Tyr Gly Leu Gly His Leu Ala Leu Glu Leu Asn Ile | |
| 85 90 95 | |
| gaa gcg gcc aaa ctc gcc aaa caa acg gct gag tcg ttc tcc acc ccg | 336 |
| Glu Ala Ala Lys Leu Ala Lys Gln Thr Ala Glu Ser Phe Ser Thr Pro | |
| 100 105 110 | |
| gac tgg ccg cgc ttt gtc gcc ggt tcg atg ggg ccg acg acg aaa acg | 384 |
| Asp Trp Pro Arg Phe Val Ala Gly Ser Met Gly Pro Thr Thr Lys Thr | |
| 115 120 125 | |
| ttg tcg gtg aca ggc ggc gca acg ttt gaa gaa ctc gtc gcc gcc tac | 432 |
| Leu Ser Val Thr Gly Gly Ala Thr Phe Glu Glu Leu Val Ala Ala Tyr | |

53

| | | | |
|---|-----|-----|------|
| 130 | 135 | 140 | |
| gaa gaa caa gcg cgc gga ctg ctc tta gga ggc gtc gac ctt ctc cta | | | 480 |
| Glu Glu Gln Ala Arg Gly Leu Leu Leu Gly Gly Val Asp Leu Leu Leu | | | |
| 145 | 150 | 155 | 160 |
| ctc gag acg tgc caa gat acg ctg aat gtc aaa gcc ggt ttt ctc ggc | | | 528 |
| Leu Glu Thr Cys Gln Asp Thr Leu Asn Val Lys Ala Gly Phe Leu Gly | | | |
| 165 | 170 | 175 | |
| att tcg aag gcg ttt gaa gcg gtc ggc cgc cgc gtg ccg ctc atg att | | | 576 |
| Ile Ser Lys Ala Phe Glu Ala Val Gly Arg Arg Val Pro Leu Met Ile | | | |
| 180 | 185 | 190 | |
| tcc gcc acg atc gaa ccg atg ggc acg acg ctc gcc ggg cag gcg atc | | | 624 |
| Ser Gly Thr Ile Glu Pro Met Gly Thr Thr Leu Ala Gly Gln Ala Ile | | | |
| 195 | 200 | 205 | |
| gat gcg ttt ttc atc tcg gtg cgc cat atg aag ccg atc gcc gtc ggc | | | 672 |
| Asp Ala Phe Phe Ile Ser Val Arg His Met Lys Pro Ile Ala Val Gly | | | |
| 210 | 215 | 220 | |
| tta aac tgc gca acc ggt ccg gag ttt atg acc gac cat ttg cgc acg | | | 720 |
| Leu Asn Cys Ala Thr Gly Pro Glu Phe Met Thr Asp His Leu Arg Thr | | | |
| 225 | 230 | 235 | 240 |
| ctc gcc tcg ctc gct gac acg gcg gtc agc tgc tac ccg aac gcc ggt | | | 768 |
| Leu Ala Ser Leu Ala Asp Thr Ala Val Ser Cys Tyr Pro Asn Ala Gly | | | |
| 245 | 250 | 255 | |
| ctg ccg gat gag gaa ggc cac tat cat gaa acg ccg aat atg ctg gca | | | 816 |
| Leu Pro Asp Glu Glu Gly His Tyr His Glu Thr Pro Asn Met Leu Ala | | | |
| 260 | 265 | 270 | |
| gag aaa atc cgc cgc ttt gcc gaa aag gga tgg atc aac atc gtc ggc | | | 864 |
| Glu Lys Ile Arg Arg Phe Ala Glu Lys Gly Trp Ile Asn Ile Val Gly | | | |
| 275 | 280 | 285 | |
| ggg tgt tgc ggc acg acg ccg gat cat atc cgc gcc att gct gaa gcg | | | 912 |
| Gly Cys Cys Gly Thr Thr Pro Asp His Ile Arg Ala Ile Ala Glu Ala | | | |
| 290 | 295 | 300 | |
| gtg cgt gat ctc ccg ccg cgg gcg att ccg tct tcg ttt gat gtc cac | | | 960 |
| Val Arg Asp Leu Pro Pro Arg Ala Ile Pro Ser Ser Phe Asp Val His | | | |
| 305 | 310 | 315 | 320 |
| gcc gtt tcc gcc atc gag gcg ctc atc tat gat gaa acg atg cgc ccg | | | 1008 |
| Ala Val Ser Gly Ile Glu Ala Leu Ile Tyr Asp Glu Thr Met Arg Pro | | | |
| 325 | 330 | 335 | |
| ctc ttt gtc ggc gag cgg aca aac gtg atc ggc tcg cgc aaa ttc aag | | | 1056 |
| Leu Phe Val Gly Glu Arg Thr Asn Val Ile Gly Ser Arg Lys Phe Lys | | | |
| 340 | 345 | 350 | |
| cgc ctc atc gcc gaa ggg aaa tac gaa gaa gcg gcg gaa atc gcc cgc | | | 1104 |
| Arg Leu Ile Ala Glu Gly Lys Tyr Glu Glu Ala Ala Glu Ile Ala Arg | | | |
| 355 | 360 | 365 | |
| gcc caa gtg aaa aac gcc gcc cat gtc atc gac att tgc ctc gcc gac | | | 1152 |
| Ala Gln Val Lys Asn Gly Ala His Val Ile Asp Ile Cys Leu Ala Asp | | | |
| 370 | 375 | 380 | |

54

| | |
|---|------|
| cca gac cgc gac gaa ctc cat gac atg gag cag ttc gtc cgc gaa gtc Pro Asp Arg Asp Glu Leu His Asp Met Glu Gln Phe Val Arg Glu Val 385 390 395 400 | 1200 |
| gtg aaa aaa gtg aaa gtg ccg ctt gtc atc gat tcg acc gac gag cgc Val Lys Lys Val Lys Val Pro Leu Val Ile Asp Ser Thr Asp Glu Arg 405 410 415 | 1248 |
| gtc atc gaa cgc gcc ctt acg tat tcg caa ggg aag gcg atc atc aac Val Ile Glu Arg Ala Leu Thr Tyr Ser Gln Gly Lys Ala Ile Ile Asn 420 425 430 | 1296 |
| tcg atc aac ctc gaa gat ggc gaa gag cgg ttt gcg aag gtc gtt cct Ser Ile Asn Leu Glu Asp Gly Glu Glu Arg Phe Ala Lys Val Val Pro 435 440 445 | 1344 |
| ctc ctg cat caa tac ggc gcc gcc gtt gtc gtc ggc acg atc gat gag Leu Leu His Gln Tyr Gly Ala Ala Val Val Val Gly Thr Ile Asp Glu 450 455 460 | 1392 |
| caa gga atg gcg gtt aca gcc gaa cgg aaa ttg gaa atc gcc ttg cgt Gln Gly Met Ala Val Thr Ala Glu Arg Lys Leu Glu Ile Ala Leu Arg 465 470 475 480 | 1440 |
| tcg tat gac ttg ctg gtg aac cgc tac ggc gtc ccc gag cgc gac atc Ser Tyr Asp Leu Leu Val Asn Arg Tyr Gly Val Pro Glu Arg Asp Ile 485 490 495 | 1488 |
| att ttc gac ccg ctc gtc ttc ccg gtc ggc acc ggc gat gag caa tac Ile Phe Asp Pro Leu Val Phe Pro Val Gly Thr Gly Asp Glu Gln Tyr 500 505 510 | 1536 |
| atc ggc gcg gcg aaa gaa acc att gag ggc atc cgc ctc att aaa gag Ile Gly Ala Ala Lys Glu Thr Ile Glu Gly Ile Arg Leu Ile Lys Glu 515 520 525 | 1584 |
| cgg ctg cct cat tgc ttg acg atg ctt ggc atc agc aac gtc tcg ttc Arg Leu Pro His Cys Leu Thr Met Leu Gly Ile Ser Asn Val Ser Phe 530 535 540 | 1632 |
| ggc ttg ccg ccg gcc gga cgc gag gtg ctc aac tcc gtc ttt ttg tac Gly Leu Pro Pro Ala Gly Arg Glu Val Leu Asn Ser Val Phe Leu Tyr 545 550 555 560 | 1680 |
| cat tgc acg caa gcc ggg ctc gat tac gcc atc gtc aac acc gag aaa His Cys Thr Gln Ala Gly Leu Asp Tyr Ala Ile Val Asn Thr Glu Lys 565 570 575 | 1728 |
| ttg gag ccg ttc gcc tcg att ccg gaa gag gaa gtg cga atg gct gag Leu Glu Arg Phe Ala Ser Ile Pro Glu Glu Glu Val Arg Met Ala Glu 580 585 590 | 1776 |
| gca ctt ctt ttt gac aca aac gac gaa aca tta aac gcc ttt atc gaa Ala Leu Leu Phe Asp Thr Asn Asp Glu Thr Leu Asn Ala Phe Ile Glu 595 600 605 | 1824 |
| ttt tac cga agc aaa atc acc gcc gcc aaa ccg gcg cag acg aac ttg Phe Tyr Arg Ser Lys Ile Thr Ala Ala Lys Pro Ala Gln Thr Asn Leu 610 615 620 | 1872 |
| agc ttg gaa gag ccg ctc gcc cgc tac gtt att gaa ggg tcg aaa gac Ser Leu Glu Glu Arg Leu Ala Arg Tyr Val Ile Glu Gly Ser Lys Asp | 1920 |

| 55 | | | | | | | | | | | | | | | | | | | |
|---|------|--|--|--|-----|--|--|--|--|-----|--|--|--|--|-----|--|--|--|--|
| 625 | | | | | 630 | | | | | 635 | | | | | 640 | | | | |
| ggg ctc att ctc gat ttg gaa aag gcg ctt gag acc tac tcc gat ccg | 1968 | | | | | | | | | | | | | | | | | | |
| Gly Leu Ile Leu Asp Leu Glu Lys Ala Leu Glu Thr Tyr Ser Asp Pro | | | | | | | | | | | | | | | | | | | |
| 645 | | | | | 650 | | | | | 655 | | | | | | | | | |
| ctg tcc atc atc aac ggt ccg ctc atg gcc ggc atg gat gaa gtc ggg | 2016 | | | | | | | | | | | | | | | | | | |
| Leu Ser Ile Ile Asn Gly Pro Leu Met Ala Gly Met Asp Glu Val Gly | | | | | | | | | | | | | | | | | | | |
| 660 | | | | | 665 | | | | | 670 | | | | | | | | | |
| cgg ctg ttc aac aac aac cag ctc atc gtc gct gaa gta ttg caa agc | 2064 | | | | | | | | | | | | | | | | | | |
| Arg Leu Phe Asn Asn Asn Gln Leu Ile Val Ala Glu Val Leu Gln Ser | | | | | | | | | | | | | | | | | | | |
| 675 | | | | | 680 | | | | | 685 | | | | | | | | | |
| gcg gaa gtg atg aaa gca gcg gtc gcc ttt tta gag ctg tat atg gaa | 2112 | | | | | | | | | | | | | | | | | | |
| Ala Glu Val Met Lys Ala Ala Val Ala Phe Leu Glu Leu Tyr Met Glu | | | | | | | | | | | | | | | | | | | |
| 690 | | | | | 695 | | | | | 700 | | | | | | | | | |
| aag aaa gaa gga agc aca aaa gga aaa gtc att ctc gcc acc gtc aaa | 2160 | | | | | | | | | | | | | | | | | | |
| Lys Lys Glu Gly Ser Thr Lys Gly Lys Val Ile Leu Ala Thr Val Lys | | | | | | | | | | | | | | | | | | | |
| 705 | | | | | 710 | | | | | 715 | | | | | | | | | |
| ggc gat gtg cat gac atc ggc aaa aac ttg gtc gac atc att tta agc | 2208 | | | | | | | | | | | | | | | | | | |
| Gly Asp Val His Asp Ile Gly Lys Asn Leu Val Asp Ile Ile Leu Ser | | | | | | | | | | | | | | | | | | | |
| 725 | | | | | 730 | | | | | 735 | | | | | | | | | |
| aac aac ggc tac gag gtg atc gac ctc ggc att aaa gtc gct ccg cag | 2256 | | | | | | | | | | | | | | | | | | |
| Asn Asn Gly Tyr Glu Val Ile Asp Leu Gly Ile Lys Val Ala Pro Gln | | | | | | | | | | | | | | | | | | | |
| 740 | | | | | 745 | | | | | 750 | | | | | | | | | |
| caa ctc att gaa gcg gtg cgc gaa cat cag ccg gac atc atc ggg ttg | 2304 | | | | | | | | | | | | | | | | | | |
| Gln Leu Ile Glu Ala Val Arg Glu His Gln Pro Asp Ile Ile Gly Leu | | | | | | | | | | | | | | | | | | | |
| 755 | | | | | 760 | | | | | 765 | | | | | | | | | |
| tcg ggc ttg ctt gtg aaa tcg gct caa cag atg gtc gtc acc gcc caa | 2352 | | | | | | | | | | | | | | | | | | |
| Ser Gly Leu Leu Val Lys Ser Ala Gln Gln Met Val Val Thr Ala Gln | | | | | | | | | | | | | | | | | | | |
| 770 | | | | | 775 | | | | | 780 | | | | | | | | | |
| gac ttg cgc caa gcg ggc atc tcg acc ccg att tta gtc ggc ggc gcc | 2400 | | | | | | | | | | | | | | | | | | |
| Asp Leu Arg Gln Ala Gly Ile Ser Thr Pro Ile Leu Val Gly Gly Ala | | | | | | | | | | | | | | | | | | | |
| 785 | | | | | 790 | | | | | 795 | | | | | | | | | |
| gcc ttg acg cgc aaa ttt acg gaa aac aaa atc gcg ccc gag tac gac | 2448 | | | | | | | | | | | | | | | | | | |
| Ala Leu Thr Arg Lys Phe Thr Glu Asn Lys Ile Ala Pro Glu Tyr Asp | | | | | | | | | | | | | | | | | | | |
| 805 | | | | | 810 | | | | | 815 | | | | | | | | | |
| ggc gtt gtc ttg tac gcg aaa gac gcc atg gac ggg ctc gcc ctt gcc | 2496 | | | | | | | | | | | | | | | | | | |
| Gly Val Val Leu Tyr Ala Lys Asp Ala Met Asp Gly Leu Ala Leu Ala | | | | | | | | | | | | | | | | | | | |
| 820 | | | | | 825 | | | | | 830 | | | | | | | | | |
| aac caa atc cag cag ggc gag att gac tac aag aaa aaa gaa acg gcc | 2544 | | | | | | | | | | | | | | | | | | |
| Asn Gln Ile Gln Gln Gly Glu Ile Asp Tyr Lys Lys Lys Glu Thr Ala | | | | | | | | | | | | | | | | | | | |
| 835 | | | | | 840 | | | | | 845 | | | | | | | | | |
| gaa agc gag cca acg cgg caa acg acg gtg gtc aca gcg gtc aaa tcg | 2592 | | | | | | | | | | | | | | | | | | |
| Glu Ser Glu Pro Thr Arg Gln Thr Thr Val Val Thr Ala Val Lys Ser | | | | | | | | | | | | | | | | | | | |
| 850 | | | | | 855 | | | | | 860 | | | | | | | | | |
| acc gtc tcg acc gac gtt ccc gtc tac atc ccg gcc gat ctc gag cgc | 2640 | | | | | | | | | | | | | | | | | | |
| Thr Val Ser Thr Asp Val Pro Val Tyr Ile Pro Ala Asp Leu Glu Arg | | | | | | | | | | | | | | | | | | | |
| 865 | | | | | 870 | | | | | 875 | | | | | | | | | |
| | | | | | | | | | | 880 | | | | | | | | | |

56

| | |
|---|------|
| cac gcg ctg cga aat gtg ccg ctt gac cac att ttg ccg tac gtc aac His Ala Leu Arg Asn Val Pro Leu Asp His Ile Leu Pro Tyr Val Asn 885 890 895 | 2688 |
| tgg caa atg gtg ctc ggc cac cac ctc ggc ttg aaa gga aaa gtg aaa Trp Gln Met Val Leu Gly His His Leu Gly Leu Lys Gly Lys Val Lys 900 905 910 | 2736 |
| cgg ctg ctt gaa gag aaa gac gaa aaa gcg ttg gcg tta aaa gcg gtc Arg Leu Leu Glu Glu Lys Asp Glu Lys Ala Leu Ala Leu Lys Ala Val 915 920 925 | 2784 |
| gtc gac gaa ctg ctc gcc gaa gcg aaa gag cgc cgc tgg att cag ccc Val Asp Glu Leu Leu Ala Glu Ala Lys Glu Arg Arg Trp Ile Gln Pro 930 935 940 | 2832 |
| gcc ggc gtc tac cgc ttc ttc ccg gcg caa agc gac ggc aac cgg gtt Ala Gly Val Tyr Arg Phe Phe Pro Ala Gln Ser Asp Gly Asn Arg Val 945 950 955 960 | 2880 |
| tac att tac gat ccg act gac ggc aaa aca gtg ctc gag atg ttc gac Tyr Ile Tyr Asp Pro Thr Asp Gly Lys Thr Val Leu Glu Met Phe Asp 965 970 975 | 2928 |
| ttt ccg cgc caa ccg cgg gcg ccg tat ctt tgc ctc gcc gat tat ttg Phe Pro Arg Gln Pro Arg Ala Pro Tyr Leu Cys Leu Ala Asp Tyr Leu 980 985 990 | 2976 |
| aaa tcg aaa gaa agc ggc gaa atg gat tac gtc ggt ttg ttc gcc gtc Lys Ser Lys Glu Ser Gly Glu Met Asp Tyr Val Gly Leu Phe Ala Val 995 1000 1005 | 3024 |
| acc gct ggg cat ggc gtc cgc gaa ctc gcc cag cgc tgg aag gaa gaa Thr Ala Gly His Gly Val Arg Glu Leu Ala Gln Arg Trp Lys Glu Glu 1010 1015 1020 | 3072 |
| ggc gaa ttt ttg aaa agc cat gcc atc caa gcg ttg gcg ctc gag att Gly Glu Phe Leu Lys Ser His Ala Ile Gln Ala Leu Ala Leu Glu Ile 1025 1030 1035 1040 | 3120 |
| gcc gaa ggg ttc gcc gaa cga atc cat caa att atg cgc gac cgc tgg Ala Glu Gly Phe Ala Glu Arg Ile His Gln Ile Met Arg Asp Arg Trp 1045 1050 1055 | 3168 |
| ggc ttc ccg gac gac ccg gat ttc acg atg gaa gag cgc ttc gcc gcc Gly Phe Pro Asp Asp Pro Asp Phe Thr Met Glu Glu Arg Phe Ala Ala 1060 1065 1070 | 3216 |
| aaa tac cag ggc cag cgc tac tcg ttc ggc tac ccg gcc tgt ccg aac Lys Tyr Gln Gly Gln Arg Tyr Ser Phe Gly Tyr Pro Ala Cys Pro Asn 1075 1080 1085 | 3264 |
| ttg gaa gac cag gag aaa ctg ttc cgt ctg ctt cat cca gaa gac atc Leu Glu Asp Gln Glu Lys Leu Phe Arg Leu Leu His Pro Glu Asp Ile 1090 1095 1100 | 3312 |
| ggc atc cgt ctc acc gac ggc tat atg atg gaa ccc gaa gca tcg gtt Gly Ile Arg Leu Thr Asp Gly Tyr Met Met Glu Pro Glu Ala Ser Val 1105 1110 1115 1120 | 3360 |
| tcg gcg atc gtc ttc gcc cat ccg gaa gcg cgg tat ttc aat gtg tta Ser Ala Ile Val Phe Ala His Pro Glu Ala Arg Tyr Phe Asn Val Leu | 3408 |

57

1125

1130

1135

taa

3411

<210> 14

<211> 1136

<212> PRT

<213> Bacillus stearothermophilus

<400> 14

Met Ala Asn Val Thr Leu Glu Gln Gln Leu Gln Arg Lys Ile Leu Val
 1 5 10 15

Ile Asp Gly Ala Met Gly Thr Met Ile Gln Ser Ala Asn Leu Ser Ala
 20 25 30

Ala Asp Phe Gly Gly Glu Ala Tyr Glu Gly Cys Asn Glu Tyr Leu Thr
 35 40 45

Leu Thr Ala Pro His Val Ile Arg Arg Ile His Glu Ala Tyr Leu Glu
 50 55 60

Ala Gly Ala Asp Ile Ile Glu Thr Asn Thr Phe Gly Ala Thr Arg Ile
 65 70 75 80

Val Leu Asp Glu Tyr Gly Leu Gly His Leu Ala Leu Glu Leu Asn Ile
 85 90 95

Glu Ala Ala Lys Leu Ala Lys Gln Thr Ala Glu Ser Phe Ser Thr Pro
 100 105 110

Asp Trp Pro Arg Phe Val Ala Gly Ser Met Gly Pro Thr Thr Lys Thr
 115 120 125

Leu Ser Val Thr Gly Gly Ala Thr Phe Glu Glu Leu Val Ala Ala Tyr
 130 135 140

Glu Glu Gln Ala Arg Gly Leu Leu Leu Gly Gly Val Asp Leu Leu Leu
 145 150 155 160

Leu Glu Thr Cys Gln Asp Thr Leu Asn Val Lys Ala Gly Phe Leu Gly
 165 170 175

Ile Ser Lys Ala Phe Glu Ala Val Gly Arg Arg Val Pro Leu Met Ile
 180 185 190

Ser Gly Thr Ile Glu Pro Met Gly Thr Thr Leu Ala Gly Gln Ala Ile
 195 200 205

Asp Ala Phe Phe Ile Ser Val Arg His Met Lys Pro Ile Ala Val Gly
 210 215 220

Leu Asn Cys Ala Thr Gly Pro Glu Phe Met Thr Asp His Leu Arg Thr
 225 230 235 240

Leu Ala Ser Leu Ala Asp Thr Ala Val Ser Cys Tyr Pro Asn Ala Gly
 245 250 255

Leu Pro Asp Glu Gly His Tyr His Glu Thr Pro Asn Met Leu Ala
 260 265 270

58

Glu Lys Ile Arg Arg Phe Ala Glu Lys Gly Trp Ile Asn Ile Val Gly
 275 280 285
 Gly Cys Cys Gly Thr Thr Pro Asp His Ile Arg Ala Ile Ala Glu Ala
 290 295 300
 Val Arg Asp Leu Pro Pro Arg Ala Ile Pro Ser Ser Phe Asp Val His
 305 310 315 320
 Ala Val Ser Gly Ile Glu Ala Leu Ile Tyr Asp Glu Thr Met Arg Pro
 325 330 335
 Leu Phe Val Gly Glu Arg Thr Asn Val Ile Gly Ser Arg Lys Phe Lys
 340 345 350
 Arg Leu Ile Ala Glu Gly Lys Tyr Glu Glu Ala Ala Glu Ile Ala Arg
 355 360 365
 Ala Gln Val Lys Asn Gly Ala His Val Ile Asp Ile Cys Leu Ala Asp
 370 375 380
 Pro Asp Arg Asp Glu Leu His Asp Met Glu Gln Phe Val Arg Glu Val
 385 390 395 400
 Val Lys Lys Val Lys Val Pro Leu Val Ile Asp Ser Thr Asp Glu Arg
 405 410 415
 Val Ile Glu Arg Ala Leu Thr Tyr Ser Gln Gly Lys Ala Ile Ile Asn
 420 425 430
 Ser Ile Asn Leu Glu Asp Gly Glu Glu Arg Phe Ala Lys Val Val Pro
 435 440 445
 Leu Leu His Gln Tyr Gly Ala Ala Val Val Val Gly Thr Ile Asp Glu
 450 455 460
 Gln Gly Met Ala Val Thr Ala Glu Arg Lys Leu Glu Ile Ala Leu Arg
 465 470 475 480
 Ser Tyr Asp Leu Leu Val Asn Arg Tyr Gly Val Pro Glu Arg Asp Ile
 485 490 495
 Ile Phe Asp Pro Leu Val Phe Pro Val Gly Thr Gly Asp Glu Gln Tyr
 500 505 510
 Ile Gly Ala Ala Lys Glu Thr Ile Glu Gly Ile Arg Leu Ile Lys Glu
 515 520 525
 Arg Leu Pro His Cys Leu Thr Met Leu Gly Ile Ser Asn Val Ser Phe
 530 535 540
 Gly Leu Pro Pro Ala Gly Arg Glu Val Leu Asn Ser Val Phe Leu Tyr
 545 550 555 560
 His Cys Thr Gln Ala Gly Leu Asp Tyr Ala Ile Val Asn Thr Glu Lys
 565 570 575
 Leu Glu Arg Phe Ala Ser Ile Pro Glu Glu Glu Val Arg Met Ala Glu
 580 585 590
 Ala Leu Leu Phe Asp Thr Asn Asp Glu Thr Leu Asn Ala Phe Ile Glu
 595 600 605

59

Phe Tyr Arg Ser Lys Ile Thr Ala Ala Lys Pro Ala Gln Thr Asn Leu
 610 615 620
 Ser Leu Glu Glu Arg Leu Ala Arg Tyr Val Ile Glu Gly Ser Lys Asp
 625 630 635 640
 Gly Leu Ile Leu Asp Leu Glu Lys Ala Leu Glu Thr Tyr Ser Asp Pro
 645 650 655
 Leu Ser Ile Ile Asn Gly Pro Leu Met Ala Gly Met Asp Glu Val Gly
 660 665 670
 Arg Leu Phe Asn Asn Asn Gln Leu Ile Val Ala Glu Val Leu Gln Ser
 675 680 685
 Ala Glu Val Met Lys Ala Ala Val Ala Phe Leu Glu Leu Tyr Met Glu
 690 695 700
 Lys Lys Glu Gly Ser Thr Lys Gly Lys Val Ile Leu Ala Thr Val Lys
 705 710 715 720
 Gly Asp Val His Asp Ile Gly Lys Asn Leu Val Asp Ile Ile Leu Ser
 725 730 735
 Asn Asn Gly Tyr Glu Val Ile Asp Leu Gly Ile Lys Val Ala Pro Gln
 740 745 750
 Gln Leu Ile Glu Ala Val Arg Glu His Gln Pro Asp Ile Ile Gly Leu
 755 760 765
 Ser Gly Leu Leu Val Lys Ser Ala Gln Gln Met Val Val Thr Ala Gln
 770 775 780
 Asp Leu Arg Gln Ala Gly Ile Ser Thr Pro Ile Leu Val Gly Gly Ala
 785 790 795 800
 Ala Leu Thr Arg Lys Phe Thr Glu Asn Lys Ile Ala Pro Glu Tyr Asp
 805 810 815
 Gly Val Val Leu Tyr Ala Lys Asp Ala Met Asp Gly Leu Ala Leu Ala
 820 825 830
 Asn Gln Ile Gln Gln Gly Glu Ile Asp Tyr Lys Lys Lys Glu Thr Ala
 835 840 845
 Glu Ser Glu Pro Thr Arg Gln Thr Thr Val Val Thr Ala Val Lys Ser
 850 855 860
 Thr Val Ser Thr Asp Val Pro Val Tyr Ile Pro Ala Asp Leu Glu Arg
 865 870 875 880
 His Ala Leu Arg Asn Val Pro Leu Asp His Ile Leu Pro Tyr Val Asn
 885 890 895
 Trp Gln Met Val Leu Gly His His Leu Gly Leu Lys Gly Lys Val Lys
 900 905 910
 Arg Leu Leu Glu Glu Lys Asp Glu Lys Ala Leu Ala Leu Lys Ala Val
 915 920 925
 Val Asp Glu Leu Leu Ala Glu Ala Lys Glu Arg Arg Trp Ile Gln Pro

60

930 935 940
 Ala Gly Val Tyr Arg Phe Phe Pro Ala Gln Ser Asp Gly Asn Arg Val
 945 950 955 960
 Tyr Ile Tyr Asp Pro Thr Asp Gly Lys Thr Val Leu Glu Met Phe Asp
 965 970 975
 Phe Pro Arg Gln Pro Arg Ala Pro Tyr Leu Cys Leu Ala Asp Tyr Leu
 980 985 990
 Lys Ser Lys Glu Ser Gly Glu Met Asp Tyr Val Gly Leu Phe Ala Val
 995 1000 1005
 Thr Ala Gly His Gly Val Arg Glu Leu Ala Gln Arg Trp Lys Glu Glu
 1010 1015 1020
 Gly Glu Phe Leu Lys Ser His Ala Ile Gln Ala Leu Ala Leu Glu Ile
 1025 1030 1035 1040
 Ala Glu Gly Phe Ala Glu Arg Ile His Gln Ile Met Arg Asp Arg Trp
 1045 1050 1055
 Gly Phe Pro Asp Asp Pro Asp Phe Thr Met Glu Glu Arg Phe Ala Ala
 1060 1065 1070
 Lys Tyr Gln Gly Gln Arg Tyr Ser Phe Gly Tyr Pro Ala Cys Pro Asn
 1075 1080 1085
 Leu Glu Asp Gln Glu Lys Leu Phe Arg Leu Leu His Pro Glu Asp Ile
 1090 1095 1100
 Gly Ile Arg Leu Thr Asp Gly Tyr Met Met Glu Pro Glu Ala Ser Val
 1105 1110 1115 1120
 Ser Ala Ile Val Phe Ala His Pro Glu Ala Arg Tyr Phe Asn Val Leu
 1125 1130 1135

<210> 15
 <211> 3681
 <212> DNA
 <213> *Vibrio cholerae*

<220>
 <221> CDS
 <222> (1) .. (3678)
 <223> RVC04265

<400> 15
 gtg gga aaa gaa gta aga caa caa ctc gaa cag caa ttg aaa caa cgt 48
 Val Gly Lys Glu Val Arg Gln Gln Leu Glu Gln Gln Leu Lys Gln Arg
 1 5 10 15
 atc cta ctg att gat ggt ggt atg ggt acc atg att cag agt tat aag 96
 Ile Leu Leu Ile Asp Gly Gly Met Gly Thr Met Ile Gln Ser Tyr Lys
 20 25 30
 tta caa gag gaa gac tat cgc ggt gca cga ttt gtc gat tgg cac tgt 144

61

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Gln | Glu | Glu | Asp | Tyr | Arg | Gly | Ala | Arg | Phe | Val | Asp | Trp | His | Cys | |
| | 35 | | | | | | 40 | | | | | 45 | | | | |
| gat | ttg | aaa | gga | aat | aac | gac | ctc | tta | gtg | ctt | act | cag | ccg | caa | att | 192 |
| Asp | Leu | Lys | Gly | Asn | Asn | Asp | Leu | Leu | Val | Leu | Thr | Gln | Pro | Gln | Ile | |
| | 50 | | | | 55 | | | | | 60 | | | | | | |
| att | aaa | gag | att | cac | tcc | gct | tac | ctt | gaa | gcg | ggg | gcg | gat | att | ctt | 240 |
| Ile | Lys | Glu | Ile | His | Ser | Ala | Tyr | Leu | Glu | Ala | Gly | Ala | Asp | Ile | Leu | |
| | 65 | | | 70 | | | | 75 | | | | | | 80 | | |
| gag | acc | aac | acc | ttt | aac | tca | acc | acg | att | gcc | atg | gca | gac | tat | gac | 288 |
| Glu | Thr | Asn | Thr | Phe | Asn | Ser | Thr | Thr | Ile | Ala | Met | Ala | Asp | Tyr | Asp | |
| | | 85 | | | | | 90 | | | | 95 | | | | | |
| atg | caa | tcg | ctc | agt | gct | gaa | att | aac | ttt | gcc | gcg | gct | aag | ctt | gca | 336 |
| Met | Gln | Ser | Leu | Ser | Ala | Glu | Ile | Asn | Phe | Ala | Ala | Ala | Lys | Leu | Ala | |
| | 100 | | | | | 105 | | | | | | 110 | | | | |
| cgt | gaa | gtc | gcg | gat | gag | tgg | acg | gct | aaa | gat | cca | agt | cgg | cca | cgc | 384 |
| Arg | Glu | Val | Ala | Asp | Glu | Trp | Thr | Ala | Lys | Asp | Pro | Ser | Arg | Pro | Arg | |
| | 115 | | | | 120 | | | 125 | | | | | | | | |
| tat | gtg | gct | ggg | gtg | ctt | ggg | cca | acc | aac | cgt | act | tgc | tct | att | tcg | 432 |
| Tyr | Val | Ala | Gly | Val | Leu | Gly | Pro | Thr | Asn | Arg | Thr | Cys | Ser | Ile | Ser | |
| | 130 | | | | 135 | | | 140 | | | | | | | | |
| cca | gat | gtg | aac | gat | cca | gga | ttt | cgt | aac | gtc | act | ttt | gat | ggg | ctt | 480 |
| Pro | Asp | Val | Asn | Asp | Pro | Gly | Phe | Arg | Asn | Val | Thr | Phe | Asp | Gly | Leu | |
| | 145 | | | 150 | | | | 155 | | | | | | 160 | | |
| gtt | gaa | gcc | tat | tcc | gaa | tcg | acg | cgc | gct | ttg | atc | aaa | ggg | ggc | agc | 528 |
| Val | Glu | Ala | Tyr | Ser | Glu | Ser | Thr | Arg | Ala | Leu | Ile | Lys | Gly | Gly | Ser | |
| | | | 165 | | | | 170 | | | | | | 175 | | | |
| gat | ctg | atc | ctc | att | gaa | acc | atc | ttc | gat | aca | ctt | aac | gcc | aaa | gcc | 576 |
| Asp | Leu | Ile | Leu | Ile | Glu | Thr | Ile | Phe | Asp | Thr | Leu | Asn | Ala | Lys | Ala | |
| | | 180 | | | | | 185 | | | | | 190 | | | | |
| tgt | gcg | ttt | gcg | gtc | gat | agc | gta | ttt | gaa | gag | ctg | ggc | atc | agc | tta | 624 |
| Cys | Ala | Phe | Ala | Val | Asp | Ser | Val | Phe | Glu | Glu | Leu | Gly | Ile | Ser | Leu | |
| | 195 | | | | | 200 | | | | | 205 | | | | | |
| cct | gtg | atg | att | tcc | ggc | acg | att | acc | gat | gcc | tct | ggg | cga | act | ctg | 672 |
| Pro | Val | Met | Ile | Ser | Gly | Thr | Ile | Thr | Asp | Ala | Ser | Gly | Arg | Thr | Leu | |
| | 210 | | | | 215 | | | 220 | | | | | | | | |
| tca | gga | cag | aca | acg | gaa | gct | ttc | tac | aac | gcc | ttg | cgt | cat | gta | cgg | 720 |
| Ser | Gly | Gln | Thr | Thr | Glu | Ala | Phe | Tyr | Asn | Ala | Leu | Arg | His | Val | Arg | |
| | 225 | | | | 230 | | | 235 | | | | | 240 | | | |
| ccg | att | tcg | ttt | ggc | ttg | aac | tgt | gcg | tta | ggg | cct | gat | gag | ctg | cgc | 768 |
| Pro | Ile | Ser | Phe | Gly | Leu | Asn | Cys | Ala | Leu | Gly | Pro | Asp | Glu | Leu | Arg | |
| | | | 245 | | | | 250 | | | | | | 255 | | | |
| cag | tac | gtg | gaa | gag | ctt | tca | cgc | att | tca | gaa | tgc | tat | gtt | tcc | gcg | 816 |
| Gln | Tyr | Val | Glu | Glu | Leu | Ser | Arg | Ile | Ser | Glu | Cys | Tyr | Val | Ser | Ala | |
| | | 260 | | | | | 265 | | | | | 270 | | | | |
| cac | cca | aat | gcc | gga | ctg | ccc | aat | gcg | ttt | ggg | gaa | tac | gat | ctc | tct | 864 |
| His | Pro | Asn | Ala | Gly | Leu | Pro | Asn | Ala | Phe | Gly | Glu | Tyr | Asp | Leu | Ser | |
| | | 275 | | | | 280 | | | | | 285 | | | | | |

| | |
|---|------|
| gcc gag gaa atg gca gaa cat att gcg gaa tgg gca caa gct ggc ttt Ala Glu Glu Met Ala Glu His Ile Ala Glu Trp Ala Gln Ala Gly Phe 290 295 300 | 912 |
| ttg aat ttg gtc ggt ggt tgc tgt gga act aca cct gag cat atc gcc Leu Asn Leu Val Gly Gly Cys Cys Gly Thr Thr Pro Glu His Ile Ala 305 310 315 320 | 960 |
| gcc att gcc aaa gcc gtc gag ggt gta aaa cca agg gct ctg cca gat Ala Ile Ala Lys Ala Val Glu Gly Val Lys Pro Arg Ala Leu Pro Asp 325 330 335 | 1008 |
| ctg aaa gta gaa tgt cgt ctc tcg ggt tta gag ccg ctc aat att ggt Leu Lys Val Glu Cys Arg Leu Ser Gly Leu Glu Pro Leu Asn Ile Gly 340 345 350 | 1056 |
| cct gaa acc ttg ttt gtt aac gtg ggc gaa cgt act aac gtc acc ggt Pro Glu Thr Leu Phe Val Asn Val Gly Glu Arg Thr Asn Val Thr Gly 355 360 365 | 1104 |
| tct gcg cgt ttt aag cgt tta att aaa gaa gag caa tac gac gaa gcg Ser Ala Arg Phe Lys Arg Leu Ile Lys Glu Glu Gln Tyr Asp Glu Ala 370 375 380 | 1152 |
| ctc gat gtg gcg cgt gag caa gtc gaa aac ggc gcg cag atc att gat Leu Asp Val Ala Arg Glu Gln Val Glu Asn Gly Ala Gln Ile Ile Asp 385 390 395 400 | 1200 |
| atc aac atg gat gaa ggc atg ttg gac gcc gag gcg tgt atg gtg cgc Ile Asn Met Asp Glu Gly Met Leu Asp Ala Glu Ala Cys Met Val Arg 405 410 415 | 1248 |
| ttt ttg aat cta tgc gcc tct gaa cca gaa ata tcc aaa gtt ccg gtg Phe Leu Asn Leu Cys Ala Ser Glu Pro Glu Ile Ser Lys Val Pro Val 420 425 430 | 1296 |
| atg gtc gac tcc tct aaa tgg gaa gtc att gaa gcg ggt ctg aaa tgc Met Val Asp Ser Ser Lys Trp Glu Val Ile Glu Ala Gly Leu Lys Cys 435 440 445 | 1344 |
| att cag ggt aaa ggc atc gtc aac tct atc tct cta aaa gaa ggg aaa Ile Gln Gly Lys Gly Ile Val Asn Ser Ile Ser Leu Lys Glu Gly Lys 450 455 460 | 1392 |
| gag aag ttt att gcc caa gcc aaa ttg gtg cgc cgc tac ggt gcc gcg Glu Lys Phe Ile Ala Gln Ala Lys Leu Val Arg Arg Tyr Gly Ala Ala 465 470 475 480 | 1440 |
| gtg att gtg atg gca ttt gac gaa gtg ggc caa gcc gat acc cgt gag Val Ile Val Met Ala Phe Asp Glu Val Gly Gln Ala Asp Thr Arg Glu 485 490 495 | 1488 |
| cgc aaa tta gag atc tgt cgt cgg gct tac cat att ttg gtc gat gag Arg Lys Leu Glu Ile Cys Arg Arg Ala Tyr His Ile Leu Val Asp Glu 500 505 510 | 1536 |
| gtg ggc ttc cca ccg gaa gat att att ttt gac ccg aac atc ttt gct Val Gly Phe Pro Pro Glu Asp Ile Ile Phe Asp Pro Asn Ile Phe Ala 515 520 525 | 1584 |
| gtt gcg acc gga att gat gag cac aat aac tac gca ctg gat ttc att | 1632 |

63

| | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|--|
| Val | Ala | Thr | Gly | Ile | Asp | Glu | His | Asn | Asn | Tyr | Ala | Leu | Asp | Phe | Ile | | |
| 530 | | | | | | 535 | | | | | 540 | | | | | | |
| aat | gca | gtg | gcg | gac | att | aag | cgt | gag | ctg | ccg | cat | gcg | atg | att | tct | 1680 | |
| Asn | Ala | Val | Ala | Asp | Ile | Lys | Arg | Glu | Leu | Pro | His | Ala | Met | Ile | Ser | | |
| 545 | | | | | 550 | | | | | 555 | | | | 560 | | | |
| ggc | ggt | gtt | tct | aac | gtt | tcc | ttc | tct | ttc | cgc | ggc | aac | aac | tat | gtg | 1728 | |
| Gly | Gly | Val | Ser | Asn | Val | Ser | Phe | Ser | Phe | Arg | Gly | Asn | Asn | Tyr | Val | | |
| | | | | 565 | | | | | 570 | | | | | 575 | | | |
| cgt | gaa | gcg | atc | cat | gct | gtt | ttc | ctt | tat | cac | tgc | ttc | aaa | cac | ggc | 1776 | |
| Arg | Glu | Ala | Ile | His | Ala | Val | Phe | Leu | Tyr | His | Cys | Phe | Lys | His | Gly | | |
| | | | 580 | | | | | 585 | | | | | 590 | | | | |
| atg | gac | atg | ggg | att | gtc | aac | gca | ggg | cag | ctt | gaa | atc | tac | gat | aac | 1824 | |
| Met | Asp | Met | Gly | Ile | Val | Asn | Ala | Gly | Gln | Leu | Glu | Ile | Tyr | Asp | Asn | | |
| | | 595 | | | | | 600 | | | | | 605 | | | | | |
| gtt | ccg | ctg | aaa | ctg | cgt | gag | gca | gtg | gaa | gat | gtg | atc | ctc | aat | cga | 1872 | |
| Val | Pro | Leu | Lys | Leu | Arg | Glu | Ala | Val | Glu | Asp | Val | Ile | Leu | Asn | Arg | | |
| | 610 | | | | | 615 | | | | | 620 | | | | | | |
| cgt | agc | gat | ggc | acg | gaa | aga | ctg | ctt | gag | atc | gcc | gaa | gcg | tat | cgc | 1920 | |
| Arg | Ser | Asp | Gly | Thr | Glu | Arg | Leu | Leu | Glu | Ile | Ala | Glu | Ala | Tyr | Arg | | |
| | 625 | | | | 630 | | | | | 635 | | | | 640 | | | |
| gaa | aac | agt | gtt | ggt | aaa | gaa | gag | gat | gct | tct | gca | tta | gag | tgg | cgc | 1968 | |
| Glu | Asn | Ser | Val | Gly | Lys | Glu | Glu | Asp | Ala | Ser | Ala | Leu | Glu | Trp | Arg | | |
| | | | 645 | | | | | 650 | | | | | | 655 | | | |
| gca | tgg | cct | gtg | gct | aag | cgc | cta | gag | cac | gct | tta | gtc | aaa | ggc | atc | 2016 | |
| Ala | Trp | Pro | Val | Ala | Lys | Arg | Leu | Glu | His | Ala | Leu | Val | Lys | Gly | Ile | | |
| | | 660 | | | | | 665 | | | | | | 670 | | | | |
| acc | gaa | ttt | atc | gtc | caa | gac | act | gaa | gaa | gca | cgt | cag | caa | gcc | agt | 2064 | |
| Thr | Glu | Phe | Ile | Val | Gln | Asp | Thr | Glu | Glu | Ala | Arg | Gln | Gln | Ala | Ser | | |
| | | 675 | | | | 680 | | | | | | 685 | | | | | |
| aaa | cca | ctg | gaa | gtg | att | gaa | ggg | ccg | ctg | atg | gat | ggt | atg | aac | gtg | 2112 | |
| Lys | Pro | Leu | Glu | Val | Ile | Glu | Gly | Pro | Leu | Met | Asp | Gly | Met | Asn | Val | | |
| | 690 | | | | | 695 | | | | | 700 | | | | | | |
| gtc | ggt | gac | ttg | ttc | ggg | gaa | ggg | aaa | atg | ttc | cta | ccg | caa | gtc | gta | 2160 | |
| Val | Gly | Asp | Leu | Phe | Gly | Glu | Gly | Lys | Met | Phe | Leu | Pro | Gln | Val | Val | | |
| | 705 | | | | 710 | | | | | 715 | | | | 720 | | | |
| aaa | tca | gcg | cgt | gtc | atg | aaa | caa | gcc | gtt | gcg | tat | ctt | gag | cct | ttc | 2208 | |
| Lys | Ser | Ala | Arg | Val | Met | Lys | Gln | Ala | Val | Ala | Tyr | Leu | Glu | Pro | Phe | | |
| | | | 725 | | | | | 730 | | | | | | 735 | | | |
| att | aat | gcg | caa | aaa | agt | ggt | agc | act | tca | aat | ggt | aag | att | ttg | ctg | 2256 | |
| Ile | Asn | Ala | Gln | Lys | Ser | Gly | Ser | Thr | Ser | Asn | Gly | Lys | Ile | Leu | Leu | | |
| | | | 740 | | | | | 745 | | | | | | 750 | | | |
| gcg | acc | gta | aaa | ggc | gat | gtg | cat | gac | att | ggt | aag | aac | att | gtt | ggc | 2304 | |
| Ala | Thr | Val | Lys | Gly | Asp | Val | His | Asp | Ile | Gly | Lys | Asn | Ile | Val | Gly | | |
| | | 755 | | | | | 760 | | | | | 765 | | | | | |
| gtc | gtg | ctg | cag | tgt | aat | aac | ttc | gag | atc | atc | gat | ctt | ggt | gtg | atg | 2352 | |
| Val | Val | Leu | Gln | Cys | Asn | Asn | Phe | Glu | Ile | Ile | Asp | Leu | Gly | Val | Met | | |
| | | 770 | | | | 775 | | | | | | 780 | | | | | |

| | |
|---|------|
| gtg cct tgc gag cag atc ctc aaa gtc gca cgc gag caa aat gtc gat | 2400 |
| Val Pro Cys Glu Gln Ile Leu Lys Val Ala Arg Glu Gln Asn Val Asp | |
| 785 790 795 800 | |
| atc atc ggt ctc tct ggg ctt atc acg ccg tct ttg gat gag atg gta | 2448 |
| Ile Ile Gly Leu Ser Gly Leu Ile Thr Pro Ser Leu Asp Glu Met Val | |
| 805 810 815 | |
| cac gtg gcg aaa gag atg gag cga caa ggg ttt gaa ctg cca ctt ttg | 2496 |
| His Val Ala Lys Glu Met Glu Arg Gln Gly Phe Glu Leu Pro Leu Leu | |
| 820 825 830 | |
| att ggt ggg gca aca acg tct aaa gcg cat act gcg gtg aag att gaa | 2544 |
| Ile Gly Gly Ala Thr Thr Ser Lys Ala His Thr Ala Val Lys Ile Glu | |
| 835 840 845 | |
| cag aat tat cat gcg cct gta gtg tac gtg aat aac gcg tcg cgc gcg | 2592 |
| Gln Asn Tyr His Ala Pro Val Val Tyr Val Asn Asn Ala Ser Arg Ala | |
| 850 855 860 | |
| gta ggg gtg tgc aca tca tta ttg tct gat gaa cag cgc ccc gga ttt | 2640 |
| Val Gly Val Cys Thr Ser Leu Leu Ser Asp Glu Gln Arg Pro Gly Phe | |
| 865 870 875 880 | |
| atc gaa cgt ttg gat ctc gat tat gag cgc acg cgt gat cag cat gct | 2688 |
| Ile Glu Arg Leu Asp Leu Asp Tyr Glu Arg Thr Arg Asp Gln His Ala | |
| 885 890 895 | |
| cgt aaa acg ccc aaa tcg cgc cca gtc acg tta gag cag gca cgt gct | 2736 |
| Arg Lys Thr Pro Lys Ser Arg Pro Val Thr Leu Glu Gln Ala Arg Ala | |
| 900 905 910 | |
| aat aaa gcg gcg ctg gat tgg gca aat tac acg ccg ccc gct cct gcg | 2784 |
| Asn Lys Ala Ala Leu Asp Trp Ala Asn Tyr Thr Pro Pro Ala Pro Ala | |
| 915 920 925 | |
| aaa ccg ggt gtg cat gtg ttt gaa aac att gcg tta gcc aca cta cgt | 2832 |
| Lys Pro Gly Val His Val Phe Glu Asn Ile Ala Leu Ala Thr Leu Arg | |
| 930 935 940 | |
| cct tat atc gat tgg acg cct ttt ttt atg act tgg tcg ctt atg ggc | 2880 |
| Pro Tyr Ile Asp Trp Thr Pro Phe Phe Met Thr Trp Ser Leu Met Gly | |
| 945 950 955 960 | |
| aaa tac cct gcc att ttg gag cat gaa gag gtc ggt gaa gag gcc aaa | 2928 |
| Lys Tyr Pro Ala Ile Leu Glu His Glu Glu Val Gly Glu Glu Ala Lys | |
| 965 970 975 | |
| cgt ctg ttt cat gat gcc aat gcc tta ctt gat aaa gta gag cga gaa | 2976 |
| Arg Leu Phe His Asp Ala Asn Ala Leu Leu Asp Lys Val Glu Arg Glu | |
| 980 985 990 | |
| gga cta ctg aaa gcc agt ggt atg tgt gca ctg ttt cca gca gcc agc | 3024 |
| Gly Leu Leu Lys Ala Ser Gly Met Cys Ala Leu Phe Pro Ala Ala Ser | |
| 995 1000 1005 | |
| gtg ggc gat gac att gag gtg tac agt gat gaa tcg cgt acg caa gtc | 3072 |
| Val Gly Asp Asp Ile Glu Val Tyr Ser Asp Glu Ser Arg Thr Gln Val | |
| 1010 1015 1020 | |
| gcg cat gtg ctg tac aac ttg cgt cag cag act gag aaa ccg aaa ggg | 3120 |

65

Ala His Val Leu Tyr Asn Leu Arg Gln Gln Thr Glu Lys Pro Lys Gly
 1025 1030 1035 1040

gcc aac tac tgt ttg tcg gac tat gtt gct ccg aaa gag agc ggt aaa 3168
 Ala Asn Tyr Cys Leu Ser Asp Tyr Val Ala Pro Lys Glu Ser Gly Lys
 1045 1050 1055

cgt gat tgg att ggc gcg ttt gca gta act ggt ggc att ggt gag cga 3216
 Arg Asp Trp Ile Gly Ala Phe Ala Val Thr Gly Gly Ile Gly Glu Arg
 1060 1065 1070

gcc ttg gcc gat gct tat aaa gct cag ggt gat gat tac aat gcg atc 3264
 Ala Leu Ala Asp Ala Tyr Lys Ala Gln Gly Asp Asp Tyr Asn Ala Ile
 1075 1080 1085

atg atc caa gcg gta gcc gat cgt ttg gcg gaa gcc ttt gcg gaa tat 3312
 Met Ile Gln Ala Val Ala Asp Arg Leu Ala Glu Ala Phe Ala Glu Tyr
 1090 1095 1100

ctg cat gaa aaa gtg cgt aaa gag att tgg ggt tat gcg agc gat gaa 3360
 Leu His Glu Lys Val Arg Lys Glu Ile Trp Gly Tyr Ala Ser Asp Glu
 1105 1110 1115 1120

aat ctc tcc aat gat gac ctg atc cgt gag cgt tat cag ggc att cga 3408
 Asn Leu Ser Asn Asp Asp Leu Ile Arg Glu Arg Tyr Gln Gly Ile Arg
 1125 1130 1135

ccc gcg ccg ggg tat ccc gcg tgt cct gag cat acc gag aaa gcg act 3456
 Pro Ala Pro Gly Tyr Pro Ala Cys Pro Glu His Thr Glu Lys Ala Thr
 1140 1145 1150

ttg tgg cag atg cta aat gtc gaa gag acc ata ggt atg tca ctg acc 3504
 Leu Trp Gln Met Leu Asn Val Glu Glu Thr Ile Gly Met Ser Leu Thr
 1155 1160 1165

aca agc tat gcg atg tgg ccg ggc gct tcg gta tcc ggt tgg tat ttc 3552
 Thr Ser Tyr Ala Met Trp Pro Gly Ala Ser Val Ser Gly Trp Tyr Phe
 1170 1175 1180

tcg cat ccc gat tct cgc tat ttt gcg gta gcg cag atc caa cca gat 3600
 Ser His Pro Asp Ser Arg Tyr Phe Ala Val Ala Gln Ile Gln Pro Asp
 1185 1190 1195 1200

caa ctg cac agc tac gct gag cgt aaa ggt tgg cgt ttg gaa gaa gct 3648
 Gln Leu His Ser Tyr Ala Glu Arg Lys Gly Trp Arg Leu Glu Glu Ala
 1205 1210 1215

gaa aag tgg cta gcg cct aac ctt gat gct taa 3681
 Glu Lys Trp Leu Ala Pro Asn Leu Asp Ala
 1220 1225

<210> 16

<211> 1226

<212> PRT

<213> Vibrio cholerae

<400> 16

Val Gly Lys Glu Val Arg Gln Gln Leu Glu Gln Gln Leu Lys Gln Arg
 1 5 10 15

Ile Leu Leu Ile Asp Gly Gly Met Gly Thr Met Ile Gln Ser Tyr Lys

66

| | | |
|---|-----|-----|
| 20 | 25 | 30 |
| Leu Gln Glu Glu Asp Tyr Arg Gly Ala Arg Phe Val Asp Trp His Cys | | |
| 35 | 40 | 45 |
| Asp Leu Lys Gly Asn Asn Asp Leu Leu Val Leu Thr Gln Pro Gln Ile | | |
| 50 | 55 | 60 |
| Ile Lys Glu Ile His Ser Ala Tyr Leu Glu Ala Gly Ala Asp Ile Leu | | |
| 65 | 70 | 75 |
| Glu Thr Asn Thr Phe Asn Ser Thr Thr Ile Ala Met Ala Asp Tyr Asp | | |
| 85 | 90 | 95 |
| Met Gln Ser Leu Ser Ala Glu Ile Asn Phe Ala Ala Ala Lys Leu Ala | | |
| 100 | 105 | 110 |
| Arg Glu Val Ala Asp Glu Trp Thr Ala Lys Asp Pro Ser Arg Pro Arg | | |
| 115 | 120 | 125 |
| Tyr Val Ala Gly Val Leu Gly Pro Thr Asn Arg Thr Cys Ser Ile Ser | | |
| 130 | 135 | 140 |
| Pro Asp Val Asn Asp Pro Gly Phe Arg Asn Val Thr Phe Asp Gly Leu | | |
| 145 | 150 | 155 |
| Val Glu Ala Tyr Ser Glu Ser Thr Arg Ala Leu Ile Lys Gly Gly Ser | | |
| 165 | 170 | 175 |
| Asp Leu Ile Leu Ile Glu Thr Ile Phe Asp Thr Leu Asn Ala Lys Ala | | |
| 180 | 185 | 190 |
| Cys Ala Phe Ala Val Asp Ser Val Phe Glu Glu Leu Gly Ile Ser Leu | | |
| 195 | 200 | 205 |
| Pro Val Met Ile Ser Gly Thr Ile Thr Asp Ala Ser Gly Arg Thr Leu | | |
| 210 | 215 | 220 |
| Ser Gly Gln Thr Thr Glu Ala Phe Tyr Asn Ala Leu Arg His Val Arg | | |
| 225 | 230 | 235 |
| Pro Ile Ser Phe Gly Leu Asn Cys Ala Leu Gly Pro Asp Glu Leu Arg | | |
| 245 | 250 | 255 |
| Gln Tyr Val Glu Glu Leu Ser Arg Ile Ser Glu Cys Tyr Val Ser Ala | | |
| 260 | 265 | 270 |
| His Pro Asn Ala Gly Leu Pro Asn Ala Phe Gly Glu Tyr Asp Leu Ser | | |
| 275 | 280 | 285 |
| Ala Glu Glu Met Ala Glu His Ile Ala Glu Trp Ala Gln Ala Gly Phe | | |
| 290 | 295 | 300 |
| Leu Asn Leu Val Gly Gly Cys Cys Gly Thr Thr Pro Glu His Ile Ala | | |
| 305 | 310 | 315 |
| Ala Ile Ala Lys Ala Val Glu Gly Val Lys Pro Arg Ala Leu Pro Asp | | |
| 325 | 330 | 335 |
| Leu Lys Val Glu Cys Arg Leu Ser Gly Leu Glu Pro Leu Asn Ile Gly | | |
| 340 | 345 | 350 |

67

Pro Glu Thr Leu Phe Val Asn Val Gly Glu Arg Thr Asn Val Thr Gly
 355 360 365
 Ser Ala Arg Phe Lys Arg Leu Ile Lys Glu Glu Gln Tyr Asp Glu Ala
 370 375 380
 Leu Asp Val Ala Arg Glu Gln Val Glu Asn Gly Ala Gln Ile Ile Asp
 385 390 395 400
 Ile Asn Met Asp Glu Gly Met Leu Asp Ala Glu Ala Cys Met Val Arg
 405 410 415
 Phe Leu Asn Leu Cys Ala Ser Glu Pro Glu Ile Ser Lys Val Pro Val
 420 425 430
 Met Val Asp Ser Ser Lys Trp Glu Val Ile Glu Ala Gly Leu Lys Cys
 435 440 445
 Ile Gln Gly Lys Gly Ile Val Asn Ser Ile Ser Leu Lys Glu Gly Lys
 450 455 460
 Glu Lys Phe Ile Ala Gln Ala Lys Leu Val Arg Arg Tyr Gly Ala Ala
 465 470 475 480
 Val Ile Val Met Ala Phe Asp Glu Val Gly Gln Ala Asp Thr Arg Glu
 485 490 495
 Arg Lys Leu Glu Ile Cys Arg Arg Ala Tyr His Ile Leu Val Asp Glu
 500 505 510
 Val Gly Phe Pro Pro Glu Asp Ile Ile Phe Asp Pro Asn Ile Phe Ala
 515 520 525
 Val Ala Thr Gly Ile Asp Glu His Asn Asn Tyr Ala Leu Asp Phe Ile
 530 535 540
 Asn Ala Val Ala Asp Ile Lys Arg Glu Leu Pro His Ala Met Ile Ser
 545 550 555 560
 Gly Gly Val Ser Asn Val Ser Phe Ser Phe Arg Gly Asn Asn Tyr Val
 565 570 575
 Arg Glu Ala Ile His Ala Val Phe Leu Tyr His Cys Phe Lys His Gly
 580 585 590
 Met Asp Met Gly Ile Val Asn Ala Gly Gln Leu Glu Ile Tyr Asp Asn
 595 600 605
 Val Pro Leu Lys Leu Arg Glu Ala Val Glu Asp Val Ile Leu Asn Arg
 610 615 620
 Arg Ser Asp Gly Thr Glu Arg Leu Leu Glu Ile Ala Glu Ala Tyr Arg
 625 630 635 640
 Glu Asn Ser Val Gly Lys Glu Glu Asp Ala Ser Ala Leu Glu Trp Arg
 645 650 655
 Ala Trp Pro Val Ala Lys Arg Leu Glu His Ala Leu Val Lys Gly Ile
 660 665 670
 Thr Glu Phe Ile Val Gln Asp Thr Glu Glu Ala Arg Gln Gln Ala Ser
 675 680 685

Lys Pro Leu Glu Val Ile Glu Gly Pro Leu Met Asp Gly Met Asn Val
 690 695 700
 Val Gly Asp Leu Phe Gly Glu Gly Lys Met Phe Leu Pro Gln Val Val
 705 710 715 720
 Lys Ser Ala Arg Val Met Lys Gln Ala Val Ala Tyr Leu Glu Pro Phe
 725 730 735
 Ile Asn Ala Gln Lys Ser Gly Ser Thr Ser Asn Gly Lys Ile Leu Leu
 740 745 750
 Ala Thr Val Lys Gly Asp Val His Asp Ile Gly Lys Asn Ile Val Gly
 755 760 765
 Val Val Leu Gln Cys Asn Asn Phe Glu Ile Ile Asp Leu Gly Val Met
 770 775 780
 Val Pro Cys Glu Gln Ile Leu Lys Val Ala Arg Glu Gln Asn Val Asp
 785 790 795 800
 Ile Ile Gly Leu Ser Gly Leu Ile Thr Pro Ser Leu Asp Glu Met Val
 805 810 815
 His Val Ala Lys Glu Met Glu Arg Gln Gly Phe Glu Leu Pro Leu Leu
 820 825 830
 Ile Gly Gly Ala Thr Thr Ser Lys Ala His Thr Ala Val Lys Ile Glu
 835 840 845
 Gln Asn Tyr His Ala Pro Val Val Tyr Val Asn Asn Ala Ser Arg Ala
 850 855 860
 Val Gly Val Cys Thr Ser Leu Leu Ser Asp Glu Gln Arg Pro Gly Phe
 865 870 875 880
 Ile Glu Arg Leu Asp Leu Asp Tyr Glu Arg Thr Arg Asp Gln His Ala
 885 890 895
 Arg Lys Thr Pro Lys Ser Arg Pro Val Thr Leu Glu Gln Ala Arg Ala
 900 905 910
 Asn Lys Ala Ala Leu Asp Trp Ala Asn Tyr Thr Pro Pro Ala Pro Ala
 915 920 925
 Lys Pro Gly Val His Val Phe Glu Asn Ile Ala Leu Ala Thr Leu Arg
 930 935 940
 Pro Tyr Ile Asp Trp Thr Pro Phe Phe Met Thr Trp Ser Leu Met Gly
 945 950 955 960
 Lys Tyr Pro Ala Ile Leu Glu His Glu Glu Val Gly Glu Glu Ala Lys
 965 970 975
 Arg Leu Phe His Asp Ala Asn Ala Leu Leu Asp Lys Val Glu Arg Glu
 980 985 990
 Gly Leu Leu Lys Ala Ser Gly Met Cys Ala Leu Phe Pro Ala Ala Ser
 995 1000 1005
 Val Gly Asp Asp Ile Glu Val Tyr Ser Asp Glu Ser Arg Thr Gln Val

69

1010 1015 1020
 Ala His Val Leu Tyr Asn Leu Arg Gln Gln Thr Glu Lys Pro Lys Gly
 1025 1030 1035 1040
 Ala Asn Tyr Cys Leu Ser Asp Tyr Val Ala Pro Lys Glu Ser Gly Lys
 1045 1050 1055
 Arg Asp Trp Ile Gly Ala Phe Ala Val Thr Gly Gly Ile Gly Glu Arg
 1060 1065 1070
 Ala Leu Ala Asp Ala Tyr Lys Ala Gln Gly Asp Asp Tyr Asn Ala Ile
 1075 1080 1085
 Met Ile Gln Ala Val Ala Asp Arg Leu Ala Glu Ala Phe Ala Glu Tyr
 1090 1095 1100
 Leu His Glu Lys Val Arg Lys Glu Ile Trp Gly Tyr Ala Ser Asp Glu
 1105 1110 1115 1120
 Asn Leu Ser Asn Asp Asp Leu Ile Arg Glu Arg Tyr Gln Gly Ile Arg
 1125 1130 1135
 Pro Ala Pro Gly Tyr Pro Ala Cys Pro Glu His Thr Glu Lys Ala Thr
 1140 1145 1150
 Leu Trp Gln Met Leu Asn Val Glu Glu Thr Ile Gly Met Ser Leu Thr
 1155 1160 1165
 Thr Ser Tyr Ala Met Trp Pro Gly Ala Ser Val Ser Gly Trp Tyr Phe
 1170 1175 1180
 Ser His Pro Asp Ser Arg Tyr Phe Ala Val Ala Gln Ile Gln Pro Asp
 1185 1190 1195 1200
 Gln Leu His Ser Tyr Ala Glu Arg Lys Gly Trp Arg Leu Glu Glu Ala
 1205 1210 1215
 Glu Lys Trp Leu Ala Pro Asn Leu Asp Ala
 1220 1225

<210> 17
 <211> 3822
 <212> DNA
 <213> Sinorhizobium meliloti

<220>
 <221> CDS
 <222> (1) .. (3819)
 <223> RSM07338

<400> 17
 gtg agt aaa tcg ata att ctt tgt cgt ttt cag aac ggg aga tct ccc 48
 Val Ser Lys Ser Ile Ile Leu Cys Arg Phe Gln Asn Gly Arg Ser Pro
 1 5 10 15
 atg tcc gcc gcc gac gcc ctc ttt gga aac gtc tcg ccc aag ccg gat 96
 Met Ser Ala Ala Asp Ala Leu Phe Gly Asn Val Ser Pro Lys Pro Asp
 20 25 30
 ggt tcg gaa gtc ttt cgg cag ctc gcc cag gcg gcg gct gaa cgc atc 144

70

| | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Gly | Ser | Glu | Val | Phe | Arg | Gln | Leu | Ala | Gln | Ala | Ala | Ala | Glu | Arg | Ile | | |
| | 35 | | | | | | 40 | | | | | | 45 | | | | |
| ctc | atc | atg | gat | ggc | gcc | atg | gga | acg | gag | atc | cag | cag | ctc | ggt | ttc | 192 | |
| Leu | Ile | Met | Asp | Gly | Ala | Met | Gly | Thr | Glu | Ile | Gln | Gln | Leu | Gly | Phe | | |
| | 50 | | | | | 55 | | | | | 60 | | | | | | |
| gtg | gag | gat | cac | ttc | cgc | ggc | gag | cgc | ttc | ggt | ggc | tgc | gcc | tgc | cat | 240 | |
| Val | Glu | Asp | His | Phe | Arg | Gly | Glu | Arg | Phe | Gly | Gly | Cys | Ala | Cys | His | | |
| | 65 | | | | 70 | | | | 75 | | | | | 80 | | | |
| cag | cag | ggc | aac | aac | gac | ctc | ctg | acg | ctc | act | cag | ccg | aag | gcg | atc | 288 | |
| Gln | Gln | Gly | Asn | Asn | Asp | Leu | Leu | Thr | Leu | Thr | Gln | Pro | Lys | Ala | Ile | | |
| | | | 85 | | | | | 90 | | | | | 95 | | | | |
| gag | gat | att | cat | tac | cac | tac | gcc | atc | gcc | ggc | gcc | gat | atc | ctc | gaa | 336 | |
| Glu | Asp | Ile | His | Tyr | His | Tyr | Ala | Ile | Ala | Gly | Ala | Asp | Ile | Leu | Glu | | |
| | 100 | | | | | | 105 | | | | | | 110 | | | | |
| acc | aac | acc | ttc | tcc | tcg | acg | cgg | atc | gcc | cag | gcc | gat | tac | ggc | atg | 384 | |
| Thr | Asn | Thr | Phe | Ser | Ser | Thr | Arg | Ile | Ala | Gln | Ala | Asp | Tyr | Gly | Met | | |
| | 115 | | | | | 120 | | | | | | 125 | | | | | |
| gag | gac | atg | gtc | tac | gat | ctc | aat | cgc | gac | ggc | gcg | cgg | ctg | gcg | cgg | 432 | |
| Glu | Asp | Met | Val | Tyr | Asp | Leu | Asn | Arg | Asp | Gly | Ala | Arg | Leu | Ala | Arg | | |
| | 130 | | | | | 135 | | | | 140 | | | | | | | |
| cga | gcc | gcg | aag | cgg | gcc | gag | gcg | gag | gat | ggc | cgg | cgg | cgc | ttc | gtg | 480 | |
| Arg | Ala | Ala | Lys | Arg | Ala | Glu | Ala | Glu | Asp | Gly | Arg | Arg | Arg | Phe | Val | | |
| | 145 | | | | 150 | | | | 155 | | | | | 160 | | | |
| gca | ggc | gcg | ctc | ggc | ccc | acc | aac | cgc | acc | gct | tcg | att | tcg | ccg | gac | 528 | |
| Ala | Gly | Ala | Leu | Gly | Pro | Thr | Asn | Arg | Thr | Ala | Ser | Ile | Ser | Pro | Asp | | |
| | | | 165 | | | | | 170 | | | | | | 175 | | | |
| gtc | aac | aac | ccc | ggc | tat | cga | gcc | gtc | agc | ttc | gac | gat | ctg | agg | ctc | 576 | |
| Val | Asn | Asn | Pro | Gly | Tyr | Arg | Ala | Val | Ser | Phe | Asp | Asp | Leu | Arg | Leu | | |
| | 180 | | | | | | 185 | | | | | | 190 | | | | |
| gcc | tat | gcc | gag | cag | gtg | cgg | ggc | ctc | atc | gac | ggc | ggt | gcc | gac | atc | 624 | |
| Ala | Tyr | Ala | Glu | Gln | Val | Arg | Gly | Leu | Ile | Asp | Gly | Gly | Ala | Asp | Ile | | |
| | 195 | | | | | 200 | | | | | | 205 | | | | | |
| atc | ctg | atc | gag | acg | atc | ttc | gac | acg | ctg | aat | gcc | aag | gcg | gcg | atc | 672 | |
| Ile | Leu | Ile | Glu | Thr | Ile | Phe | Asp | Thr | Leu | Asn | Ala | Lys | Ala | Ala | Ile | | |
| | 210 | | | | | 215 | | | | 220 | | | | | | | |
| ttc | gcg | acg | cag | gaa | gtc | ttt | gcc | gaa | aag | ggc | gtc | cgc | ctt | ccg | gtg | 720 | |
| Phe | Ala | Thr | Gln | Glu | Val | Phe | Ala | Glu | Lys | Gly | Val | Arg | Leu | Pro | Val | | |
| | 225 | | | | 230 | | | | | 235 | | | | 240 | | | |
| atg | atc | tcc | gga | acg | atc | acc | gat | ctc | tcc | ggc | cgt | acc | ctc | tcc | ggc | 768 | |
| Met | Ile | Ser | Gly | Thr | Ile | Thr | Asp | Leu | Ser | Gly | Arg | Thr | Leu | Ser | Gly | | |
| | | | 245 | | | | | 250 | | | | | 255 | | | | |
| cag | acg | cct | acg | gcc | ttc | tgg | tat | tcg | gtg | cgc | cat | gcg | gat | ccg | ttt | 816 | |
| Gln | Thr | Pro | Thr | Ala | Phe | Trp | Tyr | Ser | Val | Arg | His | Ala | Asp | Pro | Phe | | |
| | | | 260 | | | | | 265 | | | | | 270 | | | | |
| acg | atc | ggg | ctc | aac | tgc | gcg | ctc | ggc | gca | aat | gcg | atg | cgc | gcc | cat | 864 | |
| Thr | Ile | Gly | Leu | Asn | Cys | Ala | Leu | Gly | Ala | Asn | Ala | Met | Arg | Ala | His | | |
| | 275 | | | | | 280 | | | | | | 285 | | | | | |

| | |
|---|------|
| ata gac gag ctt tcg gcg gtc gcc gac acg ctc gtc tgc gcc tat ccg Ile Asp Glu Leu Ser Ala Val Ala Asp Thr Leu Val Cys Ala Tyr Pro 290 295 300 | 912 |
| aat gcc ggc ctg ccg aac gag ttc ggc cgc tat gac gaa agc ccc gag Asn Ala Gly Leu Pro Asn Glu Phe Gly Arg Tyr Asp Glu Ser Pro Glu 305 310 315 320 | 960 |
| cag atg gcg gcg cag gtc gag ggc ttc gcc cgg gac ggt ctc gtc aac Gln Met Ala Ala Gln Val Glu Gly Phe Ala Arg Asp Gly Leu Val Asn 325 330 335 | 1008 |
| atc gtc ggc ggc tgc tgc ggt tcc acg ccg gcc cat atc cgc gcc att Ile Val Gly Gly Cys Cys Gly Ser Thr Pro Ala His Ile Arg Ala Ile 340 345 350 | 1056 |
| gcc gaa gcg gtt gcc aaa tat ccg ccg cgc cgg gtg ccc gag atc gat Ala Glu Ala Val Ala Lys Tyr Pro Pro Arg Arg Val Pro Glu Ile Asp 355 360 365 | 1104 |
| cgc cgc atg cgg ctt tcc ggc ctc gaa ccc ttc acg ctt acc gac gag Arg Arg Met Arg Leu Ser Gly Leu Glu Pro Phe Thr Leu Thr Asp Glu 370 375 380 | 1152 |
| att ccc ttc gtc aac gtc ggc gaa cgc acc aac gtc acc ggc tcg gcg Ile Pro Phe Val Asn Val Gly Glu Arg Thr Asn Val Thr Gly Ser Ala 385 390 395 400 | 1200 |
| aag ttc cgc aag ctg atc acc gcc ggg gac tac gcc gcc gca ctc gat Lys Phe Arg Lys Leu Ile Thr Ala Gly Asp Tyr Ala Ala Ala Leu Asp 405 410 415 | 1248 |
| gtg gcg cgt gat cag gtg gcg aat ggc gcc cag atc atc gac gtc aac Val Ala Arg Asp Gln Val Ala Asn Gly Ala Gln Ile Ile Asp Val Asn 420 425 430 | 1296 |
| atg gac gaa ggc ctg atc gat tcg aag cag gtg atg gtc gag ttc ctg Met Asp Glu Gly Leu Ile Asp Ser Lys Gln Val Met Val Glu Phe Leu 435 440 445 | 1344 |
| aac ctc gtc gcc tcc gag ccg gat atc gcc cgt gta ccg gtg atg atc Asn Leu Val Ala Ser Glu Pro Asp Ile Ala Arg Val Pro Val Met Ile 450 455 460 | 1392 |
| gat tcg tcg aaa tgg gag gtg atc gaa gcc ggg ctc aaa tgc gtc cag Asp Ser Ser Lys Trp Glu Val Ile Glu Ala Gly Leu Lys Cys Val Gln 465 470 475 480 | 1440 |
| ggc aag gcg ctg gtg aac tcc atc tcg ctc aag gaa ggc gag gcg gct Gly Lys Ala Leu Val Asn Ser Ile Ser Leu Lys Glu Gly Glu Ala Ala 485 490 495 | 1488 |
| ttc ctg cac cat gcg cgc ctc gtg cgc gcc tat ggc gcc gcg gtc gtg Phe Leu His His Ala Arg Leu Val Arg Ala Tyr Gly Ala Ala Val Val 500 505 510 | 1536 |
| gtg atg gcg ttc gac gag aag ggc cag gcc gac acg aaa acc cgc aag Val Met Ala Phe Asp Glu Lys Gly Gln Ala Asp Thr Lys Thr Arg Lys 515 520 525 | 1584 |
| gtg gaa atc tgc cgg cgg gcc tat cgg ctg ctg acg gaa gag gtt ggc | 1632 |

| Val | Glu | Ile | Cys | Arg | Arg | Ala | Tyr | Arg | Leu | Leu | Thr | Glu | Glu | Val | Gly | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| 530 | | | | | | 535 | | | | | 540 | | | | | |
| ttc | ccc | ccg | gag | gac | atc | atc | ttc | gac | ccg | aat | atc | ttc | gcg | gtc | gcg | 1680 |
| Phe | Pro | Pro | Glu | Asp | Ile | Ile | Phe | Asp | Pro | Asn | Ile | Phe | Ala | Val | Ala | |
| 545 | | | | | 550 | | | | | 555 | | | | | 560 | |
| acc | ggc | atc | gag | gag | cac | aac | aat | tac | ggc | gtc | gac | ttc | atc | gag | gcg | 1728 |
| Thr | Gly | Ile | Glu | Glu | His | Asn | Asn | Tyr | Gly | Val | Asp | Phe | Ile | Glu | Ala | |
| | | | | 565 | | | | | 570 | | | | | 575 | | |
| acg | cac | gag | atc | atc | gcg | gca | ctg | ccg | cat | gtc | cac | gtc | tcc | ggc | ggc | 1776 |
| Thr | His | Glu | Ile | Ile | Ala | Ala | Leu | Pro | His | Val | His | Val | Ser | Gly | Gly | |
| | | | 580 | | | | | 585 | | | | | 590 | | | |
| gtg | tcg | aac | ctc | tcc | ttt | tcc | ttc | cgc | ggc | aac | gag | ccg | gtg | cgc | gag | 1824 |
| Val | Ser | Asn | Leu | Ser | Phe | Ser | Phe | Arg | Gly | Asn | Glu | Pro | Val | Arg | Glu | |
| | | 595 | | | | | 600 | | | | | 605 | | | | |
| gcg | atg | cac | gcc | atc | ttc | ctt | tat | cac | gcg | atc | cag | gcc | ggc | atg | gac | 1872 |
| Ala | Met | His | Ala | Ile | Phe | Leu | Tyr | His | Ala | Ile | Gln | Ala | Gly | Met | Asp | |
| | 610 | | | | | 615 | | | | | 620 | | | | | |
| atg | ggc | atc | gtc | aat | gcc | gga | cag | ctc | gcc | gtc | tat | gat | gcg | atc | gac | 1920 |
| Met | Gly | Ile | Val | Asn | Ala | Gly | Gln | Leu | Ala | Val | Tyr | Asp | Ala | Ile | Asp | |
| 625 | | | | | 630 | | | | | 635 | | | | | 640 | |
| ccg | gaa | ctg | cgc | gaa | acc | tgc | gag | gac | gtg | gtg | ctc | aac | cgc | cgg | gcc | 1968 |
| Pro | Glu | Leu | Arg | Glu | Thr | Cys | Glu | Asp | Val | Val | Leu | Asn | Arg | Arg | Ala | |
| | | | | 645 | | | | | 650 | | | | | 655 | | |
| gat | tcg | acc | gag | cgc | ctc | ctg | gag | atc | gcc | gag | cgc | tat | cgc | ggg | aag | 2016 |
| Asp | Ser | Thr | Glu | Arg | Leu | Leu | Glu | Ile | Ala | Glu | Arg | Tyr | Arg | Gly | Lys | |
| | | | 660 | | | | | 665 | | | | | 670 | | | |
| ggc | ggg | agc | cag | ggc | aag | gag | aag | gac | ctt | gcc | tgg | cgc | gaa | tgg | ccg | 2064 |
| Gly | Gly | Ser | Gln | Gly | Lys | Glu | Lys | Asp | Leu | Ala | Trp | Arg | Glu | Trp | Pro | |
| | | 675 | | | | | 680 | | | | | 685 | | | | |
| gtg | gag | aag | cgg | ctc | gaa | cac | gcg | ctc | gtc | aat | gga | att | acc | gaa | ttt | 2112 |
| Val | Glu | Lys | Arg | Leu | Glu | His | Ala | Leu | Val | Asn | Gly | Ile | Thr | Glu | Phe | |
| | 690 | | | | | 695 | | | | | 700 | | | | | |
| atc | gaa | gcc | gat | acg | gaa | gag | gcc | cgg | ctt | gcc | gcc | gag | cgg | ccg | ctg | 2160 |
| Ile | Glu | Ala | Asp | Thr | Glu | Glu | Ala | Arg | Leu | Ala | Ala | Glu | Arg | Pro | Leu | |
| 705 | | | | | 710 | | | | | 715 | | | | | 720 | |
| cat | gtc | atc | gaa | ggc | ccg | ctg | atg | gcc | ggg | atg | aac | gtc | gtg | ggc | gat | 2208 |
| His | Val | Ile | Glu | Gly | Pro | Leu | Met | Ala | Gly | Met | Asn | Val | Val | Gly | Asp | |
| | | | | 725 | | | | | 730 | | | | | 735 | | |
| ctc | ttc | ggt | tcc | ggc | aag | atg | ttc | | | | | | | | | |

| | |
|---|------|
| atc ctg atg gcg acc gtc aag ggc gac gtg cac gac atc ggc aag aac Ile Leu Met Ala Thr Val Lys Gly Asp Val His Asp Ile Gly Lys Asn 785 790 795 800 | 2400 |
| atc gtc ggc gtc gtg ctc gcc tgc aac aat tac gag atc atc gac ctc Ile Val Gly Val Val Leu Ala Cys Asn Tyr Glu Ile Ile Asp Leu 805 810 815 | 2448 |
| ggc gtc atg gtg ccc tcg gct aag atc ctc gaa gtg gcg cgc gaa cag Gly Val Met Val Pro Ser Ala Lys Ile Leu Glu Val Ala Arg Glu Gln 820 825 830 | 2496 |
| aag gtc gac atc gtc ggt ctt tcc ggc ctc atc acg ccg tcg ctg gac Lys Val Asp Ile Val Gly Leu Ser Gly Leu Ile Thr Pro Ser Leu Asp 835 840 845 | 2544 |
| gag atg gcg cat gtc gct tcc gag ctc gaa cgg gag ggc ttc gat gtc Glu Met Ala His Val Ala Ser Glu Leu Glu Arg Glu Gly Phe Asp Val 850 855 860 | 2592 |
| ccg ctg ctg atc ggc ggg gcg acg acc agc cgc gtg cac acg gcc gtg Pro Leu Leu Ile Gly Gly Ala Thr Thr Ser Arg Val His Thr Ala Val 865 870 875 880 | 2640 |
| aag atc aat ccg cgt tac agc ctc ggc cag acg gtc tat gtc acc gac Lys Ile Asn Pro Arg Tyr Ser Leu Gly Gln Thr Val Tyr Val Thr Asp 885 890 895 | 2688 |
| gcc agc cgc gcg gtc ggc gtc gta tcg agc ctg ctc tcg ccg gaa gtc Ala Ser Arg Ala Val Gly Val Val Ser Ser Leu Leu Ser Pro Glu Val 900 905 910 | 2736 |
| cgc gac tcc tac aag aaa acg gtc cgc gcg gag tat ctg aag gtt gcc Arg Asp Ser Tyr Lys Lys Thr Val Arg Ala Glu Tyr Leu Lys Val Ala 915 920 925 | 2784 |
| gac gca cat gcc cgc aac gaa gcc gag aag cgc cgt ctg ccg ctt tcc Asp Ala His Ala Arg Asn Glu Ala Glu Lys Arg Arg Leu Pro Leu Ser 930 935 940 | 2832 |
| cag gcg cgg gcg aat gcc ttt cgg ata gat tgg gac gcc cac cag ccg Gln Ala Arg Ala Asn Ala Phe Arg Ile Asp Trp Asp Ala His Gln Pro 945 950 955 960 | 2880 |
| aag gtt ccg tcc ttc ctc ggc acg cgt gtt ttc gag gga tgg gac ctc Lys Val Pro Ser Phe Leu Gly Thr Arg Val Phe Glu Gly Trp Asp Leu 965 970 975 | 2928 |
| gcc gaa ctc gcc cgc tat atc gac tgg acg ccg ttc ttc cag acc tgg Ala Glu Leu Ala Arg Tyr Ile Asp Trp Thr Pro Phe Phe Gln Thr Trp 980 985 990 | 2976 |
| gag ctg aag ggg gta ttc ccg aaa atc ctc gat gac gaa cgc cag ggg Glu Leu Lys Gly Val Phe Pro Lys Ile Leu Asp Asp Glu Arg Gln Gly 995 1000 1005 | 3024 |
| gct gcc gct cgc cag ctc ttc gag gat gcg cag gcg atg gtc gaa aag Ala Ala Ala Arg Gln Leu Phe Glu Asp Ala Gln Ala Met Val Glu Lys 1010 1015 1020 | 3072 |
| atc gtg gcc gag gca tgg ttc gcc ccg aag gcc gtg atc ggc ttc tgg | 3120 |

| | | | | |
|---------------------|-------------------------|-----------------------------|------|--|
| Ile Val Ala Glu Ala | Trp Phe Ala Pro Lys | Ala Val Ile Gly Phe | Trp | |
| 1025 | 1030 | 1035 | 1040 | |
| cgc gcc gcc agc atg | ggc gac gac gtc | cgc ctg ttt gcc gac gag gtg | 3168 | |
| Pro Ala Ala Ser Met | Gly Asp Asp Val Arg | Leu Phe Ala Asp Glu Val | | |
| 1045 | 1050 | 1055 | | |
| cgc gaa gcc gag ctt | gcc acc ttc ttc acg ctc | cgc cag cag atg gtg | 3216 | |
| Arg Glu Ala Glu Leu | Ala Thr Phe Phe Thr | Leu Arg Gln Gln Met Val | | |
| 1060 | 1065 | 1070 | | |
| aag cgc gac ggc cgg | ccg aac gtc gcc ctt | gcc gac ttc gtc gcc ccg | 3264 | |
| Lys Arg Asp Gly Arg | Pro Asn Val Ala Leu | Ala Asp Phe Val Ala Pro | | |
| 1075 | 1080 | 1085 | | |
| gcg gcg agc ggc aag | cgg gac tat gtc ggc | ggt ttc gtg gtg acg gcc | 3312 | |
| Ala Ala Ser Gly Lys | Arg Asp Tyr Val Gly | Gly Phe Val Val Thr Ala | | |
| 1090 | 1095 | 1100 | | |
| ggc atc gag gaa gtg | gcg atc gcc gaa cgc | ttc gaa cgg gcg aac gac | 3360 | |
| Gly Ile Glu Glu Val | Ala Ile Ala Glu Arg | Phe Glu Arg Ala Asn Asp | | |
| 1105 | 1110 | 1115 | 1120 | |
| gat tat tcc tcg atc | atg gtc aag gcg ctt | gcg gac cgc ttc gca gag | 3408 | |
| Asp Tyr Ser Ser Ile | Met Val Lys Ala Leu | Ala Asp Arg Phe Ala Glu | | |
| 1125 | 1130 | 1135 | | |
| gcc ttt gcc gag cgc | atg cat gaa tat gtc | cgc aag gag ctc tgg ggc | 3456 | |
| Ala Phe Ala Glu Arg | Met His Glu Tyr Val | Arg Lys Glu Leu Trp Gly | | |
| 1140 | 1145 | 1150 | | |
| tat gct ccg gac gaa | gcc ttc acg ccg cag | gaa ttg atc gcc gag ccc | 3504 | |
| Tyr Ala Pro Asp Glu | Ala Phe Thr Pro Gln | Glu Leu Ile Ala Glu Pro | | |
| 1155 | 1160 | 1165 | | |
| tat gcc ggc atc cgc | cct gcg ccc ggc tac | ccg gcg cag ccc gac cac | 3552 | |
| Tyr Ala Gly Ile Arg | Pro Ala Pro Gly Tyr | Pro Ala Gln Pro Asp His | | |
| 1170 | 1175 | 1180 | | |
| acg gaa aag gag acg | ctt ttc cgg ctc ctg | gat gcg gaa gcc gct atc | 3600 | |
| Thr Glu Lys Glu Thr | Leu Phe Arg Leu Leu | Asp Ala Glu Ala Ala Ile | | |
| 1185 | 1190 | 1195 | 1200 | |
| ggc gtc cgg ctc acc | gag agc tat gcg atg | tgg ccg ggc tct tcg gta | 3648 | |
| Gly Val Arg Leu Thr | Glu Ser Tyr Ala Met | Trp Pro Gly Ser Ser Val | | |
| 1205 | 1210 | 1215 | | |
| tcg ggc ctc tat gtc | ggc cac ccc gat tcc | tat tac ttc ggc gtc gca | 3696 | |
| Ser Gly Leu Tyr Val | Gly His Pro Asp Ser | Tyr Tyr Phe Gly Val Ala | | |
| 1220 | 1225 | 1230 | | |
| aag atc gag cgc gat | cag gtg gag gac tat | gcc gat cgc aag cgc atg | 3744 | |
| Lys Ile Glu Arg Asp | Gln Val Glu Asp Tyr | Ala Asp Arg Lys Arg Met | | |
| 1235 | 1240 | 1245 | | |
| agc gtc cgc gag gtc | gag cgc tgg ctt tcg | ccg atc ctc aat tac gtg | 3792 | |
| Ser Val Arg Glu Val | Glu Arg Trp Leu Ser | Pro Ile Leu Asn Tyr Val | | |
| 1250 | 1255 | 1260 | | |
| ccg atg ccg gag acg | gaa gcg gcg gag tag | | 3822 | |
| Pro Met Pro Glu Thr | Glu Ala Ala Glu | | | |
| 1265 | 1270 | | | |

<210> 18
 <211> 1273
 <212> PRT
 <213> Sinorhizobium meliloti

<400> 18

Val Ser Lys Ser Ile Ile Leu Cys Arg Phe Gln Asn Gly Arg Ser Pro
 1 5 10 15
 Met Ser Ala Ala Asp Ala Leu Phe Gly Asn Val Ser Pro Lys Pro Asp
 20 25 30
 Gly Ser Glu Val Phe Arg Gln Leu Ala Gln Ala Ala Ala Glu Arg Ile
 35 40 45
 Leu Ile Met Asp Gly Ala Met Gly Thr Glu Ile Gln Gln Leu Gly Phe
 50 55 60
 Val Glu Asp His Phe Arg Gly Glu Arg Phe Gly Gly Cys Ala Cys His
 65 70 75 80
 Gln Gln Gly Asn Asn Asp Leu Leu Thr Leu Thr Gln Pro Lys Ala Ile
 85 90 95
 Glu Asp Ile His Tyr His Tyr Ala Ile Ala Gly Ala Asp Ile Leu Glu
 100 105 110
 Thr Asn Thr Phe Ser Ser Thr Arg Ile Ala Gln Ala Asp Tyr Gly Met
 115 120 125
 Glu Asp Met Val Tyr Asp Leu Asn Arg Asp Gly Ala Arg Leu Ala Arg
 130 135 140
 Arg Ala Ala Lys Arg Ala Glu Ala Glu Asp Gly Arg Arg Arg Phe Val
 145 150 155 160
 Ala Gly Ala Leu Gly Pro Thr Asn Arg Thr Ala Ser Ile Ser Pro Asp
 165 170 175
 Val Asn Asn Pro Gly Tyr Arg Ala Val Ser Phe Asp Asp Leu Arg Leu
 180 185 190
 Ala Tyr Ala Glu Gln Val Arg Gly Leu Ile Asp Gly Gly Ala Asp Ile
 195 200 205
 Ile Leu Ile Glu Thr Ile Phe Asp Thr Leu Asn Ala Lys Ala Ala Ile
 210 215 220
 Phe Ala Thr Gln Glu Val Phe Ala Glu Lys Gly Val Arg Leu Pro Val
 225 230 235 240
 Met Ile Ser Gly Thr Ile Thr Asp Leu Ser Gly Arg Thr Leu Ser Gly
 245 250 255
 Gln Thr Pro Thr Ala Phe Trp Tyr Ser Val Arg His Ala Asp Pro Phe
 260 265 270
 Thr Ile Gly Leu Asn Cys Ala Leu Gly Ala Asn Ala Met Arg Ala His
 275 280 285

76

Ile Asp Glu Leu Ser Ala Val Ala Asp Thr Leu Val Cys Ala Tyr Pro
 290 295 300

Asn Ala Gly Leu Pro Asn Glu Phe Gly Arg Tyr Asp Glu Ser Pro Glu
 305 310 315 320

Gln Met Ala Ala Gln Val Glu Gly Phe Ala Arg Asp Gly Leu Val Asn
 325 330 335

Ile Val Gly Gly Cys Cys Gly Ser Thr Pro Ala His Ile Arg Ala Ile
 340 345 350

Ala Glu Ala Val Ala Lys Tyr Pro Pro Arg Arg Val Pro Glu Ile Asp
 355 360 365

Arg Arg Met Arg Leu Ser Gly Leu Glu Pro Phe Thr Leu Thr Asp Glu
 370 375 380

Ile Pro Phe Val Asn Val Gly Glu Arg Thr Asn Val Thr Gly Ser Ala
 385 390 395 400

Lys Phe Arg Lys Leu Ile Thr Ala Gly Asp Tyr Ala Ala Ala Leu Asp
 405 410 415

Val Ala Arg Asp Gln Val Ala Asn Gly Ala Gln Ile Ile Asp Val Asn
 420 425 430

Met Asp Glu Gly Leu Ile Asp Ser Lys Gln Val Met Val Glu Phe Leu
 435 440 445

Asn Leu Val Ala Ser Glu Pro Asp Ile Ala Arg Val Pro Val Met Ile
 450 455 460

Asp Ser Ser Lys Trp Glu Val Ile Glu Ala Gly Leu Lys Cys Val Gln
 465 470 475 480

Gly Lys Ala Leu Val Asn Ser Ile Ser Leu Lys Glu Gly Glu Ala Ala
 485 490 495

Phe Leu His His Ala Arg Leu Val Arg Ala Tyr Gly Ala Ala Val Val
 500 505 510

Val Met Ala Phe Asp Glu Lys Gly Gln Ala Asp Thr Lys Thr Arg Lys
 515 520 525

Val Glu Ile Cys Arg Arg Ala Tyr Arg Leu Leu Thr Glu Glu Val Gly
 530 535 540

Phe Pro Pro Glu Asp Ile Ile Phe Asp Pro Asn Ile Phe Ala Val Ala
 545 550 555 560

Thr Gly Ile Glu Glu His Asn Asn Tyr Gly Val Asp Phe Ile Glu Ala
 565 570 575

Thr His Glu Ile Ile Ala Ala Leu Pro His Val His Val Ser Gly Gly
 580 585 590

Val Ser Asn Leu Ser Phe Ser Phe Arg Gly Asn Glu Pro Val Arg Glu
 595 600 605

Ala Met His Ala Ile Phe Leu Tyr His Ala Ile Gln Ala Gly Met Asp
 610 615 620

Met Gly Ile Val Asn Ala Gly Gln Leu Ala Val Tyr Asp Ala Ile Asp
 625 630 635 640
 Pro Glu Leu Arg Glu Thr Cys Glu Asp Val Val Leu Asn Arg Arg Ala
 645 650 655
 Asp Ser Thr Glu Arg Leu Leu Glu Ile Ala Glu Arg Tyr Arg Gly Lys
 660 665 670
 Gly Gly Ser Gln Gly Lys Glu Lys Asp Leu Ala Trp Arg Glu Trp Pro
 675 680 685
 Val Glu Lys Arg Leu Glu His Ala Leu Val Asn Gly Ile Thr Glu Phe
 690 695 700
 Ile Glu Ala Asp Thr Glu Glu Ala Arg Leu Ala Ala Glu Arg Pro Leu
 705 710 715 720
 His Val Ile Glu Gly Pro Leu Met Ala Gly Met Asn Val Val Gly Asp
 725 730 735
 Leu Phe Gly Ser Gly Lys Met Phe Leu Pro Gln Val Val Lys Ser Ala
 740 745 750
 Arg Val Met Lys Gln Ala Val Ala Val Leu Leu Pro His Met Glu Glu
 755 760 765
 Glu Lys Arg Ala Asn Gly Gly Gly Glu Ala Arg Glu Ser Ala Gly Lys
 770 775 780
 Ile Leu Met Ala Thr Val Lys Gly Asp Val His Asp Ile Gly Lys Asn
 785 790 795 800
 Ile Val Gly Val Val Leu Ala Cys Asn Asn Tyr Glu Ile Ile Asp Leu
 805 810 815
 Gly Val Met Val Pro Ser Ala Lys Ile Leu Glu Val Ala Arg Glu Gln
 820 825 830
 Lys Val Asp Ile Val Gly Leu Ser Gly Leu Ile Thr Pro Ser Leu Asp
 835 840 845
 Glu Met Ala His Val Ala Ser Glu Leu Glu Arg Glu Gly Phe Asp Val
 850 855 860
 Pro Leu Leu Ile Gly Gly Ala Thr Thr Ser Arg Val His Thr Ala Val
 865 870 875 880
 Lys Ile Asn Pro Arg Tyr Ser Leu Gly Gln Thr Val Tyr Val Thr Asp
 885 890 895
 Ala Ser Arg Ala Val Gly Val Val Ser Ser Leu Leu Ser Pro Glu Val
 900 905 910
 Arg Asp Ser Tyr Lys Lys Thr Val Arg Ala Glu Tyr Leu Lys Val Ala
 915 920 925
 Asp Ala His Ala Arg Asn Glu Ala Glu Lys Arg Arg Leu Pro Leu Ser
 930 935 940
 Gln Ala Arg Ala Asn Ala Phe Arg Ile Asp Trp Asp Ala His Gln Pro

78

945 950 955 960
 Lys Val Pro Ser Phe Leu Gly Thr Arg Val Phe Glu Gly Trp Asp Leu
 965 970 975
 Ala Glu Leu Ala Arg Tyr Ile Asp Trp Thr Pro Phe Phe Gln Thr Trp
 980 985 990
 Glu Leu Lys Gly Val Phe Pro Lys Ile Leu Asp Asp Glu Arg Gln Gly
 995 1000 1005
 Ala Ala Ala Arg Gln Leu Phe Glu Asp Ala Gln Ala Met Val Glu Lys
 1010 1015 1020
 Ile Val Ala Glu Ala Trp Phe Ala Pro Lys Ala Val Ile Gly Phe Trp
 1025 1030 1035 1040
 Pro Ala Ala Ser Met Gly Asp Asp Val Arg Leu Phe Ala Asp Glu Val
 1045 1050 1055
 Arg Glu Ala Glu Leu Ala Thr Phe Phe Thr Leu Arg Gln Gln Met Val
 1060 1065 1070
 Lys Arg Asp Gly Arg Pro Asn Val Ala Leu Ala Asp Phe Val Ala Pro
 1075 1080 1085
 Ala Ala Ser Gly Lys Arg Asp Tyr Val Gly Gly Phe Val Val Thr Ala
 1090 1095 1100
 Gly Ile Glu Glu Val Ala Ile Ala Glu Arg Phe Glu Arg Ala Asn Asp
 1105 1110 1115 1120
 Asp Tyr Ser Ser Ile Met Val Lys Ala Leu Ala Asp Arg Phe Ala Glu
 1125 1130 1135
 Ala Phe Ala Glu Arg Met His Glu Tyr Val Arg Lys Glu Leu Trp Gly
 1140 1145 1150
 Tyr Ala Pro Asp Glu Ala Phe Thr Pro Gln Glu Leu Ile Ala Glu Pro
 1155 1160 1165
 Tyr Ala Gly Ile Arg Pro Ala Pro Gly Tyr Pro Ala Gln Pro Asp His
 1170 1175 1180
 Thr Glu Lys Glu Thr Leu Phe Arg Leu Leu Asp Ala Glu Ala Ala Ile
 1185 1190 1195 1200
 Gly Val Arg Leu Thr Glu Ser Tyr Ala Met Trp Pro Gly Ser Ser Val
 1205 1210 1215
 Ser Gly Leu Tyr Val Gly His Pro Asp Ser Tyr Tyr Phe Gly Val Ala
 1220 1225 1230
 Lys Ile Glu Arg Asp Gln Val Glu Asp Tyr Ala Asp Arg Lys Arg Met
 1235 1240 1245
 Ser Val Arg Glu Val Glu Arg Trp Leu Ser Pro Ile Leu Asn Tyr Val
 1250 1255 1260
 Pro Met Pro Glu Thr Glu Ala Ala Glu
 1265 1270

<210> 19
 <211> 3684
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1) .. (3681)
 <223> REC03905

<400> 19
 gtg agc agc aaa gtg gaa caa ctg cgt gcg cag tta aat gaa cgt att 48
 Val Ser Ser Lys Val Glu Gln Leu Arg Ala Gln Leu Asn Glu Arg Ile
 1 5 10 15
 ctg gtg ctg gac ggc ggt atg ggc acc atg atc cag agt tat cga ctg 96
 Leu Val Leu Asp Gly Gly Met Gly Thr Met Ile Gln Ser Tyr Arg Leu
 20 25 30
 aac gaa gcc gat ttt cgt ggt gaa cgc ttt gcc gac tgg cca tgc gac 144
 Asn Glu Ala Asp Phe Arg Gly Glu Arg Phe Ala Asp Trp Pro Cys Asp
 35 40 45
 ctc aaa ggc aac aac gac ctg ctg gta ctc agt aaa ccg gaa gtg atc 192
 Leu Lys Gly Asn Asn Asp Leu Leu Val Leu Ser Lys Pro Glu Val Ile
 50 55 60
 gcc gct atc cac aac gcc tac ttt gaa gcg ggc gcg gat atc atc gaa 240
 Ala Ala Ile His Asn Ala Tyr Phe Glu Ala Gly Ala Asp Ile Ile Glu
 65 70 75 80
 acc aac acc ttc aac tcc acg acc att gcg atg gcg gat tac cag atg 288
 Thr Asn Thr Phe Asn Ser Thr Thr Ile Ala Met Ala Asp Tyr Gln Met
 85 90 95
 gaa tcc ctg tcg gcg gaa atc aac ttt gcg gcg gcg aaa ctg gcg cga 336
 Glu Ser Leu Ser Ala Glu Ile Asn Phe Ala Ala Ala Lys Leu Ala Arg
 100 105 110
 gct tgt gct gac gag tgg acc gcg cgc acg cca gag aaa ccg cgc tac 384
 Ala Cys Ala Asp Glu Trp Thr Ala Arg Thr Pro Glu Lys Pro Arg Tyr
 115 120 125
 gtt gcc ggt gtt ctc ggc ccg acc aac cgc acg gcg tct att tct ccg 432
 Val Ala Gly Val Leu Gly Pro Thr Asn Arg Thr Ala Ser Ile Ser Pro
 130 135 140
 gac gtc aac gat ccg gca ttt cgt aat atc act ttt gac ggg ctg gtg 480
 Asp Val Asn Asp Pro Ala Phe Arg Asn Ile Thr Phe Asp Gly Leu Val
 145 150 155 160
 gcg gct tat cga gag tcc acc aaa gcg ctg gtg gaa ggt ggc gcg gat 528
 Ala Ala Tyr Arg Glu Ser Thr Lys Ala Leu Val Glu Gly Gly Ala Asp
 165 170 175
 ctg atc ctg att gaa acc gtt ttc gac acc ctt aac gcc aaa gcg gcg 576
 Leu Ile Leu Ile Glu Thr Val Phe Asp Thr Leu Asn Ala Lys Ala Ala
 180 185 190
 gta ttt gcg gtg aaa acg gag ttt gaa gcg ctg ggc gtt gag ctg ccg 624
 Val Phe Ala Val Lys Thr Glu Phe Glu Ala Leu Gly Val Glu Leu Pro

80

| 195 | 200 | 205 | |
|---|-----|-----|------|
| att atg atc tcc ggc acc atc acc gac gcc tcc ggg cgc acg ctc tcc Ile Met Ile Ser Gly Thr Ile Thr Asp Ala Ser Gly Arg Thr Leu Ser 210 215 220 | | | 672 |
| ggg cag acc acc gaa gca ttt tac aac tca ttg cgc cac gcc gaa gct Gly Gln Thr Thr Glu Ala Phe Tyr Asn Ser Leu Arg His Ala Glu Ala 225 230 235 240 | | | 720 |
| ctg acc ttt ggc ctg aac tgt gcg ctg ggg ccc gat gaa ctg cgc cag Leu Thr Phe Gly Leu Asn Cys Ala Leu Gly Pro Asp Glu Leu Arg Gln 245 250 255 | | | 768 |
| tac gtg cag gag ctg tca cgg att gcg gaa tgc tac gtc acc gcg cac Tyr Val Gln Glu Leu Ser Arg Ile Ala Glu Cys Tyr Val Thr Ala His 260 265 270 | | | 816 |
| ccg aac gcc ggg cta ccc aac gcc ttt ggt gag tac gat ctc gac gcc Pro Asn Ala Gly Leu Pro Asn Ala Phe Gly Glu Tyr Asp Leu Asp Ala 275 280 285 | | | 864 |
| gac acg atg gca aaa cag ata cgt gaa tgg gcg caa gcg ggt ttt ctc Asp Thr Met Ala Lys Gln Ile Arg Glu Trp Ala Gln Ala Gly Phe Leu 290 295 300 | | | 912 |
| aat atc gtc ggc ggc tgc tgt ggc acc acg cca caa cat att gca gcg Asn Ile Val Gly Gly Cys Cys Gly Thr Thr Pro Gln His Ile Ala Ala 305 310 315 320 | | | 960 |
| atg agt cgt gca gta gaa gga tta gcg ccg cgc aaa ctg ccg gaa att Met Ser Arg Ala Val Glu Gly Leu Ala Pro Arg Lys Leu Pro Glu Ile 325 330 335 | | | 1008 |
| ccc gta gcc tgc cgt ttg tcc ggc ctg gag ccg ctg aac att ggc gaa Pro Val Ala Cys Arg Leu Ser Gly Leu Glu Pro Leu Asn Ile Gly Glu 340 345 350 | | | 1056 |
| gat agc ctg ttt gtg aac gtg ggt gaa cgc acc aac gtc acc ggt tcc Asp Ser Leu Phe Val Asn Val Gly Glu Arg Thr Asn Val Thr Gly Ser 355 360 365 | | | 1104 |
| gct aag ttc aag cgc ctg atc aaa gaa gag aaa tac agc gag gcg ctg Ala Lys Phe Lys Arg Leu Ile Lys Glu Glu Lys Tyr Ser Glu Ala Leu 370 375 380 | | | 1152 |
| gat gtc gcg cgt caa cag gtg gaa aac ggc gcg cag att atc gat atc Asp Val Ala Arg Gln Gln Val Glu Asn Gly Ala Gln Ile Ile Asp Ile 385 390 395 400 | | | 1200 |
| aac atg gat gaa ggg atg ctc gat gcc gaa gcg gcg atg gtg cgt ttt Asn Met Asp Glu Gly Met Leu Asp Ala Glu Ala Ala Met Val Arg Phe 405 410 415 | | | 1248 |
| ctc aat ctg att gcc ggt gaa ccg gat atc gct cgc gtg ccg att atg Leu Asn Leu Ile Ala Gly Glu Pro Asp Ile Ala Arg Val Pro Ile Met 420 425 430 | | | 1296 |
| atc gac tcc tca aaa tgg gac gtc att gaa aaa ggt ctg aag tgt atc Ile Asp Ser Ser Lys Trp Asp Val Ile Glu Lys Gly Leu Lys Cys Ile 435 440 445 | | | 1344 |

81

| | |
|---|------|
| cag ggc aaa ggc att gtt aac tct atc tcg atg aaa gag ggc gtc gat Gln Gly Lys Gly Ile Val Asn Ser Ile Ser Met Lys Glu Gly Val Asp 450 455 460 | 1392 |
| gcc ttt atc cat cac gcg aaa ttg ttg cgt cgc tac ggt gcg gca gtg Ala Phe Ile His His Ala Lys Leu Leu Arg Arg Tyr Gly Ala Ala Val 465 470 475 480 | 1440 |
| gtg gta atg gcc ttt gac gaa cag gga cag gcc gat act cgc gca cgg Val Val Met Ala Phe Asp Glu Gln Gly Gln Ala Asp Thr Arg Ala Arg 485 490 495 | 1488 |
| aaa atc gag att tgc cgt cgg gcg tac aaa atc ctc acc gaa gag gtt Lys Ile Glu Ile Cys Arg Arg Ala Tyr Lys Ile Leu Thr Glu Glu Val 500 505 510 | 1536 |
| ggc ttc ccg cca gaa gat atc atc ttc gac cca aac atc ttc gcg gtc Gly Phe Pro Pro Glu Asp Ile Ile Phe Asp Pro Asn Ile Phe Ala Val 515 520 525 | 1584 |
| gca act ggc att gaa gag cac aac aac tac gcg cag gac ttt atc ggc Ala Thr Gly Ile Glu Glu His Asn Asn Tyr Ala Gln Asp Phe Ile Gly 530 535 540 | 1632 |
| gcg tgt gaa gac atc aaa cgc gaa ctg ccg cac gcg ctg att tcc ggc Ala Cys Glu Asp Ile Lys Arg Glu Leu Pro His Ala Leu Ile Ser Gly 545 550 555 560 | 1680 |
| ggc gta tct aac gtt tct ttc tcg ttc cgt ggc aac gat ccg gtg cgc Gly Val Ser Asn Val Ser Phe Ser Phe Arg Gly Asn Asp Pro Val Arg 565 570 575 | 1728 |
| gaa gcc att cac gca gtg ttc ctc tac tac gct att cgc aat ggc atg Glu Ala Ile His Ala Val Phe Leu Tyr Tyr Ala Ile Arg Asn Gly Met 580 585 590 | 1776 |
| gat atg ggg atc gtc aac gcc ggg caa ctg gcg att tac gac gac cta Asp Met Gly Ile Val Asn Ala Gly Gln Leu Ala Ile Tyr Asp Asp Leu 595 600 605 | 1824 |
| ccc gct gaa ctg cgc gac gcg gtg gaa gat gtg att ctt aat cgt cgc Pro Ala Glu Leu Arg Asp Ala Val Glu Asp Val Ile Leu Asn Arg Arg 610 615 620 | 1872 |
| gac gat ggc acc gag cgt tta ctg gag ctt gcc gag aaa tat cgc ggc Asp Asp Gly Thr Glu Arg Leu Leu Glu Leu Ala Glu Lys Tyr Arg Gly 625 630 635 640 | 1920 |
| agc aaa acc gac gac acc gcc aac gcc cag cag gcg gag tgg cgc tcg Ser Lys Thr Asp Asp Thr Ala Asn Ala Gln Gln Ala Glu Trp Arg Ser 645 650 655 | 1968 |
| tgg gaa gtg aat aaa cgt ctg gaa tac tcg ctg gtc aaa ggc att acc Trp Glu Val Asn Lys Arg Leu Glu Tyr Ser Leu Val Lys Gly Ile Thr 660 665 670 | 2016 |
| gag ttt atc gag cag gat acc gaa gaa gcc cgc cag cag gct acg cgc Glu Phe Ile Glu Gln Asp Thr Glu Glu Ala Arg Gln Gln Ala Thr Arg 675 680 685 | 2064 |
| ccg att gaa gtg att gaa ggc ccg ttg atg gac ggc atg aat gtg gtc Pro Ile Glu Val Ile Glu Gly Pro Leu Met Asp Gly Met Asn Val Val | 2112 |

82

| 690 | 695 | 700 | |
|---|-----|-----|------|
| ggc gac ctg ttt ggc gaa ggg aaa atg ttc ctg cca cag gtg gtc aaa Gly Asp Leu Phe Gly Glu Gly Lys Met Phe Leu Pro Gln Val Val Lys 705 710 715 720 | | | 2160 |
| tcg gcg cgc gtc atg aaa cag gcg gtg gcc tac ctc gaa ccg ttt att Ser Ala Arg Val Met Lys Gln Ala Val Ala Tyr Leu Glu Pro Phe Ile 725 730 735 | | | 2208 |
| gaa gcc agc aaa gag cag ggc aaa acc aac ggc aag atg gtg atc gcc Glu Ala Ser Lys Gly Glu Gln Gly Lys Thr Asn Gly Lys Met Val Ile Ala 740 745 750 | | | 2256 |
| acc gtg aag ggc gac gtc cac gac atc ggt aaa aat atc gtt ggt gtg Thr Val Lys Gly Asp Val His Asp Ile Gly Lys Asn Ile Val Gly Val 755 760 765 | | | 2304 |
| gtg ctg caa tgt aac aac tac gaa att gtc gat ctc ggc gtt atg gtg Val Leu Gln Cys Asn Asn Tyr Glu Ile Val Asp Leu Gly Val Met Val 770 775 780 | | | 2352 |
| cct gcg gaa aaa att ctc cgt acc gct aaa gaa gtg aat gct gat ctg Pro Ala Glu Lys Ile Leu Arg Thr Ala Lys Glu Val Asn Ala Asp Leu 785 790 795 800 | | | 2400 |
| att ggc ctt tcg ggg ctt atc acg ccg tcg ctg gac gag atg gtt aac Ile Gly Leu Ser Gly Leu Ile Thr Pro Ser Leu Asp Glu Met Val Asn 805 810 815 | | | 2448 |
| gtg gcg aaa gag atg gag cgt cag ggc ttc act att ccg tta ctg att Val Ala Lys Glu Met Glu Arg Gln Gly Phe Thr Ile Pro Leu Leu Ile 820 825 830 | | | 2496 |
| ggc ggc gcg acg acc tca aaa gcg cac acg gcg gtg aaa atc gag cag Gly Gly Ala Thr Thr Ser Lys Ala His Thr Ala Val Lys Ile Glu Gln 835 840 845 | | | 2544 |
| aac tac agc ggc ccg acg gtg tat gtg cag aat gcc tcg cgt acc gtt Asn Tyr Ser Gly Pro Thr Val Tyr Val Gln Asn Ala Ser Arg Thr Val 850 855 860 | | | 2592 |
| ggt gtg gtg gcg gcg ctg ctt tcc gat acc cag cgt gat gat ttt gtc Gly Val Val Ala Ala Leu Leu Ser Asp Thr Gln Arg Asp Asp Phe Val 865 870 875 880 | | | 2640 |
| gct cgt acc cgc aag gag tac gaa acc gta cgt att cag cac ggg cgc Ala Arg Thr Arg Lys Glu Tyr Glu Thr Val Arg Ile Gln His Gly Arg 885 890 895 | | | 2688 |
| aag aaa ccg cgc aca cca ccg gtc acg ctg gaa gcg gcg cgc gat aac Lys Lys Pro Arg Thr Pro Pro Val Thr Leu Glu Ala Ala Arg Asp Asn 900 905 910 | | | 2736 |
| gat ttc gct ttt gac tgg cag gct tac acg ccg ccg gtg gcg cac cgt Asp Phe Ala Phe Asp Trp Gln Ala Tyr Thr Pro Pro Val Ala His Arg 915 920 925 | | | 2784 |
| ctc ggc gtg cag gaa gtc gaa gcc agc atc gaa acg ctg cgt aat tac Leu Gly Val Gln Glu Val Glu Ala Ser Ile Glu Thr Leu Arg Asn Tyr 930 935 940 | | | 2832 |

| | |
|---|------|
| atc gac tgg aca ccg ttc ttt atg acc tgg tgc ctg gcc ggg aag tat | 2880 |
| Ile Asp Trp Thr Pro Phe Phe Met Thr Trp Ser Leu Ala Gly Lys Tyr | |
| 945 950 955 960 | |
| ccg cgc att ctg gaa gat gaa gtg gtg ggc gtt gag gcg cag cgg ctg | 2928 |
| Pro Arg Ile Leu Glu Asp Glu Val Val Gly Val Glu Ala Gln Arg Leu | |
| 965 970 975 | |
| ttt aaa gac gcc aac gac atg ctg gat aaa tta agc gcc gag aaa acg | 2976 |
| Phe Lys Asp Ala Asn Asp Met Leu Asp Lys Leu Ser Ala Glu Lys Thr | |
| 980 985 990 | |
| ctg aat ccg cgt ggc gtg gtg ggc ctg ttc ccg gca aac cgt gtg ggc | 3024 |
| Leu Asn Pro Arg Gly Val Val Gly Leu Phe Pro Ala Asn Arg Val Gly | |
| 995 1000 1005 | |
| gat gac att gaa atc tac cgt gac gaa acg cgt acc cat gtg atc aac | 3072 |
| Asp Asp Ile Glu Ile Tyr Arg Asp Glu Thr Arg Thr His Val Ile Asn | |
| 1010 1015 1020 | |
| gtc agc cac cat ctg cgt caa cag acc gaa aaa aca ggc ttc gct aac | 3120 |
| Val Ser His His Leu Arg Gln Gln Thr Glu Lys Thr Gly Phe Ala Asn | |
| 1025 1030 1035 1040 | |
| tac tgt ctc gct gac ttc gtt gcg ccg aag ctt tct ggt aaa gca gat | 3168 |
| Tyr Cys Leu Ala Asp Phe Val Ala Pro Lys Leu Ser Gly Lys Ala Asp | |
| 1045 1050 1055 | |
| tac atc ggc gca ttt gcc gtg act ggc ggg ctg gaa gag gac gca ctg | 3216 |
| Tyr Ile Gly Ala Phe Ala Val Thr Gly Gly Leu Glu Glu Asp Ala Leu | |
| 1060 1065 1070 | |
| gct gat gcc ttt gaa gcg cag cac gat gat tac aac aaa atc atg gtg | 3264 |
| Ala Asp Ala Phe Glu Ala Gln His Asp Asp Tyr Asn Lys Ile Met Val | |
| 1075 1080 1085 | |
| aaa gcg ctt gcc gac cgt tta gcc gaa gcc ttt gcg gag tat ctc cat | 3312 |
| Lys Ala Leu Ala Asp Arg Leu Ala Glu Ala Phe Ala Glu Tyr Leu His | |
| 1090 1095 1100 | |
| gag cgt gtg cgt aaa gtc tac tgg ggc tat gcg ccg aac gag aac ctc | 3360 |
| Glu Arg Val Arg Lys Val Tyr Trp Gly Tyr Ala Pro Asn Glu Asn Leu | |
| 1105 1110 1115 1120 | |
| agc aac gaa gag ctg atc cgc gaa aac tac cag ggc atc cgt ccg gca | 3408 |
| Ser Asn Glu Glu Leu Ile Arg Glu Asn Tyr Gln Gly Ile Arg Pro Ala | |
| 1125 1130 1135 | |
| ccg ggc tat ccg gcc tgc ccg gaa cat acg gaa aaa gcc acc atc tgg | 3456 |
| Pro Gly Tyr Pro Ala Cys Pro Glu His Thr Glu Lys Ala Thr Ile Trp | |
| 1140 1145 1150 | |
| gag ctg ctg gaa gtg gaa aaa cac act ggc atg aaa ctc aca gaa tct | 3504 |
| Glu Leu Leu Glu Val Glu Lys His Thr Gly Met Lys Leu Thr Glu Ser | |
| 1155 1160 1165 | |
| ttc gcc atg tgg ccc ggt gca tgc gtt tgc ggt tgg tac ttc agc cac | 3552 |
| Phe Ala Met Trp Pro Gly Ala Ser Val Ser Gly Trp Tyr Phe Ser His | |
| 1170 1175 1180 | |
| ccg gac agc aag tac tac gct gta gca caa att cag gcg gat cag gtt | 3600 |
| Pro Asp Ser Lys Tyr Tyr Ala Val Ala Gln Ile Gln Arg Asp Gln Val | |

84

1185 1190 1195 1200
 gaa gat tat gcc cgc cgt aaa ggt atg agc gtt acc gaa gtt gag cgc 3648
 Glu Asp Tyr Ala Arg Arg Lys Gly Met Ser Val Thr Glu Val Glu Arg
 1205 1210 1215

tgg ctg gca cgc aat ctg ggg tat gac gcg gac tga 3684
 Trp Leu Ala Pro Asn Leu Gly Tyr Asp Ala Asp
 1220 1225

<210> 20
 <211> 1227
 <212> PRT
 <213> Escherichia coli

<400> 20
 Val Ser Ser Lys Val Glu Gln Leu Arg Ala Gln Leu Asn Glu Arg Ile
 1 5 10 15

Leu Val Leu Asp Gly Gly Met Gly Thr Met Ile Gln Ser Tyr Arg Leu
 20 25 30

Asn Glu Ala Asp Phe Arg Gly Glu Arg Phe Ala Asp Trp Pro Cys Asp
 35 40 45

Leu Lys Gly Asn Asn Asp Leu Leu Val Leu Ser Lys Pro Glu Val Ile
 50 55 60

Ala Ala Ile His Asn Ala Tyr Phe Glu Ala Gly Ala Asp Ile Ile Glu
 65 70 75 80

Thr Asn Thr Phe Asn Ser Thr Thr Ile Ala Met Ala Asp Tyr Gln Met
 85 90 95

Glu Ser Leu Ser Ala Glu Ile Asn Phe Ala Ala Ala Lys Leu Ala Arg
 100 105 110

Ala Cys Ala Asp Glu Trp Thr Ala Arg Thr Pro Glu Lys Pro Arg Tyr
 115 120 125

Val Ala Gly Val Leu Gly Pro Thr Asn Arg Thr Ala Ser Ile Ser Pro
 130 135 140

Asp Val Asn Asp Pro Ala Phe Arg Asn Ile Thr Phe Asp Gly Leu Val
 145 150 155 160

Ala Ala Tyr Arg Glu Ser Thr Lys Ala Leu Val Glu Gly Gly Ala Asp
 165 170 175

Leu Ile Leu Ile Glu Thr Val Phe Asp Thr Leu Asn Ala Lys Ala Ala
 180 185 190

Val Phe Ala Val Lys Thr Glu Phe Glu Ala Leu Gly Val Glu Leu Pro
 195 200 205

Ile Met Ile Ser Gly Thr Ile Thr Asp Ala Ser Gly Arg Thr Leu Ser
 210 215 220

Gly Gln Thr Thr Glu Ala Phe Tyr Asn Ser Leu Arg His Ala Glu Ala
 225 230 235 240

85

Leu Thr Phe Gly Leu Asn Cys Ala Leu Gly Pro Asp Glu Leu Arg Gln
 245 250 255
 Tyr Val Gln Glu Leu Ser Arg Ile Ala Glu Cys Tyr Val Thr Ala His
 260 265 270
 Pro Asn Ala Gly Leu Pro Asn Ala Phe Gly Glu Tyr Asp Leu Asp Ala
 275 280 285
 Asp Thr Met Ala Lys Gln Ile Arg Glu Trp Ala Gln Ala Gly Phe Leu
 290 295 300
 Asn Ile Val Gly Gly Cys Cys Gly Thr Thr Pro Gln His Ile Ala Ala
 305 310 315 320
 Met Ser Arg Ala Val Glu Gly Leu Ala Pro Arg Lys Leu Pro Glu Ile
 325 330 335
 Pro Val Ala Cys Arg Leu Ser Gly Leu Glu Pro Leu Asn Ile Gly Glu
 340 345 350
 Asp Ser Leu Phe Val Asn Val Gly Glu Arg Thr Asn Val Thr Gly Ser
 355 360 365
 Ala Lys Phe Lys Arg Leu Ile Lys Glu Glu Lys Tyr Ser Glu Ala Leu
 370 375 380
 Asp Val Ala Arg Gln Gln Val Glu Asn Gly Ala Gln Ile Ile Asp Ile
 385 390 395 400
 Asn Met Asp Glu Gly Met Leu Asp Ala Glu Ala Ala Met Val Arg Phe
 405 410 415
 Leu Asn Leu Ile Ala Gly Glu Pro Asp Ile Ala Arg Val Pro Ile Met
 420 425 430
 Ile Asp Ser Ser Lys Trp Asp Val Ile Glu Lys Gly Leu Lys Cys Ile
 435 440 445
 Gln Gly Lys Gly Ile Val Asn Ser Ile Ser Met Lys Glu Gly Val Asp
 450 455 460
 Ala Phe Ile His His Ala Lys Leu Leu Arg Arg Tyr Gly Ala Ala Val
 465 470 475 480
 Val Val Met Ala Phe Asp Glu Gln Gly Gln Ala Asp Thr Arg Ala Arg
 485 490 495
 Lys Ile Glu Ile Cys Arg Arg Ala Tyr Lys Ile Leu Thr Glu Glu Val
 500 505 510
 Gly Phe Pro Pro Glu Asp Ile Ile Phe Asp Pro Asn Ile Phe Ala Val
 515 520 525
 Ala Thr Gly Ile Glu Glu His Asn Asn Tyr Ala Gln Asp Phe Ile Gly
 530 535 540
 Ala Cys Glu Asp Ile Lys Arg Glu Leu Pro His Ala Leu Ile Ser Gly
 545 550 555 560
 Gly Val Ser Asn Val Ser Phe Ser Phe Arg Gly Asn Asp Pro Val Arg
 565 570 575

Glu Ala Ile His Ala Val Phe Leu Tyr Tyr Ala Ile Arg Asn Gly Met
 580 585 590
 Asp Met Gly Ile Val Asn Ala Gly Gln Leu Ala Ile Tyr Asp Asp Leu
 595 600 605
 Pro Ala Glu Leu Arg Asp Ala Val Glu Asp Val Ile Leu Asn Arg Arg
 610 615 620
 Asp Asp Gly Thr Glu Arg Leu Leu Glu Leu Ala Glu Lys Tyr Arg Gly
 625 630 635 640
 Ser Lys Thr Asp Asp Thr Ala Asn Ala Gln Gln Ala Glu Trp Arg Ser
 645 650 655
 Trp Glu Val Asn Lys Arg Leu Glu Tyr Ser Leu Val Lys Gly Ile Thr
 660 665 670
 Glu Phe Ile Glu Gln Asp Thr Glu Glu Ala Arg Gln Gln Ala Thr Arg
 675 680 685
 Pro Ile Glu Val Ile Glu Gly Pro Leu Met Asp Gly Met Asn Val Val
 690 695 700
 Gly Asp Leu Phe Gly Glu Gly Lys Met Phe Leu Pro Gln Val Val Lys
 705 710 715 720
 Ser Ala Arg Val Met Lys Gln Ala Val Ala Tyr Leu Glu Pro Phe Ile
 725 730 735
 Glu Ala Ser Lys Glu Gln Gly Lys Thr Asn Gly Lys Met Val Ile Ala
 740 745 750
 Thr Val Lys Gly Asp Val His Asp Ile Gly Lys Asn Ile Val Gly Val
 755 760 765
 Val Leu Gln Cys Asn Asn Tyr Glu Ile Val Asp Leu Gly Val Met Val
 770 775 780
 Pro Ala Glu Lys Ile Leu Arg Thr Ala Lys Glu Val Asn Ala Asp Leu
 785 790 795 800
 Ile Gly Leu Ser Gly Leu Ile Thr Pro Ser Leu Asp Glu Met Val Asn
 805 810 815
 Val Ala Lys Glu Met Glu Arg Gln Gly Phe Thr Ile Pro Leu Leu Ile
 820 825 830
 Gly Gly Ala Thr Thr Ser Lys Ala His Thr Ala Val Lys Ile Glu Gln
 835 840 845
 Asn Tyr Ser Gly Pro Thr Val Tyr Val Gln Asn Ala Ser Arg Thr Val
 850 855 860
 Gly Val Val Ala Ala Leu Leu Ser Asp Thr Gln Arg Asp Asp Phe Val
 865 870 875 880
 Ala Arg Thr Arg Lys Glu Tyr Glu Thr Val Arg Ile Gln His Gly Arg
 885 890 895
 Lys Lys Pro Arg Thr Pro Pro Val Thr Leu Glu Ala Ala Arg Asp Asn

| | | |
|--|-----|-----|
| 900 | 905 | 910 |
| Asp Phe Ala Phe Asp Trp Gln Ala Tyr Thr Pro Pro Val Ala His Arg 915 920 925 | | |
| Leu Gly Val Gln Glu Val Glu Ala Ser Ile Glu Thr Leu Arg Asn Tyr 930 935 940 | | |
| Ile Asp Trp Thr Pro Phe Phe Met Thr Trp Ser Leu Ala Gly Lys Tyr 945 950 955 960 | | |
| Pro Arg Ile Leu Glu Asp Glu Val Val Gly Val Glu Ala Gln Arg Leu 965 970 975 | | |
| Phe Lys Asp Ala Asn Asp Met Leu Asp Lys Leu Ser Ala Glu Lys Thr 980 985 990 | | |
| Leu Asn Pro Arg Gly Val Val Gly Leu Phe Pro Ala Asn Arg Val Gly 995 1000 1005 | | |
| Asp Asp Ile Glu Ile Tyr Arg Asp Glu Thr Arg Thr His Val Ile Asn 1010 1015 1020 | | |
| Val Ser His His Leu Arg Gln Gln Thr Glu Lys Thr Gly Phe Ala Asn 1025 1030 1035 1040 | | |
| Tyr Cys Leu Ala Asp Phe Val Ala Pro Lys Leu Ser Gly Lys Ala Asp 1045 1050 1055 | | |
| Tyr Ile Gly Ala Phe Ala Val Thr Gly Gly Leu Glu Glu Asp Ala Leu 1060 1065 1070 | | |
| Ala Asp Ala Phe Glu Ala Gln His Asp Asp Tyr Asn Lys Ile Met Val 1075 1080 1085 | | |
| Lys Ala Leu Ala Asp Arg Leu Ala Glu Ala Phe Ala Glu Tyr Leu His 1090 1095 1100 | | |
| Glu Arg Val Arg Lys Val Tyr Trp Gly Tyr Ala Pro Asn Glu Asn Leu 1105 1110 1115 1120 | | |
| Ser Asn Glu Glu Leu Ile Arg Glu Asn Tyr Gln Gly Ile Arg Pro Ala 1125 1130 1135 | | |
| Pro Gly Tyr Pro Ala Cys Pro Glu His Thr Glu Lys Ala Thr Ile Trp 1140 1145 1150 | | |
| Glu Leu Leu Glu Val Glu Lys His Thr Gly Met Lys Leu Thr Glu Ser 1155 1160 1165 | | |
| Phe Ala Met Trp Pro Gly Ala Ser Val Ser Gly Trp Tyr Phe Ser His 1170 1175 1180 | | |
| Pro Asp Ser Lys Tyr Tyr Ala Val Ala Gln Ile Gln Arg Asp Gln Val 1185 1190 1195 1200 | | |
| Glu Asp Tyr Ala Arg Arg Lys Gly Met Ser Val Thr Glu Val Glu Arg 1205 1210 1215 | | |
| Trp Leu Ala Pro Asn Leu Gly Tyr Asp Ala Asp 1220 1225 | | |

<210> 21
 <211> 3771
 <212> DNA
 <213> Salmonella typhimurium

<220>
 <221> CDS
 <222> (1)..(3768)
 <223> RSY02996

<400> 21
 atg tct cat gtt gcc cgt tgt tct ctt ttc cgc cag cac gct ttg tgc 48
 Met Ser His Val Ala Arg Cys Ser Leu Phe Arg Gln His Ala Leu Cys
 1 5 10 15
 cag tat ggc tcg tta cgt gga gcg ttg tcg gga gcg agt gtg agc agc 96
 Gln Tyr Gly Ser Leu Arg Gly Ala Leu Ser Gly Ala Ser Val Ser Ser
 20 25 30
 aaa gtt gaa caa ctg cgt gcg cag tta aat gaa cgt att ctg gtg ctg 144
 Lys Val Glu Gln Leu Arg Ala Gln Leu Asn Glu Arg Ile Leu Val Leu
 35 40 45
 gac ggc ggt atg ggc act atg atc cag agc tat cgt cta cat gaa gaa 192
 Asp Gly Gly Met Gly Thr Met Ile Gln Ser Tyr Arg Leu His Glu Glu
 50 55 60
 gat ttc cgc ggg gag cgc ttt gcc gac tgg ccc tgc gac ctg aaa ggc 240
 Asp Phe Arg Gly Glu Arg Phe Ala Asp Trp Pro Cys Asp Leu Lys Gly
 65 70 75 80
 aac aat gac ctg ctg gtc ctc agc aag ccg gag gtg atc gcc gct atc 288
 Asn Asn Asp Leu Leu Val Leu Ser Lys Pro Glu Val Ile Ala Ala Ile
 85 90 95
 cac aac gcc tac ttt gag gct ggc gcg gat atc atc gaa acc aac acc 336
 His Asn Ala Tyr Phe Glu Ala Gly Ala Asp Ile Ile Glu Thr Asn Thr
 100 105 110
 ttt aac tcg aca acc att gcg atg gcg gat tac cgg atg gaa tcc ctg 384
 Phe Asn Ser Thr Thr Ile Ala Met Ala Asp Tyr Arg Met Glu Ser Leu
 115 120 125
 tcg gcg gaa att aac tat gcg gcg gcc aaa ctg gcg cgc gcc tgc gcc 432
 Ser Ala Glu Ile Asn Tyr Ala Ala Ala Lys Leu Ala Arg Ala Cys Ala
 130 135 140
 gat gaa tgg acg gcg cga aca cca gaa aaa cca cgc ttt gtt gcg ggc 480
 Asp Glu Trp Thr Ala Arg Thr Pro Glu Lys Pro Arg Phe Val Ala Gly
 145 150 155 160
 gtg ctt ggt cca act aac cgc acg gcc tcc att tcg ccg gac gtc aac 528
 Val Leu Gly Pro Thr Asn Arg Thr Ala Ser Ile Ser Pro Asp Val Asn
 165 170 175
 gac ccg gcg ttt cgt aat atc acc ttc gat cag ctg gtg gcg gcc tac 576
 Asp Pro Ala Phe Arg Asn Ile Thr Phe Asp Gln Leu Val Ala Ala Tyr
 180 185 190
 cgt gaa tcc acc aaa gcg ctg gtg gaa ggt ggc gca gat ctg att ctg 624
 Arg Glu Ser Thr Lys Ala Leu Val Glu Gly Gly Ala Asp Leu Ile Leu

| 195 | 200 | 205 | |
|---|-----|-----|------|
| att gag acc gtt ttt gac acc ctg aat gcg aaa gcg gcg gtg ttt gcg Ile Glu Thr Val Phe Asp Thr Leu Asn Ala Lys Ala Ala Val Phe Ala 210 215 220 | | | 672 |
| gtg aaa gaa gag ttt gaa gcg ctg ggc gtt gac ctg ccg atc atg att Val Lys Glu Glu Phe Glu Ala Leu Gly Val Asp Leu Pro Ile Met Ile 225 230 235 240 | | | 720 |
| tcc ggc acc atc acc gac gcc tct ggc cgt acg ctt tcc ggc cag act Ser Gly Thr Ile Thr Asp Ala Ser Gly Arg Thr Leu Ser Gly Gln Thr 245 250 255 | | | 768 |
| acc gaa gcc ttt tat aac tcg ctg cgc cac gcc gag gcg ctc act ttt Thr Glu Ala Phe Tyr Asn Ser Leu Arg His Ala Glu Ala Leu Thr Phe 260 265 270 | | | 816 |
| ggc ctt aac tgc gca ctg ggg cca gat gaa ctg cgc cag tac gtc cag Gly Leu Asn Cys Ala Leu Gly Pro Asp Glu Leu Arg Gln Tyr Val Gln 275 280 285 | | | 864 |
| gaa ctg tcg cgg att gcc gaa tgc tac gtc acc gcg cac ccg aac gcc Glu Leu Ser Arg Ile Ala Glu Cys Tyr Val Thr Ala His Pro Asn Ala 290 295 300 | | | 912 |
| ggc ctg ccg aac gct ttc ggc gag tat gac ctc gac gcc gac acc atg Gly Leu Pro Asn Ala Phe Gly Glu Tyr Asp Leu Asp Ala Asp Thr Met 305 310 315 320 | | | 960 |
| gcg aaa cag att cgc gaa tgg gcg gaa gcg ggc ttc ctg aat atc gtt Ala Lys Gln Ile Arg Glu Trp Ala Glu Ala Gly Phe Leu Asn Ile Val 325 330 335 | | | 1008 |
| ggc ggc tgc tgc ggc acc acg ccg gag cat att gcg gcg atg agc cgc Gly Gly Cys Cys Gly Thr Thr Pro Glu His Ile Ala Ala Met Ser Arg 340 345 350 | | | 1056 |
| gcc gtt gcc ggt ttg ctg ccg cgc cag ctg ccg gat atc ccg gtc gcc Ala Val Ala Gly Leu Leu Pro Arg Gln Leu Pro Asp Ile Pro Val Ala 355 360 365 | | | 1104 |
| tgc cgc ctt tcc ggc ctg gag ccg ctg aac att ggc gac gat agc ctg Cys Arg Leu Ser Gly Leu Glu Pro Leu Asn Ile Gly Asp Asp Ser Leu 370 375 380 | | | 1152 |
| ttt gtg aac gtc ggc gaa cgt act aac gtc acc ggc tcg gcc aaa ttt Phe Val Asn Val Gly Glu Arg Thr Asn Val Thr Gly Ser Ala Lys Phe 385 390 395 400 | | | 1200 |
| aaa cgg ctg atc aaa gaa gag aaa tac agc gaa gcg ctg gat gtc gcc Lys Arg Leu Ile Lys Glu Glu Lys Tyr Ser Glu Ala Leu Asp Val Ala 405 410 415 | | | 1248 |
| cgt cag cag gta gaa agc ggc gcg cag att att gat atc aat atg gat Arg Gln Gln Val Glu Ser Gly Ala Gln Ile Ile Asp Ile Asn Met Asp 420 425 430 | | | 1296 |
| gag ggg atg ctc gac gcc gaa gcg gcg atg gtg cgt ttc ctc agc ctg Glu Gly Met Leu Asp Ala Glu Ala Ala Met Val Arg Phe Leu Ser Leu 435 440 445 | | | 1344 |

90

| | |
|---|------|
| att gcc ggt gag ccg gac att gcc cgt gta cca atc atg atc gac tcc Ile Ala Gly Glu Pro Asp Ile Ala Arg Val Pro Ile Met Ile Asp Ser 450 455 460 | 1392 |
| tcc aaa tgg gag gtt atc gaa aaa ggg ctg aag tgc att cag ggt aaa Ser Lys Trp Glu Val Ile Glu Lys Gly Leu Lys Cys Ile Gln Gly Lys 465 470 475 480 | 1440 |
| ggc atc gtc aac tct att tcg atg aaa gag ggc gtg gaa gcc ttt att Gly Ile Val Asn Ser Ile Ser Met Lys Glu Gly Val Glu Ala Phe Ile 485 490 495 | 1488 |
| cat cat gcg aag ctt ctg cgt cgc tac ggc gcg gca gtg gtg gtg atg His His Ala Lys Leu Leu Arg Arg Tyr Gly Ala Ala Val Val Val Met 500 505 510 | 1536 |
| gcc ttt gat gag cag ggg cag gcc gat acc cgc gcg cgt aaa atc gaa Ala Phe Asp Glu Gln Gly Gln Ala Asp Thr Arg Ala Arg Lys Ile Glu 515 520 525 | 1584 |
| att tgc cgc cga gcc tac aaa att ctc acc gaa gag gtg ggt ttc ccg Ile Cys Arg Arg Ala Tyr Lys Ile Leu Thr Glu Glu Val Gly Phe Pro 530 535 540 | 1632 |
| ccg gaa gac atc atc ttc gac ccg aat atc ttc gcc gtg gcg acc ggt Pro Glu Asp Ile Ile Phe Asp Pro Asn Ile Phe Ala Val Ala Thr Gly 545 550 555 560 | 1680 |
| att gaa gag cac aac aac tac gcg cag gac ttt atc ggc gct tgc gaa Ile Glu Glu His Asn Asn Tyr Ala Gln Asp Phe Ile Gly Ala Cys Glu 565 570 575 | 1728 |
| gac atc aaa cgc gag ctg ccg cac gcg ctg atc tcc ggc ggc gtg tct Asp Ile Lys Arg Glu Leu Pro His Ala Leu Ile Ser Gly Gly Val Ser 580 585 590 | 1776 |
| aac gtg tcc ttc tcg ttc cgc ggc aac gac ccg gta cgt gag gct atc Asn Val Ser Phe Ser Phe Arg Gly Asn Asp Pro Val Arg Glu Ala Ile 595 600 605 | 1824 |
| cac gcg gta ttc ctc tac tac gcc atc cgc aac ggt atg gac atg ggc His Ala Val Phe Leu Tyr Tyr Ala Ile Arg Asn Gly Met Asp Met Gly 610 615 620 | 1872 |
| atc gtc aac gcc gga cag ctg gct atc tac gac gac ctg ccc gcc gag Ile Val Asn Ala Gly Gln Leu Ala Ile Tyr Asp Asp Leu Pro Ala Glu 625 630 635 640 | 1920 |
| ctg cgc gat gcg gtt gaa gat gtc att ctt aac cgt cgc gat gac ggc Leu Arg Asp Ala Val Glu Asp Val Ile Leu Asn Arg Arg Asp Asp Gly 645 650 655 | 1968 |
| act gag cgt ttg ctg gat ttg gcg gag aaa tac cgc ggc agc aaa acc Thr Glu Arg Leu Leu Asp Leu Ala Glu Lys Tyr Arg Gly Ser Lys Thr 660 665 670 | 2016 |
| gac gaa gct gcc aac gcc cag cag gcg gaa tgg cgt agc tgg gac gtg Asp Glu Ala Ala Asn Ala Gln Gln Ala Glu Trp Arg Ser Trp Asp Val 675 680 685 | 2064 |
| aaa aag cgt ctc gaa tac tcg ctg gtg aaa ggc att acc gaa ttt atc Lys Lys Arg Leu Glu Tyr Ser Leu Val Lys Gly Ile Thr Glu Phe Ile | 2112 |

| 690 | 695 | 700 | |
|---|-----|-----|------|
| gaa cag gat acc gaa gaa gcc cgt cag cag gcc gcc cgc ccg att gag Glu Gln Asp Thr Glu Glu Ala Arg Gln Gln Ala Ala Arg Pro Ile Glu 705 710 715 720 | | | 2160 |
| gtg att gaa ggg ccg ttg atg gac ggc atg aac gtg gtc ggc gac ctg Val Ile Glu Gly Pro Leu Met Asp Gly Met Asn Val Val Gly Asp Leu 725 730 735 | | | 2208 |
| ttc ggc gaa ggg aaa atg ttc ctg ccg cag gtg gtg aaa tcc gct cgc Phe Gly Glu Gly Lys Met Phe Leu Pro Gln Val Val Lys Ser Ala Arg 740 745 750 | | | 2256 |
| gtg atg aaa caa gcg gtg gcc tac ctg gag ccg ttt att gaa gcc agc Val Met Lys Gln Ala Val Ala Tyr Leu Glu Pro Phe Ile Glu Ala Ser 755 760 765 | | | 2304 |
| aaa gaa aaa ggc tcc agc aac ggc aag atg gtg atc gcc acc gtg aag Lys Glu Lys Gly Ser Ser Asn Gly Lys Met Val Ile Ala Thr Val Lys 770 775 780 | | | 2352 |
| ggc gat gtg cac gat att ggt aaa aat atc gtt ggc gtg gtg ctg caa Gly Asp Val His Asp Ile Gly Lys Asn Ile Val Gly Val Val Leu Gln 785 790 795 800 | | | 2400 |
| tgt aac aac tac gaa atc gtc gat ctt ggc gtg atg gtg cca gcg gag Cys Asn Asn Tyr Glu Ile Val Asp Leu Gly Val Met Val Pro Ala Glu 805 810 815 | | | 2448 |
| aaa atc ctc aga acg gcg cgt gaa gtg aat gcc gat ctg atc ggt ctt Lys Ile Leu Arg Thr Ala Arg Glu Val Asn Ala Asp Leu Ile Gly Leu 820 825 830 | | | 2496 |
| tcc ggg ctg att acc ccg tcg ctg gac gaa atg gtc aac gtg gcg aaa Ser Gly Leu Ile Thr Pro Ser Leu Asp Glu Met Val Asn Val Ala Lys 835 840 845 | | | 2544 |
| gag atg gag cgt cag ggc ttt act atc ccg cta ctg atc ggc ggc gca Glu Met Glu Arg Gln Gly Phe Thr Ile Pro Leu Leu Ile Gly Gly Ala 850 855 860 | | | 2592 |
| acc act tcg aaa gcg cat acg gcg gtg aaa atc gag cag aac tac agc Thr Thr Ser Lys Ala His Thr Ala Val Lys Ile Glu Gln Asn Tyr Ser 865 870 875 880 | | | 2640 |
| ggt ccg acg gtc tac gtg cag aat gct tcg cgt acc gtg ggc gtg gtg Gly Pro Thr Val Tyr Val Gln Asn Ala Ser Arg Thr Val Gly Val Val 885 890 895 | | | 2688 |
| gcg gcg cta ctc tcc gac acc cag cgt gat gac ttt gtc gcc cgt acc Ala Ala Leu Leu Ser Asp Thr Gln Arg Asp Asp Phe Val Ala Arg Thr 900 905 910 | | | 2736 |
| cgc aaa gag tac gaa acc gtg cgt att cag cac gcc cgc aaa aaa ccg Arg Lys Glu Tyr Glu Thr Val Arg Ile Gln His Ala Arg Lys Lys Pro 915 920 925 | | | 2784 |
| cgc acg ccg ccg gtc acg ctg gag gcg gcg cgc gat aac gat ctg gca Arg Thr Pro Pro Val Thr Leu Glu Ala Ala Arg Asp Asn Asp Leu Ala 930 935 940 | | | 2832 |

92

| | |
|---|------|
| ttc gat tgg gaa cgc tac acc ccg ccg gta gcc cac cgt ctg ggc gtg | 2880 |
| Phe Asp Trp Glu Arg Tyr Thr Pro Pro Val Ala His Arg Leu Gly Val | |
| 945 950 955 960 | |
| cag gag gtg gaa gcc agc atc gaa act ctg cgc aac tat atc gac tgg | 2928 |
| Gln Glu Val Glu Ala Ser Ile Glu Thr Leu Arg Asn Tyr Ile Asp Trp | |
| 965 970 975 | |
| acg ccg ttc ttt atg acc tgg tgc ctg gcc ggc aaa tac ccg cgc att | 2976 |
| Thr Pro Phe Phe Met Thr Trp Ser Leu Ala Gly Lys Tyr Pro Arg Ile | |
| 980 985 990 | |
| ctg gaa gat gag gtg gtg ggc gtt gag gcg cag cgt ctg ttt aaa gac | 3024 |
| Leu Glu Asp Glu Val Val Gly Val Glu Ala Gln Arg Leu Phe Lys Asp | |
| 995 1000 1005 | |
| gcc aat gat atg ctg gat aaa ctg agc gcc gag aaa ctg ttg aat ccg | 3072 |
| Ala Asn Asp Met Leu Asp Lys Leu Ser Ala Glu Lys Leu Leu Asn Pro | |
| 1010 1015 1020 | |
| cgt ggc gtg gtg ggc ctg ttc ccg gcg aac cgt gtg ggt gac gac atc | 3120 |
| Arg Gly Val Val Gly Leu Phe Pro Ala Asn Arg Val Gly Asp Asp Ile | |
| 1025 1030 1035 1040 | |
| gaa atc tat cgc gac gaa acc cgt act cat gtt ctg acg gtc agc cac | 3168 |
| Glu Ile Tyr Arg Asp Glu Thr Arg Thr His Val Leu Thr Val Ser His | |
| 1045 1050 1055 | |
| cac ctg cgc cag cag acc gag aaa gtc ggt ttt gcc aac tac tgt ctg | 3216 |
| His Leu Arg Gln Gln Thr Glu Lys Val Gly Phe Ala Asn Tyr Cys Leu | |
| 1060 1065 1070 | |
| gcg gat ttt gtc gcg ccg aaa ctg agc gcc aaa gcg gat tac atc ggt | 3264 |
| Ala Asp Phe Val Ala Pro Lys Leu Ser Gly Lys Ala Asp Tyr Ile Gly | |
| 1075 1080 1085 | |
| gct ttc gcg gtg acc ggc ggt ctg gag gag gat gcg ctg gcg gac gcc | 3312 |
| Ala Phe Ala Val Thr Gly Leu Glu Glu Asp Ala Leu Ala Asp Ala | |
| 1090 1095 1100 | |
| ttc gaa gcg caa cac gac gac tat aac aag atc atg gtg aaa gcg att | 3360 |
| Phe Glu Ala Gln His Asp Asp Tyr Asn Lys Ile Met Val Lys Ala Ile | |
| 1105 1110 1115 1120 | |
| gcc gac cgt ctg gcg gaa gcg ttc gcg gaa tat ctg cat gag cgt gta | 3408 |
| Ala Asp Arg Leu Ala Glu Ala Phe Ala Glu Tyr Leu His Glu Arg Val | |
| 1125 1130 1135 | |
| cgt aag gtt tac tgg gga tat gcg ccg aac gag agc ctg agt aac gac | 3456 |
| Arg Lys Val Tyr Trp Gly Tyr Ala Pro Asn Glu Ser Leu Ser Asn Asp | |
| 1140 1145 1150 | |
| gaa tta atc cgc gaa aac tac cag ggg att cgc ccg gcg ccg ggt tat | 3504 |
| Glu Leu Ile Arg Glu Asn Tyr Gln Gly Ile Arg Pro Ala Pro Gly Tyr | |
| 1155 1160 1165 | |
| cct gcc tgc ccg gaa cat acc gaa aaa ggc act atc tgg cag cta ctg | 3552 |
| Pro Ala Cys Pro Glu His Thr Glu Lys Gly Thr Ile Trp Gln Leu Leu | |
| 1170 1175 1180 | |
| gat gtc gaa aaa cac acc ggg atg aag ctc acc gaa tct ttc gcc atg | 3600 |
| Asp Val Glu Lys His Thr Gly Met Lys Leu Thr Glu Ser Phe Ala Met | |

93

1185 1190 1195 1200
 tgg cca ggc gcg tcg gtc tcc ggc tgg tac ttc agc cat cct gag agc 3648
 Trp Pro Gly Ala Ser Val Ser Gly Trp Tyr Phe Ser His Pro Glu Ser
 1205 1210 1215
 aaa tac ttc gcg gta gcg cag atc caa cgc gat cag gtg aca gat tat 3696
 Lys Tyr Phe Ala Val Ala Gln Ile Gln Arg Asp Gln Val Thr Asp Tyr
 1220 1225 1230
 gct ttc cgt aaa gga atg agc gtt gag gat gtt gag cgg tgg ctc gcg 3744
 Ala Phe Arg Lys Gly Met Ser Val Glu Asp Val Glu Arg Trp Leu Ala
 1235 1240 1245
 ccg aac ctg ggt tac gat gcg gac tga 3771
 Pro Asn Leu Gly Tyr Asp Ala Asp
 1250 1255

 <210> 22
 <211> 1256
 <212> PRT
 <213> Salmonella typhimurium

 <400> 22
 Met Ser His Val Ala Arg Cys Ser Leu Phe Arg Gln His Ala Leu Cys
 1 5 10 15
 Gln Tyr Gly Ser Leu Arg Gly Ala Leu Ser Gly Ala Ser Val Ser Ser
 20 25 30
 Lys Val Glu Gln Leu Arg Ala Gln Leu Asn Glu Arg Ile Leu Val Leu
 35 40 45
 Asp Gly Gly Met Gly Thr Met Ile Gln Ser Tyr Arg Leu His Glu Glu
 50 55 60
 Asp Phe Arg Gly Glu Arg Phe Ala Asp Trp Pro Cys Asp Leu Lys Gly
 65 70 75 80
 Asn Asn Asp Leu Leu Val Leu Ser Lys Pro Glu Val Ile Ala Ala Ile
 85 90 95
 His Asn Ala Tyr Phe Glu Ala Gly Ala Asp Ile Ile Glu Thr Asn Thr
 100 105 110
 Phe Asn Ser Thr Thr Ile Ala Met Ala Asp Tyr Arg Met Glu Ser Leu
 115 120 125
 Ser Ala Glu Ile Asn Tyr Ala Ala Ala Lys Leu Ala Arg Ala Cys Ala
 130 135 140
 Asp Glu Trp Thr Ala Arg Thr Pro Glu Lys Pro Arg Phe Val Ala Gly
 145 150 155 160
 Val Leu Gly Pro Thr Asn Arg Thr Ala Ser Ile Ser Pro Asp Val Asn
 165 170 175
 Asp Pro Ala Phe Arg Asn Ile Thr Phe Asp Gln Leu Val Ala Ala Tyr
 180 185 190
 Arg Glu Ser Thr Lys Ala Leu Val Glu Gly Gly Ala Asp Leu Ile Leu

| | | |
|---|-----|---------|
| 195 | 200 | 205 |
| Ile Glu Thr Val Phe Asp Thr Leu Asn Ala Lys Ala Ala Val Phe Ala | | |
| 210 | 215 | 220 |
| Val Lys Glu Glu Phe Glu Ala Leu Gly Val Asp Leu Pro Ile Met Ile | | |
| 225 | 230 | 235 240 |
| Ser Gly Thr Ile Thr Asp Ala Ser Gly Arg Thr Leu Ser Gly Gln Thr | | |
| | 245 | 250 255 |
| Thr Glu Ala Phe Tyr Asn Ser Leu Arg His Ala Glu Ala Leu Thr Phe | | |
| | 260 | 265 270 |
| Gly Leu Asn Cys Ala Leu Gly Pro Asp Glu Leu Arg Gln Tyr Val Gln | | |
| | 275 | 280 285 |
| Glu Leu Ser Arg Ile Ala Glu Cys Tyr Val Thr Ala His Pro Asn Ala | | |
| | 290 | 295 300 |
| Gly Leu Pro Asn Ala Phe Gly Glu Tyr Asp Leu Asp Ala Asp Thr Met | | |
| 305 | 310 | 315 320 |
| Ala Lys Gln Ile Arg Glu Trp Ala Glu Ala Gly Phe Leu Asn Ile Val | | |
| | 325 | 330 335 |
| Gly Gly Cys Cys Gly Thr Thr Pro Glu His Ile Ala Ala Met Ser Arg | | |
| | 340 | 345 350 |
| Ala Val Ala Gly Leu Leu Pro Arg Gln Leu Pro Asp Ile Pro Val Ala | | |
| | 355 | 360 365 |
| Cys Arg Leu Ser Gly Leu Glu Pro Leu Asn Ile Gly Asp Asp Ser Leu | | |
| | 370 | 375 380 |
| Phe Val Asn Val Gly Glu Arg Thr Asn Val Thr Gly Ser Ala Lys Phe | | |
| 385 | 390 | 395 400 |
| Lys Arg Leu Ile Lys Glu Glu Lys Tyr Ser Glu Ala Leu Asp Val Ala | | |
| | 405 | 410 415 |
| Arg Gln Gln Val Glu Ser Gly Ala Gln Ile Ile Asp Ile Asn Met Asp | | |
| | 420 | 425 430 |
| Glu Gly Met Leu Asp Ala Glu Ala Ala Met Val Arg Phe Leu Ser Leu | | |
| | 435 | 440 445 |
| Ile Ala Gly Glu Pro Asp Ile Ala Arg Val Pro Ile Met Ile Asp Ser | | |
| | 450 | 455 460 |
| Ser Lys Trp Glu Val Ile Glu Lys Gly Leu Lys Cys Ile Gln Gly Lys | | |
| 465 | 470 | 475 480 |
| Gly Ile Val Asn Ser Ile Ser Met Lys Glu Gly Val Glu Ala Phe Ile | | |
| | 485 | 490 495 |
| His His Ala Lys Leu Leu Arg Arg Tyr Gly Ala Ala Val Val Val Met | | |
| | 500 | 505 510 |
| Ala Phe Asp Glu Gln Gly Gln Ala Asp Thr Arg Ala Arg Lys Ile Glu | | |
| | 515 | 520 525 |

95

Ile Cys Arg Arg Ala Tyr Lys Ile Leu Thr Glu Glu Val Gly Phe Pro
 530 535 540

Pro Glu Asp Ile Ile Phe Asp Pro Asn Ile Phe Ala Val Ala Thr Gly
 545 550 555 560

Ile Glu Glu His Asn Asn Tyr Ala Gln Asp Phe Ile Gly Ala Cys Glu
 565 570 575

Asp Ile Lys Arg Glu Leu Pro His Ala Leu Ile Ser Gly Gly Val Ser
 580 585 590

Asn Val Ser Phe Ser Phe Arg Gly Asn Asp Pro Val Arg Glu Ala Ile
 595 600 605

His Ala Val Phe Leu Tyr Tyr Ala Ile Arg Asn Gly Met Asp Met Gly
 610 615 620

Ile Val Asn Ala Gly Gln Leu Ala Ile Tyr Asp Asp Leu Pro Ala Glu
 625 630 635 640

Leu Arg Asp Ala Val Glu Asp Val Ile Leu Asn Arg Arg Asp Asp Gly
 645 650 655

Thr Glu Arg Leu Leu Asp Leu Ala Glu Lys Tyr Arg Gly Ser Lys Thr
 660 665 670

Asp Glu Ala Ala Asn Ala Gln Gln Ala Glu Trp Arg Ser Trp Asp Val
 675 680 685

Lys Lys Arg Leu Glu Tyr Ser Leu Val Lys Gly Ile Thr Glu Phe Ile
 690 695 700

Glu Gln Asp Thr Glu Glu Ala Arg Gln Gln Ala Ala Arg Pro Ile Glu
 705 710 715 720

Val Ile Glu Gly Pro Leu Met Asp Gly Met Asn Val Val Gly Asp Leu
 725 730 735

Phe Gly Glu Gly Lys Met Phe Leu Pro Gln Val Val Lys Ser Ala Arg
 740 745 750

Val Met Lys Gln Ala Val Ala Tyr Leu Glu Pro Phe Ile Glu Ala Ser
 755 760 765

Lys Glu Lys Gly Ser Ser Asn Gly Lys Met Val Ile Ala Thr Val Lys
 770 775 780

Gly Asp Val His Asp Ile Gly Lys Asn Ile Val Gly Val Val Leu Gln
 785 790 795 800

Cys Asn Asn Tyr Glu Ile Val Asp Leu Gly Val Met Val Pro Ala Glu
 805 810 815

Lys Ile Leu Arg Thr Ala Arg Glu Val Asn Ala Asp Leu Ile Gly Leu
 820 825 830

Ser Gly Leu Ile Thr Pro Ser Leu Asp Glu Met Val Asn Val Ala Lys
 835 840 845

Glu Met Glu Arg Gln Gly Phe Thr Ile Pro Leu Leu Ile Gly Gly Ala
 850 855 860

Thr Thr Ser Lys Ala His Thr Ala Val Lys Ile Glu Gln Asn Tyr Ser
 865 870 875 880
 Gly Pro Thr Val Tyr Val Gln Asn Ala Ser Arg Thr Val Gly Val Val
 885 890 895
 Ala Ala Leu Leu Ser Asp Thr Gln Arg Asp Asp Phe Val Ala Arg Thr
 900 905 910
 Arg Lys Glu Tyr Glu Thr Val Arg Ile Gln His Ala Arg Lys Lys Pro
 915 920 925
 Arg Thr Pro Pro Val Thr Leu Glu Ala Ala Arg Asp Asn Asp Leu Ala
 930 935 940
 Phe Asp Trp Glu Arg Tyr Thr Pro Pro Val Ala His Arg Leu Gly Val
 945 950 955 960
 Gln Glu Val Glu Ala Ser Ile Glu Thr Leu Arg Asn Tyr Ile Asp Trp
 965 970 975
 Thr Pro Phe Phe Met Thr Trp Ser Leu Ala Gly Lys Tyr Pro Arg Ile
 980 985 990
 Leu Glu Asp Glu Val Val Gly Val Glu Ala Gln Arg Leu Phe Lys Asp
 995 1000 1005
 Ala Asn Asp Met Leu Asp Lys Leu Ser Ala Glu Lys Leu Leu Asn Pro
 1010 1015 1020
 Arg Gly Val Val Gly Leu Phe Pro Ala Asn Arg Val Gly Asp Asp Ile
 1025 1030 1035 1040
 Glu Ile Tyr Arg Asp Glu Thr Arg Thr His Val Leu Thr Val Ser His
 1045 1050 1055
 His Leu Arg Gln Gln Thr Glu Lys Val Gly Phe Ala Asn Tyr Cys Leu
 1060 1065 1070
 Ala Asp Phe Val Ala Pro Lys Leu Ser Gly Lys Ala Asp Tyr Ile Gly
 1075 1080 1085
 Ala Phe Ala Val Thr Gly Gly Leu Glu Glu Asp Ala Leu Ala Asp Ala
 1090 1095 1100
 Phe Glu Ala Gln His Asp Asp Tyr Asn Lys Ile Met Val Lys Ala Ile
 1105 1110 1115 1120
 Ala Asp Arg Leu Ala Glu Ala Phe Ala Glu Tyr Leu His Glu Arg Val
 1125 1130 1135
 Arg Lys Val Tyr Trp Gly Tyr Ala Pro Asn Glu Ser Leu Ser Asn Asp
 1140 1145 1150
 Glu Leu Ile Arg Glu Asn Tyr Gln Gly Ile Arg Pro Ala Pro Gly Tyr
 1155 1160 1165
 Pro Ala Cys Pro Glu His Thr Glu Lys Gly Thr Ile Trp Gln Leu Leu
 1170 1175 1180
 Asp Val Glu Lys His Thr Gly Met Lys Leu Thr Glu Ser Phe Ala Met

| | | | | |
|---|------|-----|------|------|
| 1185 | 1190 | 97 | 1195 | 1200 |
| Trp Pro Gly Ala Ser Val Ser Gly Trp Tyr Phe Ser His Pro Glu Ser | 1205 | | 1210 | 1215 |
| Lys Tyr Phe Ala Val Ala Gln Ile Gln Arg Asp Gln Val Thr Asp Tyr | 1220 | | 1225 | 1230 |
| Ala Phe Arg Lys Gly Met Ser Val Glu Asp Val Glu Arg Trp Leu Ala | 1235 | | 1240 | 1245 |
| Pro Asn Leu Gly Tyr Asp Ala Asp | 1250 | | 1255 | |
| <p><210> 23</p> <p><211> 3771</p> <p><212> DNA</p> <p><213> Salmonella typhi</p> <p><220></p> <p><221> CDS</p> <p><222> (1)..(3768)</p> <p><223> RTY03686</p> <p><400> 23</p> | | | | |
| atg tct cat gtt gcc cgt tgt tct ctt ttc cgc cag cac gct ttg tgc | | | | 48 |
| Met Ser His Val Ala Arg Cys Ser Leu Phe Arg Gln His Ala Leu Cys | 1 | 5 | 10 | 15 |
| cag tat ggc tcg tta cgt gga gcg ttg tcg gga gcg agt gtg agc agc | | | | 96 |
| Gln Tyr Gly Ser Leu Arg Gly Ala Leu Ser Gly Ala Ser Val Ser Ser | 20 | 25 | 30 | |
| aaa gtt gaa caa ctg cgt gcg cag tta aat gaa cgt att ctg gtg ctg | | | | 144 |
| Lys Val Glu Gln Leu Arg Ala Gln Leu Asn Glu Arg Ile Leu Val Leu | 35 | 40 | 45 | |
| gac ggc ggt atg ggc acc atg atc cag agc tat cgt cta cat gaa gaa | | | | 192 |
| Asp Gly Gly Met Gly Thr Met Ile Gln Ser Tyr Arg Leu His Glu Glu | 50 | 55 | 60 | |
| gat ttc cgc ggg gag cgc ttt gcc gac tgg ccc tgc gac ctg aaa ggc | | | | 240 |
| Asp Phe Arg Gly Glu Arg Phe Ala Asp Trp Pro Cys Asp Leu Lys Gly | 65 | 70 | 75 | 80 |
| aac aat gac ctg ctg gtc ctc agc aag ccg gag gtg atc gcc gct atc | | | | 288 |
| Asn Asn Asp Leu Leu Val Leu Ser Lys Pro Glu Val Ile Ala Ala Ile | 85 | 90 | 95 | |
| cac aac gcc tac ttt gag gct ggc gcg gat atc atc gaa acc aac acc | | | | 336 |
| His Asn Ala Tyr Phe Glu Ala Gly Ala Asp Ile Ile Glu Thr Asn Thr | 100 | 105 | 110 | |
| ttt aac tcg aca acc att gcg atg gcg gat tac cgg atg gaa tcc ctg | | | | 384 |
| Phe Asn Ser Thr Thr Ile Ala Met Ala Asp Tyr Arg Met Glu Ser Leu | 115 | 120 | 125 | |
| tcg gcg gaa att aac tat gcg gcg gcc aaa ctg gcg cgc gcc tgc gcc | | | | 432 |
| Ser Ala Glu Ile Asn Tyr Ala Ala Lys Leu Ala Arg Ala Cys Ala | 130 | 135 | 140 | |

98

| | |
|---|------|
| gat gaa tgg acg gcg cga aca cca gaa aaa cca cgc ttt gtt gcg ggc | 480 |
| Asp Glu Trp Thr Ala Arg Thr Pro Glu Lys Pro Arg Phe Val Ala Gly | |
| 145 150 155 160 | |
| gtg ctt ggt cca act aac cgc acg gcc tcc att tcg ccg gac gtc aac | 528 |
| Val Leu Gly Pro Thr Asn Arg Thr Ala Ser Ile Ser Pro Asp Val Asn | |
| 165 170 175 | |
| gac ccg gcg ttt cgt aat atc acc ttc gat cag ctg gtg gcg gcc tac | 576 |
| Asp Pro Ala Phe Arg Asn Ile Thr Phe Asp Gln Leu Val Ala Ala Tyr | |
| 180 185 190 | |
| cgt gaa tcc acc aaa gcg ctg gtg gaa ggc ggg gcg gac ctg atc ctg | 624 |
| Arg Glu Ser Thr Lys Ala Leu Val Glu Gly Gly Ala Asp Leu Ile Leu | |
| 195 200 205 | |
| att gaa act gtc ttc gac acc ctc aac gcc aaa gcg gcg gtg ttt gcg | 672 |
| Ile Glu Thr Val Phe Asp Thr Leu Asn Ala Lys Ala Ala Val Phe Ala | |
| 210 215 220 | |
| gtg aaa gaa gag ttt gaa gcg ctg ggc gtt gat ctg ccg atc atg att | 720 |
| Val Lys Glu Glu Phe Glu Ala Leu Gly Val Asp Leu Pro Ile Met Ile | |
| 225 230 235 240 | |
| tcc ggc acc atc acc gac gcc tct ggc cgt acg ctt tcc ggc cag acg | 768 |
| Ser Gly Thr Ile Thr Asp Ala Ser Gly Arg Thr Leu Ser Gly Gln Thr | |
| 245 250 255 | |
| acc gaa gcc ttt tat aac tcg ctg cgc cac gcc gag gcg ctc act ttt | 816 |
| Thr Glu Ala Phe Tyr Asn Ser Leu Arg His Ala Glu Ala Leu Thr Phe | |
| 260 265 270 | |
| ggc ctt aac tgc gcg ctg ggg cca gat gaa ctg cgc cag tac gtc cag | 864 |
| Gly Leu Asn Cys Ala Leu Gly Pro Asp Glu Leu Arg Gln Tyr Val Gln | |
| 275 280 285 | |
| gaa ctg tcg cgg att gcc gaa tgc tac gtc acc gcg cac ccg aac gcc | 912 |
| Glu Leu Ser Arg Ile Ala Glu Cys Tyr Val Thr Ala His Pro Asn Ala | |
| 290 295 300 | |
| ggc ctg ccg aac gct ttc ggc gag tac gac ctc gac gcc gac acc atg | 960 |
| Gly Leu Pro Asn Ala Phe Gly Glu Tyr Asp Leu Asp Ala Asp Thr Met | |
| 305 310 315 320 | |
| gcg aaa cag att cgc gaa tgg gcg gaa gcg ggc ttc ctg aat atc gtt | 1008 |
| Ala Lys Gln Ile Arg Glu Trp Ala Glu Ala Gly Phe Leu Asn Ile Val | |
| 325 330 335 | |
| ggc ggc tgc tgc ggc acc acg ccg gag cat att gcg gcg atg agc cgc | 1056 |
| Gly Gly Cys Cys Gly Thr Thr Pro Glu His Ile Ala Ala Met Ser Arg | |
| 340 345 350 | |
| gcc gtt gcc ggt ttg tcg ccg cgc cag ctg ccg gat atc ccg gtg gcc | 1104 |
| Ala Val Ala Gly Leu Ser Pro Arg Gln Leu Pro Asp Ile Pro Val Ala | |
| 355 360 365 | |
| tgc cgc ctt tcc ggc ctg gag ccg ctg aac att ggt gac gat agc ctg | 1152 |
| Cys Arg Leu Ser Gly Leu Glu Pro Leu Asn Ile Gly Asp Asp Ser Leu | |
| 370 375 380 | |
| ttt gtc aac gtc ggc gaa cgt act aac gtc acc ggc tcg gcc aaa ttt | 1200 |
| Phe Val Asn Val Gly Glu Arg Thr Asn Val Thr Gly Ser Ala Lys Phe | |

| 99 | | | | | | | | | | | | | | | | | | | |
|-----------------|-------------|-------------|-------------|-------------|------|-----------------|-------------------------------------|-----------------|-------------|-----|-----|--|--|--|-----|--|--|--|--|
| 385 | | | | | 390 | | | | | 395 | | | | | 400 | | | | |
| aaa cgc ttg atc | aaa gaa gag | aaa tac agc | gaa gcg ctg | gat gtc gcc | 1248 | Lys Arg Leu Ile | Lys Glu Glu Lys Tyr | Ser Glu Ala Leu | Asp Val Ala | | | | | | | | | | |
| 405 | | | | | | 410 | | | | | 415 | | | | | | | | |
| cgt cag cag gtc | gaa agc ggc | gcg cag att | att att gat | atc aat atg | 1296 | Arg Gln Gln Val | Glu Ser Gly Ala Gln Ile Ile | Asp Ile Asn Met | Asp | | | | | | | | | | |
| 420 | | | | | | 425 | | | | | 430 | | | | | | | | |
| gag ggg atg ctc | gac gcc gaa | gcg gcg atg | gtg cgt ttc | ctc agc ctg | 1344 | Glu Gly Met Leu | Asp Ala Glu Ala Ala Met Val | Arg Phe Leu | Ser Leu | | | | | | | | | | |
| 435 | | | | | | 440 | | | | | 445 | | | | | | | | |
| att gcc ggt gag | ccg gac att | gcc cgt gta | cca atc atg | att gac tcc | 1392 | Ile Ala Gly Glu | Pro Asp Ile Ala Arg Val Pro | Ile Met Ile | Asp Ser | | | | | | | | | | |
| 450 | | | | | | 455 | | | | | 460 | | | | | | | | |
| tcc aaa tgg gag | gtt atc gaa | aaa ggg ctg | aag tgc att | cag ggt aaa | 1440 | Ser Lys Trp Glu | Val Ile Glu Lys Gly Leu Lys Cys | Ile Gln Gly | Lys | | | | | | | | | | |
| 465 | | | | | | 470 | | | | | 480 | | | | | | | | |
| ggc atc gtc aac | tct att tcg | atg aaa gag | ggc gtg gaa | gcc ttt att | 1488 | Gly Ile Val Asn | Ser Ile Ser Met Lys Glu Gly Val | Glu Ala Phe | Ile | | | | | | | | | | |
| 485 | | | | | | 490 | | | | | 495 | | | | | | | | |
| cat cat gcg aag | ttg cta cgt | cgc tac ggc | gcc gca gtg | gtg gtg atg | 1536 | His His Ala Lys | Leu Leu Arg Arg Tyr Gly Ala Ala | Val Val Val | Met | | | | | | | | | | |
| 500 | | | | | | 505 | | | | | 510 | | | | | | | | |
| gct ttt gat gag | cag ggg cag | gcc gac acc | cgc gaa cgt | aaa atc gag | 1584 | Ala Phe Asp Glu | Gln Gly Gln Ala Asp Thr Arg Glu Arg | Lys Ile Glu | | | | | | | | | | | |
| 515 | | | | | | 520 | | | | | 525 | | | | | | | | |
| att tgc cgc cgc | gct tac aaa | att ttg ctc | gaa gag gta | ggc ttt ccg | 1632 | Ile Cys Arg Arg | Ala Tyr Lys Ile Leu Leu Glu Glu | Val Gly Phe | Pro | | | | | | | | | | |
| 530 | | | | | | 535 | | | | | 540 | | | | | | | | |
| ccg gaa gac atc | atc ttc gac | ccg aat atc | ttc gcc gtc | gcc acc ggt | 1680 | Pro Glu Asp Ile | Ile Phe Asp Pro Asn Ile Phe Ala Val | Ala Thr Gly | | | | | | | | | | | |
| 545 | | | | | | 550 | | | | | 555 | | | | | | | | |
| att gaa gag cac | aac aac tac | gcg cag gac | ttt atc ggc | gct tgt gaa | 1728 | Ile Glu Glu His | Asn Asn Tyr Ala Gln Asp Phe Ile Gly | Ala Cys Glu | | | | | | | | | | | |
| 565 | | | | | | 570 | | | | | 575 | | | | | | | | |
| gac atc aaa cgc | gag ctg ccg | cac gcg ctg | atc tcc ggc | ggc gtg tct | 1776 | Asp Ile Lys Arg | Glu Leu Pro His Ala Leu Ile Ser Gly | Gly Val Ser | | | | | | | | | | | |
| 580 | | | | | | 585 | | | | | 590 | | | | | | | | |
| aac gtg tcc ttc | tcg ttt cgc | ggc aac gac | ccg gta cgt | gag gct atc | 1824 | Asn Val Ser Phe | Ser Phe Arg Gly Asn Asp Pro Val Arg | Glu Ala Ile | | | | | | | | | | | |
| 595 | | | | | | 600 | | | | | 605 | | | | | | | | |
| cac gcg gta ttc | ctc tac tac | gcc atc cgc | aac ggc atg | gac atg ggc | 1872 | His Ala Val Phe | Leu Tyr Tyr Ala Ile Arg Asn Gly | Met Asp Met | Gly | | | | | | | | | | |
| 610 | | | | | | 615 | | | | | 620 | | | | | | | | |
| atc gtc aac gcc | ggg caa ctg | gcg att tat | gac aac ctg | cct gcc gaa | 1920 | Ile Val Asn Ala | Gly Gln Leu Ala Ile Tyr Asp Asn | Leu Pro Ala | Glu | | | | | | | | | | |
| 625 | | | | | | 630 | | | | | 635 | | | | | | | | |
| | | | | | | | | | | | 640 | | | | | | | | |

100

| | |
|---|------|
| ctg cgc gat gca gtt gaa gat gtc att ctt aac cgt cgc gat gac ggc Leu Arg Asp Ala Val Glu Asp Val Ile Leu Asn Arg Arg Asp Asp Gly 645 650 655 | 1968 |
| acc gag cgt ttg ctg gat ttg gcg gag aaa tat cgc ggc agc aaa acc Thr Glu Arg Leu Leu Asp Leu Ala Glu Lys Tyr Arg Gly Ser Lys Thr 660 665 670 | 2016 |
| gac gag gct gcc agt gcc cag cag gcg gaa tgg cgt agc tgg gac gtg Asp Glu Ala Ala Ser Ala Gln Gln Ala Glu Trp Arg Ser Trp Asp Val 675 680 685 | 2064 |
| aaa aag cgt ctc gaa tac tcg ctg gtg aaa ggc att acc gag ttt atc Lys Lys Arg Leu Glu Tyr Ser Leu Val Lys Gly Ile Thr Glu Phe Ile 690 695 700 | 2112 |
| gaa cag gat acc gaa gaa gcc cgt cag cag gcc gcc cgc ccg att gag Glu Gln Asp Thr Glu Glu Ala Arg Gln Gln Ala Ala Arg Pro Ile Glu 705 710 715 720 | 2160 |
| gtg att gaa ggg ccg ctg atg gac ggc atg aac gtg gtc ggc gac ctg Val Ile Glu Gly Pro Leu Met Asp Gly Met Asn Val Val Gly Asp Leu 725 730 735 | 2208 |
| ttc ggc gaa ggg aaa atg ttc ctg ccg cag gtg gtg aaa tcc gct cgc Phe Gly Glu Gly Lys Met Phe Leu Pro Gln Val Val Lys Ser Ala Arg 740 745 750 | 2256 |
| gtg atg aaa caa gcg gtg gcc tac ctg gag ccg ttt att gaa gcc agc Val Met Lys Gln Ala Val Ala Tyr Leu Glu Pro Phe Ile Glu Ala Ser 755 760 765 | 2304 |
| aaa gaa aaa ggc tcc agc aac ggc aag atg gtg att gcc acc gtg aag Lys Glu Lys Gly Ser Ser Asn Gly Lys Met Val Ile Ala Thr Val Lys 770 775 780 | 2352 |
| ggc gat gtg cac gac att ggc aag aac att gtc ggc gtg gtg ctg caa Gly Asp Val His Asp Ile Gly Lys Asn Ile Val Gly Val Val Leu Gln 785 790 795 800 | 2400 |
| tgc aac aac tac gaa atc gtc gat ctt ggc gtg atg gtg cca gcg gag Cys Asn Asn Tyr Glu Ile Val Asp Leu Gly Val Met Val Pro Ala Glu 805 810 815 | 2448 |
| aaa atc ctc aga acg gcg cgt gaa gtg aat gcc gat ctg att ggt ctt Lys Ile Leu Arg Thr Ala Arg Glu Val Asn Ala Asp Leu Ile Gly Leu 820 825 830 | 2496 |
| tcc ggg ctt atc acc ccg tcg ctg gac gaa atg gtc aac gtg gcg aaa Ser Gly Leu Ile Thr Pro Ser Leu Asp Glu Met Val Asn Val Ala Lys 835 840 845 | 2544 |
| gag atg gag cgt cag ggc ttt act atc ccg cta ctg atc ggc ggc gca Glu Met Glu Arg Gln Gly Phe Thr Ile Pro Leu Leu Ile Gly Gly Ala 850 855 860 | 2592 |
| acc act tcg aaa gcg cat acg gcg gtg aaa atc gag cag aac tac agc Thr Thr Ser Lys Ala His Thr Ala Val Lys Ile Glu Gln Asn Tyr Ser 865 870 875 880 | 2640 |
| ggc ccg acg gtc tac gtg cag aat gct tcg cgt acc gtg ggc gtg gtg Gly Pro Thr Val Tyr Val Gln Asn Ala Ser Arg Thr Val Gly Val Val 885 890 895 900 | 2688 |

101

| 885 | 890 | 895 | |
|---|------|------|------|
| gcg gcg cta ctc tcc gac acc cag cgt gat gac ttt gtc gcc cgt acc | | | 2736 |
| Ala Ala Leu Leu Ser Asp Thr Gln Arg Asp Asp Phe Val Ala Arg Thr | | | |
| 900 | 905 | 910 | |
| cgc aaa gag tac gaa acc gtg cgt att cag cac gcc cgc aaa aaa ccg | | | 2784 |
| Arg Lys Glu Tyr Glu Thr Val Arg Ile Gln His Ala Arg Lys Lys Pro | | | |
| 915 | 920 | 925 | |
| cgc acg ccg ccg gtc acg ctg gaa gcg gcg cgc gat aat gat ctg gca | | | 2832 |
| Arg Thr Pro Pro Val Thr Leu Glu Ala Ala Arg Asp Asn Asp Leu Ala | | | |
| 930 | 935 | 940 | |
| ttt gat tgg gaa cgc tac acc ccg ccg gta gcc cac cgt ctg ggc gtg | | | 2880 |
| Phe Asp Trp Glu Arg Tyr Thr Pro Pro Val Ala His Arg Leu Gly Val | | | |
| 945 | 950 | 955 | 960 |
| cag gag gtg gaa gcc agc atc gaa acg ctg cgc aac tac atc gac tgg | | | 2928 |
| Gln Glu Val Glu Ala Ser Ile Glu Thr Leu Arg Asn Tyr Ile Asp Trp | | | |
| 965 | 970 | 975 | |
| acg ccg ttc ttt atg acc tgg tgg ctg gcc ggc aaa tac ccg cgc att | | | 2976 |
| Thr Pro Phe Phe Met Thr Trp Ser Leu Ala Gly Lys Tyr Pro Arg Ile | | | |
| 980 | 985 | 990 | |
| ctg gaa gat gag gtg gtg ggc gtt gag gcg cag cgt ctg ttt aaa gac | | | 3024 |
| Leu Glu Asp Glu Val Val Gly Val Glu Ala Gln Arg Leu Phe Lys Asp | | | |
| 995 | 1000 | 1005 | |
| gcc aat gat atg ctg gat aaa ctg agc gcc gag aaa ctg ttg aat ccg | | | 3072 |
| Ala Asn Asp Met Leu Asp Lys Leu Ser Ala Glu Lys Leu Leu Asn Pro | | | |
| 1010 | 1015 | 1020 | |
| cgt ggc gtg gtg ggc ctg ttc ccg gcg aac cgt gtg ggt gac gac atc | | | 3120 |
| Arg Gly Val Val Gly Leu Phe Pro Ala Asn Arg Val Gly Asp Asp Ile | | | |
| 1025 | 1030 | 1035 | 1040 |
| gaa atc tat cgc gac gaa acc cgt act cat gtt ctg acg gtc agc cac | | | 3168 |
| Glu Ile Tyr Arg Asp Glu Thr Arg Thr His Val Leu Thr Val Ser His | | | |
| 1045 | 1050 | 1055 | |
| cac ctg cgc cag cag acc gag aaa gtt ggt ttt gct aac tac tgt ctg | | | 3216 |
| His Leu Arg Gln Gln Thr Glu Lys Val Gly Phe Ala Asn Tyr Cys Leu | | | |
| 1060 | 1065 | 1070 | |
| gcg gat ttt gtc gcg ccg aaa ctg agc ggc aaa gcg gac tac atc ggt | | | 3264 |
| Ala Asp Phe Val Ala Pro Lys Leu Ser Gly Lys Ala Asp Tyr Ile Gly | | | |
| 1075 | 1080 | 1085 | |
| gct ttc gcg gtg acc ggc ggt ctg aag gag gat gcg ctg gcg gac gcc | | | 3312 |
| Ala Phe Ala Val Thr Gly Gly Leu Lys Glu Asp Ala Leu Ala Asp Ala | | | |
| 1090 | 1095 | 1100 | |
| ttc gaa gcg caa cac gac gac tat aac aag atc atg gtg aaa gcg att | | | 3360 |
| Phe Glu Ala Gln His Asp Asp Tyr Asn Lys Ile Met Val Lys Ala Ile | | | |
| 1105 | 1110 | 1115 | 1120 |
| gcc gac cgt ctg gcg gaa gcg ttt gcc gag tat ctg cat gag cgt gta | | | 3408 |
| Ala Asp Arg Leu Ala Glu Ala Phe Ala Glu Tyr Leu His Glu Arg Val | | | |
| 1125 | 1130 | 1135 | |

102

cgt aag gtt tac tgg gga tat gcg ccg aac gag agc ctg agt aac gac 3456
 Arg Lys Val Tyr Trp Gly Tyr Ala Pro Asn Glu Ser Leu Ser Asn Asp
 1140 1145 1150

gaa tta atc cgc gaa aac tac cag ggg att cgc ccg gcg ccg ggt tat 3504
 Glu Leu Ile Arg Glu Asn Tyr Gln Gly Ile Arg Pro Ala Pro Gly Tyr
 1155 1160 1165

cct gcc tgc ccg gaa cat acc gaa aaa ggc act atc tgg cag cta ctg 3552
 Pro Ala Cys Pro Glu His Thr Glu Lys Gly Thr Ile Trp Gln Leu Leu
 1170 1175 1180

gat gtc gaa aaa cac acc ggg atg aag ctc acc gaa tct ttc gcc atg 3600
 Asp Val Glu Lys His Thr Gly Met Lys Leu Thr Glu Ser Phe Ala Met
 1185 1190 1195 1200

tgg cct ggc gcg tcg gtc tcc ggc tgg tac ttc agc cat cct gag agc 3648
 Trp Pro Gly Ala Ser Val Ser Gly Trp Tyr Phe Ser His Pro Glu Ser
 1205 1210 1215

aaa tac ttc gcg gta gcg cag atc caa cgc gat cag gtg aca gat tat 3696
 Lys Tyr Phe Ala Val Ala Gln Ile Gln Arg Asp Gln Val Thr Asp Tyr
 1220 1225 1230

gct ttc cgt aaa gga atg agc gtt gag gac gtt gag cgg tgg ctc gcg 3744
 Ala Phe Arg Lys Gly Met Ser Val Glu Asp Val Glu Arg Trp Leu Ala
 1235 1240 1245

ccg aac ctg ggt tac gat gcg gac tga 3771
 Pro Asn Leu Gly Tyr Asp Ala Asp
 1250 1255

<210> 24

<211> 1256

<212> PRT

<213> Salmonella typhi

<400> 24

Met Ser His Val Ala Arg Cys Ser Leu Phe Arg Gln His Ala Leu Cys
 1 5 10 15

Gln Tyr Gly Ser Leu Arg Gly Ala Leu Ser Gly Ala Ser Val Ser Ser
 20 25 30

Lys Val Glu Gln Leu Arg Ala Gln Leu Asn Glu Arg Ile Leu Val Leu
 35 40 45

Asp Gly Gly Met Gly Thr Met Ile Gln Ser Tyr Arg Leu His Glu Glu
 50 55 60

Asp Phe Arg Gly Glu Arg Phe Ala Asp Trp Pro Cys Asp Leu Lys Gly
 65 70 75 80

Asn Asn Asp Leu Leu Val Leu Ser Lys Pro Glu Val Ile Ala Ala Ile
 85 90 95

His Asn Ala Tyr Phe Glu Ala Gly Ala Asp Ile Ile Glu Thr Asn Thr
 100 105 110

Phe Asn Ser Thr Thr Ile Ala Met Ala Asp Tyr Arg Met Glu Ser Leu
 115 120 125

103

Ser Ala Glu Ile Asn Tyr Ala Ala Ala Lys Leu Ala Arg Ala Cys Ala
 130 135 140
 Asp Glu Trp Thr Ala Arg Thr Pro Glu Lys Pro Arg Phe Val Ala Gly
 145 150 155 160
 Val Leu Gly Pro Thr Asn Arg Thr Ala Ser Ile Ser Pro Asp Val Asn
 165 170 175
 Asp Pro Ala Phe Arg Asn Ile Thr Phe Asp Gln Leu Val Ala Ala Tyr
 180 185 190
 Arg Glu Ser Thr Lys Ala Leu Val Glu Gly Gly Ala Asp Leu Ile Leu
 195 200 205
 Ile Glu Thr Val Phe Asp Thr Leu Asn Ala Lys Ala Ala Val Phe Ala
 210 215 220
 Val Lys Glu Glu Phe Glu Ala Leu Gly Val Asp Leu Pro Ile Met Ile
 225 230 235 240
 Ser Gly Thr Ile Thr Asp Ala Ser Gly Arg Thr Leu Ser Gly Gln Thr
 245 250 255
 Thr Glu Ala Phe Tyr Asn Ser Leu Arg His Ala Glu Ala Leu Thr Phe
 260 265 270
 Gly Leu Asn Cys Ala Leu Gly Pro Asp Glu Leu Arg Gln Tyr Val Gln
 275 280 285
 Glu Leu Ser Arg Ile Ala Glu Cys Tyr Val Thr Ala His Pro Asn Ala
 290 295 300
 Gly Leu Pro Asn Ala Phe Gly Glu Tyr Asp Leu Asp Ala Asp Thr Met
 305 310 315 320
 Ala Lys Gln Ile Arg Glu Trp Ala Glu Ala Gly Phe Leu Asn Ile Val
 325 330 335
 Gly Gly Cys Cys Gly Thr Thr Pro Glu His Ile Ala Ala Met Ser Arg
 340 345 350
 Ala Val Ala Gly Leu Ser Pro Arg Gln Leu Pro Asp Ile Pro Val Ala
 355 360 365
 Cys Arg Leu Ser Gly Leu Glu Pro Leu Asn Ile Gly Asp Asp Ser Leu
 370 375 380
 Phe Val Asn Val Gly Glu Arg Thr Asn Val Thr Gly Ser Ala Lys Phe
 385 390 395 400
 Lys Arg Leu Ile Lys Glu Glu Lys Tyr Ser Glu Ala Leu Asp Val Ala
 405 410 415
 Arg Gln Gln Val Glu Ser Gly Ala Gln Ile Ile Asp Ile Asn Met Asp
 420 425 430
 Glu Gly Met Leu Asp Ala Glu Ala Ala Met Val Arg Phe Leu Ser Leu
 435 440 445
 Ile Ala Gly Glu Pro Asp Ile Ala Arg Val Pro Ile Met Ile Asp Ser

104

450 455 460
 Ser Lys Trp Glu Val Ile Glu Lys Gly Leu Lys Cys Ile Gln Gly Lys
 465 470 475 480
 Gly Ile Val Asn Ser Ile Ser Met Lys Glu Gly Val Glu Ala Phe Ile
 485 490 495
 His His Ala Lys Leu Leu Arg Arg Tyr Gly Ala Ala Val Val Val Met
 500 505 510
 Ala Phe Asp Glu Gln Gly Gln Ala Asp Thr Arg Glu Arg Lys Ile Glu
 515 520 525
 Ile Cys Arg Arg Ala Tyr Lys Ile Leu Leu Glu Glu Val Gly Phe Pro
 530 535 540
 Pro Glu Asp Ile Ile Phe Asp Pro Asn Ile Phe Ala Val Ala Thr Gly
 545 550 555 560
 Ile Glu Glu His Asn Asn Tyr Ala Gln Asp Phe Ile Gly Ala Cys Glu
 565 570 575
 Asp Ile Lys Arg Glu Leu Pro His Ala Leu Ile Ser Gly Gly Val Ser
 580 585 590
 Asn Val Ser Phe Ser Phe Arg Gly Asn Asp Pro Val Arg Glu Ala Ile
 595 600 605
 His Ala Val Phe Leu Tyr Tyr Ala Ile Arg Asn Gly Met Asp Met Gly
 610 615 620
 Ile Val Asn Ala Gly Gln Leu Ala Ile Tyr Asp Asn Leu Pro Ala Glu
 625 630 635 640
 Leu Arg Asp Ala Val Glu Asp Val Ile Leu Asn Arg Arg Asp Asp Gly
 645 650 655
 Thr Glu Arg Leu Leu Asp Leu Ala Glu Lys Tyr Arg Gly Ser Lys Thr
 660 665 670
 Asp Glu Ala Ala Ser Ala Gln Gln Ala Glu Trp Arg Ser Trp Asp Val
 675 680 685
 Lys Lys Arg Leu Glu Tyr Ser Leu Val Lys Gly Ile Thr Glu Phe Ile
 690 695 700
 Glu Gln Asp Thr Glu Glu Ala Arg Gln Gln Ala Ala Arg Pro Ile Glu
 705 710 715 720
 Val Ile Glu Gly Pro Leu Met Asp Gly Met Asn Val Val Gly Asp Leu
 725 730 735
 Phe Gly Glu Gly Lys Met Phe Leu Pro Gln Val Val Lys Ser Ala Arg
 740 745 750
 Val Met Lys Gln Ala Val Ala Tyr Leu Glu Pro Phe Ile Glu Ala Ser
 755 760 765
 Lys Glu Lys Gly Ser Ser Asn Gly Lys Met Val Ile Ala Thr Val Lys
 770 775 780

105

Gly Asp Val His Asp Ile Gly Lys Asn Ile Val Gly Val Val Leu Gln
 785 790 795 800
 Cys Asn Asn Tyr Glu Ile Val Asp Leu Gly Val Met Val Pro Ala Glu
 805 810 815
 Lys Ile Leu Arg Thr Ala Arg Glu Val Asn Ala Asp Leu Ile Gly Leu
 820 825 830
 Ser Gly Leu Ile Thr Pro Ser Leu Asp Glu Met Val Asn Val Ala Lys
 835 840 845
 Glu Met Glu Arg Gln Gly Phe Thr Ile Pro Leu Leu Ile Gly Gly Ala
 850 855 860
 Thr Thr Ser Lys Ala His Thr Ala Val Lys Ile Glu Gln Asn Tyr Ser
 865 870 875 880
 Gly Pro Thr Val Tyr Val Gln Asn Ala Ser Arg Thr Val Gly Val Val
 885 890 895
 Ala Ala Leu Leu Ser Asp Thr Gln Arg Asp Asp Phe Val Ala Arg Thr
 900 905 910
 Arg Lys Glu Tyr Glu Thr Val Arg Ile Gln His Ala Arg Lys Lys Pro
 915 920 925
 Arg Thr Pro Pro Val Thr Leu Glu Ala Ala Arg Asp Asn Asp Leu Ala
 930 935 940
 Phe Asp Trp Glu Arg Tyr Thr Pro Pro Val Ala His Arg Leu Gly Val
 945 950 955 960
 Gln Glu Val Glu Ala Ser Ile Glu Thr Leu Arg Asn Tyr Ile Asp Trp
 965 970 975
 Thr Pro Phe Phe Met Thr Trp Ser Leu Ala Gly Lys Tyr Pro Arg Ile
 980 985 990
 Leu Glu Asp Glu Val Val Gly Val Glu Ala Gln Arg Leu Phe Lys Asp
 995 1000 1005
 Ala Asn Asp Met Leu Asp Lys Leu Ser Ala Glu Lys Leu Leu Asn Pro
 1010 1015 1020
 Arg Gly Val Val Gly Leu Phe Pro Ala Asn Arg Val Gly Asp Asp Ile
 1025 1030 1035 1040
 Glu Ile Tyr Arg Asp Glu Thr Arg Thr His Val Leu Thr Val Ser His
 1045 1050 1055
 His Leu Arg Gln Gln Thr Glu Lys Val Gly Phe Ala Asn Tyr Cys Leu
 1060 1065 1070
 Ala Asp Phe Val Ala Pro Lys Leu Ser Gly Lys Ala Asp Tyr Ile Gly
 1075 1080 1085
 Ala Phe Ala Val Thr Gly Gly Leu Lys Glu Asp Ala Leu Ala Asp Ala
 1090 1095 1100
 Phe Glu Ala Gln His Asp Asp Tyr Asn Lys Ile Met Val Lys Ala Ile
 1105 1110 1115 1120

Ala Asp Arg Leu Ala Glu Ala Phe Ala Glu Tyr Leu His Glu Arg Val
 1125 1130 1135

Arg Lys Val Tyr Trp Gly Tyr Ala Pro Asn Glu Ser Leu Ser Asn Asp
 1140 1145 1150

Glu Leu Ile Arg Glu Asn Tyr Gln Gly Ile Arg Pro Ala Pro Gly Tyr
 1155 1160 1165

Pro Ala Cys Pro Glu His Thr Glu Lys Gly Thr Ile Trp Gln Leu Leu
 1170 1175 1180

Asp Val Glu Lys His Thr Gly Met Lys Leu Thr Glu Ser Phe Ala Met
 1185 1190 1195 1200

Trp Pro Gly Ala Ser Val Ser Gly Trp Tyr Phe Ser His Pro Glu Ser
 1205 1210 1215

Lys Tyr Phe Ala Val Ala Gln Ile Gln Arg Asp Gln Val Thr Asp Tyr
 1220 1225 1230

Ala Phe Arg Lys Gly Met Ser Val Glu Asp Val Glu Arg Trp Leu Ala
 1235 1240 1245

Pro Asn Leu Gly Tyr Asp Ala Asp
 1250 1255

<210> 25

<211> 3711

<212> DNA

<213> *Pseudomonas fluorescens*

<220>

<221> CDS

<222> (1) .. (3708)

<223> RPU03563

<400> 25

atg tcc gat cgc agc gtc cgc ctt caa gct ctc aag caa gct ctc aaa 48
 Met Ser Asp Arg Ser Val Arg Leu Gln Ala Leu Lys Gln Ala Leu Lys
 1 5 10 15

gag cgc atc ctg att ctc gac ggc ggc atg ggc acg atg atc cag agc 96
 Glu Arg Ile Leu Ile Leu Asp Gly Gly Met Gly Thr Met Ile Gln Ser
 20 25 30

tac aag ctc gaa gag cag gat tat cgc ggc aaa cgc ttc gcc gac tgg 144
 Tyr Lys Leu Glu Glu Gln Asp Tyr Arg Gly Lys Arg Phe Ala Asp Trp
 35 40 45

ccg agc gac gtc aag ggc aac aac gac ctg ttg gtg ctg acc cgc ccg 192
 Pro Ser Asp Val Lys Gly Asn Asn Asp Leu Leu Val Leu Thr Arg Pro
 50 55 60

gac gtg atc ggc ggc atc gag aaa gcc tat ctg gat gcc ggt gcc gac 240
 Asp Val Ile Gly Gly Ile Glu Lys Ala Tyr Leu Asp Ala Gly Ala Asp
 65 70 75 80

atc ctc gag acc aac acc ttc aac gcc acg cag att tcc atg gcc gac 288
 Ile Leu Glu Thr Asn Thr Phe Asn Ala Thr Gln Ile Ser Met Ala Asp

| | | | | | | | | | | 107 | | | | | | | | | | |
|---|------|-----|-----|--|--|--|--|--|--|-----|----|--|--|--|--|--|--|--|--|--|
| 85 | | | | | | | | | | 90 | 95 | | | | | | | | | |
| tac ggc atg gaa gaa ctg gtc tac gaa ctc aac gta gaa ggc gcc cgt | 336 | | | | | | | | | | | | | | | | | | | |
| Tyr Gly Met Glu Glu Leu Val Tyr Glu Leu Asn Val Glu Gly Ala Arg | | | | | | | | | | | | | | | | | | | | |
| 100 | 105 | 110 | | | | | | | | | | | | | | | | | | |
| ctg gca cgc aag gtc gcc gac gcg aaa acc ctc gag acc ccc gac aag | 384 | | | | | | | | | | | | | | | | | | | |
| Leu Ala Arg Lys Val Ala Asp Ala Lys Thr Leu Glu Thr Pro Asp Lys | | | | | | | | | | | | | | | | | | | | |
| 115 | 120 | 125 | | | | | | | | | | | | | | | | | | |
| ccg cgc ttc gtc gcc ggc gtt ctc ggc ccg acc agc cgc acc tgc tcg | 432 | | | | | | | | | | | | | | | | | | | |
| Pro Arg Phe Val Ala Gly Val Leu Gly Pro Thr Ser Arg Thr Cys Ser | | | | | | | | | | | | | | | | | | | | |
| 130 | 135 | 140 | | | | | | | | | | | | | | | | | | |
| ctg tcg ccg gac gtc aac aac ccg ggc tat cgc aac gtc acc ttc gat | 480 | | | | | | | | | | | | | | | | | | | |
| Leu Ser Pro Asp Val Asn Asn Pro Gly Tyr Arg Asn Val Thr Phe Asp | | | | | | | | | | | | | | | | | | | | |
| 145 | 150 | 155 | 160 | | | | | | | | | | | | | | | | | |
| gag ctg gtc gaa aac tac acc gag gcc acc aaa ggc ctg atc gag ggc | 528 | | | | | | | | | | | | | | | | | | | |
| Glu Leu Val Glu Asn Tyr Thr Glu Ala Thr Lys Gly Leu Ile Glu Gly | | | | | | | | | | | | | | | | | | | | |
| 165 | 170 | 175 | | | | | | | | | | | | | | | | | | |
| ggc gcg gat ctg atc ctg atc gaa acc atc ttc gac acc ctc aac gcc | 576 | | | | | | | | | | | | | | | | | | | |
| Gly Ala Asp Leu Ile Leu Ile Glu Thr Ile Phe Asp Thr Leu Asn Ala | | | | | | | | | | | | | | | | | | | | |
| 180 | 185 | 190 | | | | | | | | | | | | | | | | | | |
| aaa gcc gcg atc ttc gcc gtg caa ggc gtg ttc gaa gaa ctg ggc ttc | 624 | | | | | | | | | | | | | | | | | | | |
| Lys Ala Ala Ile Phe Ala Val Gln Gly Val Phe Glu Glu Leu Gly Phe | | | | | | | | | | | | | | | | | | | | |
| 195 | 200 | 205 | | | | | | | | | | | | | | | | | | |
| gaa ttg ccg atc atg atc tcc ggc acc atc acc gac gcc tcc ggc cgt | 672 | | | | | | | | | | | | | | | | | | | |
| Glu Leu Pro Ile Met Ile Ser Gly Thr Ile Thr Asp Ala Ser Gly Arg | | | | | | | | | | | | | | | | | | | | |
| 210 | 215 | 220 | | | | | | | | | | | | | | | | | | |
| acc ctg tcg ggc cag acc acc gaa gcg ttc tgg aac tcc gtg gct cac | 720 | | | | | | | | | | | | | | | | | | | |
| Thr Leu Ser Gly Gln Thr Thr Glu Ala Phe Trp Asn Ser Val Ala His | | | | | | | | | | | | | | | | | | | | |
| 225 | 230 | 235 | 240 | | | | | | | | | | | | | | | | | |
| gcc aaa ccg att tcc gtc ggt ctt aac tgc gcc ctc ggc gcc cgc gaa | 768 | | | | | | | | | | | | | | | | | | | |
| Ala Lys Pro Ile Ser Val Gly Leu Asn Cys Ala Leu Gly Ala Arg Glu | | | | | | | | | | | | | | | | | | | | |
| 245 | 250 | 255 | | | | | | | | | | | | | | | | | | |
| ctg cgt ccg tac ctg gaa gag ctg tcg gac aag gcc agc acc cac gtt | 816 | | | | | | | | | | | | | | | | | | | |
| Leu Arg Pro Tyr Leu Glu Glu Leu Ser Asp Lys Ala Ser Thr His Val | | | | | | | | | | | | | | | | | | | | |
| 260 | 265 | 270 | | | | | | | | | | | | | | | | | | |
| tcg gcg cac ccg aac gcc ggc ctg ccg aac gaa ttc ggc gag tac gac | 864 | | | | | | | | | | | | | | | | | | | |
| Ser Ala His Pro Asn Ala Gly Leu Pro Asn Glu Phe Gly Glu Tyr Asp | | | | | | | | | | | | | | | | | | | | |
| 275 | 280 | 285 | | | | | | | | | | | | | | | | | | |
| gag ctg ccg gtg gac acc gcc aag gtc atc gaa gag ttc gcc cag agc | 912 | | | | | | | | | | | | | | | | | | | |
| Glu Leu Pro Val Asp Thr Ala Lys Val Ile Glu Glu Phe Ala Gln Ser | | | | | | | | | | | | | | | | | | | | |
| 290 | 295 | 300 | | | | | | | | | | | | | | | | | | |
| ggt ttc ctc aac atc gtc ggc ggt tgc tgc ggc acc acg ccg ggc cat | 960 | | | | | | | | | | | | | | | | | | | |
| Gly Phe Leu Asn Ile Val Gly Gly Cys Cys Gly Thr Thr Pro Gly His | | | | | | | | | | | | | | | | | | | | |
| 305 | 310 | 315 | 320 | | | | | | | | | | | | | | | | | |
| atc gaa gcc atc gcc aaa gcc gtt gcc ggt tac gcg cca cgg cag att | 1008 | | | | | | | | | | | | | | | | | | | |
| Ile Glu Ala Ile Ala Lys Ala Val Ala Gly Tyr Ala Pro Arg Gln Ile | | | | | | | | | | | | | | | | | | | | |
| 325 | 330 | 335 | | | | | | | | | | | | | | | | | | |

108

| | |
|---|------|
| ccg gac att ccc aag gcc tgc cgc ctg tcg ggt ctg gaa ccg ttc acc Pro Asp Ile Pro Lys Ala Cys Arg Leu Ser Gly Leu Glu Pro Phe Thr 340 345 350 | 1056 |
| att gat cgc agc tcg ctg ttc gtc aac gtc ggc gag cgg acc aac atc Ile Asp Arg Ser Ser Leu Phe Val Asn Val Gly Glu Arg Thr Asn Ile 355 360 365 | 1104 |
| acc ggg tcc gcg aaa ttt gcc cgg ctg atc cgt gaa gac aac tac acc Thr Gly Ser Ala Lys Phe Ala Arg Leu Ile Arg Glu Asp Asn Tyr Thr 370 375 380 | 1152 |
| gaa gcc ctg gaa gtc gcc ctg cag cag gtc gag gcc ggc gcc cag gtg Glu Ala Leu Glu Val Ala Leu Gln Gln Val Glu Ala Gly Ala Gln Val 385 390 395 400 | 1200 |
| atc gac atc aac atg gac gaa ggg atg ctc gat tcg aag aag gcc atg Ile Asp Ile Asn Met Asp Glu Gly Met Leu Asp Ser Lys Lys Ala Met 405 410 415 | 1248 |
| gtg acc ttc ctc aat ctg att gcc ggc gaa ccg gac atc tcc cgc gta Val Thr Phe Leu Asn Leu Ile Ala Gly Glu Pro Asp Ile Ser Arg Val 420 425 430 | 1296 |
| ccg atc atg atc gac tcc tcg aaa tgg gac gtg atc gaa gcc ggc ctc Pro Ile Met Ile Asp Ser Ser Lys Trp Asp Val Ile Glu Ala Gly Leu 435 440 445 | 1344 |
| aag tgc att cag ggc aag ggc atc gtc aac tcg atc agc atg aaa gaa Lys Cys Ile Gln Gly Lys Gly Ile Val Asn Ser Ile Ser Met Lys Glu 450 455 460 | 1392 |
| ggc gtc gag cag ttc atc cac cac gcc aaa ctg tgc aag cgc tat ggc Gly Val Glu Gln Phe Ile His His Ala Lys Leu Cys Lys Arg Tyr Gly 465 470 475 480 | 1440 |
| gcc gcc gtg gtg gtg atg gcg ttc gac gaa gcc ggc cag gct gac acc Ala Ala Val Val Val Met Ala Phe Asp Glu Ala Gly Gln Ala Asp Thr 485 490 495 | 1488 |
| gaa gcg cgc aag aaa gag atc tgc aaa cgc tcc tac gac att ctg gtc Glu Ala Arg Lys Lys Glu Ile Cys Lys Arg Ser Tyr Asp Ile Leu Val 500 505 510 | 1536 |
| aac gaa gtc ggc ttc ccg ccg gaa gac atc att ttc gac ccg aac atc Asn Glu Val Gly Phe Pro Pro Glu Asp Ile Ile Phe Asp Pro Asn Ile 515 520 525 | 1584 |
| ttc gcc gtg gcc acc ggc atc gaa gaa cac aac aac tac gct gtg gac Phe Ala Val Ala Thr Gly Ile Glu Glu His Asn Asn Tyr Ala Val Asp 530 535 540 | 1632 |
| ttc atc aac gcc tgt gcc tac atc cgc gac gag ctg ccg tat gcc ctg Phe Ile Asn Ala Cys Ala Tyr Ile Arg Asp Glu Leu Pro Tyr Ala Leu 545 550 555 560 | 1680 |
| agc tcc ggc ggc gtg tcc aac gtg tcg ttc tcg ttc cgc ggc aac aac Ser Ser Gly Gly Val Ser Asn Val Ser Phe Ser Phe Arg Gly Asn Asn 565 570 575 | 1728 |
| ccg gtg cgc gag gcg atc cac tcg gtg ttc ctg ctg tac gcg atc cgc Pro Val Arg Glu Ala Ile His Ser Val Phe Leu Leu Tyr Ala Ile Arg | 1776 |

109

| 580 | 585 | 590 | |
|---|-----|-----|------|
| gcc ggc ctg acc atg ggt atc gtc aac gcc ggt cag ctg gag atc tac Ala Gly Leu Thr Met Gly Ile Val Asn Ala Gly Gln Leu Glu Ile Tyr 595 600 605 | | | 1824 |
| gac cag atc ccg cag gaa ctg cgc gac gcc gtt gaa gac gtg atc ctc Asp Gln Ile Pro Gln Glu Leu Arg Asp Ala Val Glu Asp Val Ile Leu 610 615 620 | | | 1872 |
| aac cgc acg ccg gaa ggc acc gac gcc ctc ctc gcc atc gcc gac aag Asn Arg Thr Pro Glu Gly Thr Asp Ala Leu Leu Ala Ile Ala Asp Lys 625 630 635 640 | | | 1920 |
| tac aag ggc gac ggc agc gtc aag gaa gcc gag acc gaa gaa tgg cgc Tyr Lys Gly Asp Gly Ser Val Lys Glu Ala Glu Thr Glu Glu Trp Arg 645 650 655 | | | 1968 |
| ggc tgg gac gtc aac aaa cgt ctg gaa cat gcg ctg gtc aag ggc atc Gly Trp Asp Val Asn Lys Arg Leu Glu His Ala Leu Val Lys Gly Ile 660 665 670 | | | 2016 |
| acc acc cac atc gtc gaa gac acc gaa gaa tcc cgt cag tcc ttc gcc Thr Thr His Ile Val Glu Asp Thr Glu Glu Ser Arg Gln Ser Phe Ala 675 680 685 | | | 2064 |
| cgc ccg atc gaa gtg atc gaa ggc ccg ctg atg tcc ggc atg aac atc Arg Pro Ile Glu Val Ile Glu Gly Pro Leu Met Ser Gly Met Asn Ile 690 695 700 | | | 2112 |
| gtc ggc gac ctg ttc ggc gcc ggc aaa atg ttc ctg ccg caa gtg gtg Val Gly Asp Leu Phe Gly Ala Gly Lys Met Phe Leu Pro Gln Val Val 705 710 715 720 | | | 2160 |
| aaa tcc gcc cgc gtg atg aag cag gcc gtg gcg cac ctg att ccg ttc Lys Ser Ala Arg Val Met Lys Gln Ala Val Ala His Leu Ile Pro Phe 725 730 735 | | | 2208 |
| atc gaa ctg gaa aaa ggc gac aag ccg gaa gcc aag ggc aag atc ctg Ile Glu Leu Glu Lys Gly Asp Lys Pro Glu Ala Lys Gly Lys Ile Leu 740 745 750 | | | 2256 |
| atg gcc acg gtc aaa ggc gac gtg cac gac atc ggc aag aac atc gtc Met Ala Thr Val Lys Gly Asp Val His Asp Ile Gly Lys Asn Ile Val 755 760 765 | | | 2304 |
| ggc gtg gtg ctg ggt tgc aac ggc tac gac atc gtc gac ctc ggc gtg Gly Val Val Leu Gly Cys Asn Gly Tyr Asp Ile Val Asp Leu Gly Val 770 775 780 | | | 2352 |
| atg gtg ccg gcg gag aag atc ctg cag gtg gcc aag gag cag aag tgc Met Val Pro Ala Glu Lys Ile Leu Gln Val Ala Lys Glu Gln Lys Cys 785 790 795 800 | | | 2400 |
| gac atc atc ggc ctg tcc ggt ctg atc acc ccg tcg ctg gat gag atg Asp Ile Ile Gly Leu Ser Gly Leu Ile Thr Pro Ser Leu Asp Glu Met 805 810 815 | | | 2448 |
| gtc cat gtg gcc cgc gag atg cag cgc cag gac ttc cac ctg ccg ctg Val His Val Ala Arg Glu Met Gln Arg Gln Asp Phe His Leu Pro Leu 820 825 830 | | | 2496 |

110

| | |
|---|------|
| atg atc ggc ggc gcg acc acc tcc aag gcg cac acg gcg gtg aag atc Met Ile Gly Gly Ala Thr Thr Ser Lys Ala His Thr Ala Val Lys Ile 835 840 845 | 2544 |
| gag ccc aag tac agc aac gac gca gtg gtc tac gtg acc gac gcc tcc Glu Pro Lys Tyr Ser Asn Asp Ala Val Val Tyr Val Thr Asp Ala Ser 850 855 860 | 2592 |
| cgc gcc gtg ggc gtg gcg acg cag ttg ctg tcc aag gaa ctg aaa gcc Arg Ala Val Gly Val Ala Thr Gln Leu Leu Ser Lys Glu Leu Lys Ala 865 870 875 880 | 2640 |
| ggt ttc gtc cag aag acc cgc gaa gag tac atc gac gtc cgc gag cgc Gly Phe Val Gln Lys Thr Arg Glu Glu Tyr Ile Asp Val Arg Glu Arg 885 890 895 | 2688 |
| acc gcc aac cgc agc gcc cgc acc gaa cgc ctg agc tac gcc gcc gcg Thr Ala Asn Arg Ser Ala Arg Thr Glu Arg Leu Ser Tyr Ala Ala Ala 900 905 910 | 2736 |
| atc gcc aag aag ccg cag ttc gac tgg gcc act tac acc ccg gtc aaa Ile Ala Lys Lys Pro Gln Phe Asp Trp Ala Thr Tyr Thr Pro Val Lys 915 920 925 | 2784 |
| ccg acc ttc acc ggc acc cgc gtg ctg gac aac atc gac ctc aac gtt Pro Thr Phe Thr Gly Thr Arg Val Leu Asp Asn Ile Asp Leu Asn Val 930 935 940 | 2832 |
| ctc gcc gag tac atc gac tgg acg ccg ttc ttc atc tcc tgg gac ctg Leu Ala Glu Tyr Ile Asp Trp Thr Pro Phe Phe Ile Ser Trp Asp Leu 945 950 955 960 | 2880 |
| gcc ggc aag ttc ccg cgc atc ctc gaa gac gaa gtg gtc gcc gaa gcg Ala Gly Lys Phe Pro Arg Ile Leu Glu Asp Glu Val Val Gly Glu Ala 965 970 975 | 2928 |
| gcg acc gcg ctg tac aag gac gct cgc gag atg ctg acc aag ctg atc Ala Thr Ala Leu Tyr Lys Asp Ala Arg Glu Met Leu Thr Lys Leu Ile 980 985 990 | 2976 |
| gac gag aaa ctg atc agc gcc cgt gcg gtg ttc ggc ttc tgg ccg gcc Asp Glu Lys Leu Ile Ser Ala Arg Ala Val Phe Gly Phe Trp Pro Ala 995 1000 1005 | 3024 |
| aat cag gtg cac gac gac gat atc gag ctg tac ggc gat gac ggc aag Asn Gln Val His Asp Asp Asp Ile Glu Leu Tyr Gly Asp Asp Gly Lys 1010 1015 1020 | 3072 |
| cca atg gcg cgc ctg cat cac ctg cgc cag cag atc atc aag acc gac Pro Met Ala Arg Leu His His Leu Arg Gln Gln Ile Ile Lys Thr Asp 1025 1030 1035 1040 | 3120 |
| ggc aaa ccg aac ttc tcc ctc gcc gac ttc gtc gcg ccg aag gac agc Gly Lys Pro Asn Phe Ser Leu Ala Asp Phe Val Ala Pro Lys Asp Ser 1045 1050 1055 | 3168 |
| gaa gtg acc gac tac gtt ggt ggt ttc atc acc acc gcc ggg atc gcc Glu Val Thr Asp Tyr Val Gly Gly Phe Ile Thr Thr Ala Gly Ile Gly 1060 1065 1070 | 3216 |
| gcc gaa gaa gtg gcc aag gcc tat cag gac gcc ggc gac gat tac aac Ala Glu Glu Val Ala Lys Ala Tyr Gln Asp Ala Gly Asp Asp Tyr Asn | 3264 |

111

1075 1080 1085
 tcg atc atg gtc aag gcc ctg gcc gac cgt ctg gcc gag gcg tgc gcc 3312
 Ser Ile Met Val Lys Ala Leu Ala Asp Arg Leu Ala Glu Ala Cys Ala
 1090 1095 1100
 gag tgg ctg cac cag cag gtg cgc aaa gag cac tgg ggt tac gcc aag 3360
 Glu Trp Leu His Gln Gln Val Arg Lys Glu His Trp Gly Tyr Ala Lys
 1105 1110 1115 1120
 gat gaa gcc ctc gat aac gag gcg ctg atc aaa gag cag tat tcc ggc 3408
 Asp Glu Ala Leu Asp Asn Glu Ala Leu Ile Lys Glu Gln Tyr Ser Gly
 1125 1130 1135
 atc cgc cct gcc ccc ggc tac ccg gcg tgc ccg gat cac acc gag aag 3456
 Ile Arg Pro Ala Pro Gly Tyr Pro Ala Cys Pro Asp His Thr Glu Lys
 1140 1145 1150
 gcc acc ctg ttc gcc ctg ctc gac cct gaa gca cag gaa atg cgc gcc 3504
 Ala Thr Leu Phe Ala Leu Leu Asp Pro Glu Ala Gln Glu Met Arg Ala
 1155 1160 1165
 ggc cgc agc ggt gtg ttc ctc acc gag cac tac gcg atg ttc ccg gcg 3552
 Gly Arg Ser Gly Val Phe Leu Thr Glu His Tyr Ala Met Phe Pro Ala
 1170 1175 1180
 gca gcc gtc agc ggc tgg tac ttc gcc cat ccg cag gcg cag tac ttc 3600
 Ala Ala Val Ser Gly Trp Tyr Phe Ala His Pro Gln Ala Gln Tyr Phe
 1185 1190 1195 1200
 gcc gtg ggc aag gtc gac aag gat cag gtg cag agc tac acc tcg cgc 3648
 Ala Val Gly Lys Val Asp Lys Asp Gln Val Gln Ser Tyr Thr Ser Arg
 1205 1210 1215
 aaa ggc cag gaa ctg agc ctg acc gag cgc tgg ctg gca ccc aat ctg 3696
 Lys Gly Gln Glu Leu Ser Leu Thr Glu Arg Trp Leu Ala Pro Asn Leu
 1220 1225 1230
 ggc tac gac aac tga 3711
 Gly Tyr Asp Asn
 1235
 <210> 26
 <211> 1236
 <212> PRT
 <213> *Pseudomonas fluorescens*
 <400> 26
 Met Ser Asp Arg Ser Val Arg Leu Gln Ala Leu Lys Gln Ala Leu Lys
 1 5 10 15
 Glu Arg Ile Leu Ile Leu Asp Gly Gly Met Gly Thr Met Ile Gln Ser
 20 25 30
 Tyr Lys Leu Glu Glu Gln Asp Tyr Arg Gly Lys Arg Phe Ala Asp Trp
 35 40 45
 Pro Ser Asp Val Lys Gly Asn Asn Asp Leu Leu Val Leu Thr Arg Pro
 50 55 60
 Asp Val Ile Gly Gly Ile Glu Lys Ala Tyr Leu Asp Ala Gly Ala Asp

112

| | | | |
|---|-----|-----|-----|
| 65 | 70 | 75 | 80 |
| Ile Leu Glu Thr Asn Thr Phe Asn Ala Thr Gln Ile Ser Met Ala Asp | 85 | 90 | 95 |
| Tyr Gly Met Glu Glu Leu Val Tyr Glu Leu Asn Val Glu Gly Ala Arg | 100 | 105 | 110 |
| Leu Ala Arg Lys Val Ala Asp Ala Lys Thr Leu Glu Thr Pro Asp Lys | 115 | 120 | 125 |
| Pro Arg Phe Val Ala Gly Val Leu Gly Pro Thr Ser Arg Thr Cys Ser | 130 | 135 | 140 |
| Leu Ser Pro Asp Val Asn Asn Pro Gly Tyr Arg Asn Val Thr Phe Asp | 145 | 150 | 155 |
| Glu Leu Val Glu Asn Tyr Thr Glu Ala Thr Lys Gly Leu Ile Glu Gly | 165 | 170 | 175 |
| Gly Ala Asp Leu Ile Leu Ile Glu Thr Ile Phe Asp Thr Leu Asn Ala | 180 | 185 | 190 |
| Lys Ala Ala Ile Phe Ala Val Gln Gly Val Phe Glu Glu Leu Gly Phe | 195 | 200 | 205 |
| Glu Leu Pro Ile Met Ile Ser Gly Thr Ile Thr Asp Ala Ser Gly Arg | 210 | 215 | 220 |
| Thr Leu Ser Gly Gln Thr Thr Glu Ala Phe Trp Asn Ser Val Ala His | 225 | 230 | 235 |
| Ala Lys Pro Ile Ser Val Gly Leu Asn Cys Ala Leu Gly Ala Arg Glu | 245 | 250 | 255 |
| Leu Arg Pro Tyr Leu Glu Glu Leu Ser Asp Lys Ala Ser Thr His Val | 260 | 265 | 270 |
| Ser Ala His Pro Asn Ala Gly Leu Pro Asn Glu Phe Gly Glu Tyr Asp | 275 | 280 | 285 |
| Glu Leu Pro Val Asp Thr Ala Lys Val Ile Glu Glu Phe Ala Gln Ser | 290 | 295 | 300 |
| Gly Phe Leu Asn Ile Val Gly Gly Cys Cys Gly Thr Thr Pro Gly His | 305 | 310 | 315 |
| Ile Glu Ala Ile Ala Lys Ala Val Ala Gly Tyr Ala Pro Arg Gln Ile | 325 | 330 | 335 |
| Pro Asp Ile Pro Lys Ala Cys Arg Leu Ser Gly Leu Glu Pro Phe Thr | 340 | 345 | 350 |
| Ile Asp Arg Ser Ser Leu Phe Val Asn Val Gly Glu Arg Thr Asn Ile | 355 | 360 | 365 |
| Thr Gly Ser Ala Lys Phe Ala Arg Leu Ile Arg Glu Asp Asn Tyr Thr | 370 | 375 | 380 |
| Glu Ala Leu Glu Val Ala Leu Gln Gln Val Glu Ala Gly Ala Gln Val | 385 | 390 | 395 |
| | | | 400 |

113

Ile Asp Ile Asn Met Asp Glu Gly Met Leu Asp Ser Lys Lys Ala Met
 405 410 415
 Val Thr Phe Leu Asn Leu Ile Ala Gly Glu Pro Asp Ile Ser Arg Val
 420 425 430
 Pro Ile Met Ile Asp Ser Ser Lys Trp Asp Val Ile Glu Ala Gly Leu
 435 440 445
 Lys Cys Ile Gln Gly Lys Gly Ile Val Asn Ser Ile Ser Met Lys Glu
 450 455 460
 Gly Val Glu Gln Phe Ile His His Ala Lys Leu Cys Lys Arg Tyr Gly
 465 470 475 480
 Ala Ala Val Val Val Met Ala Phe Asp Glu Ala Gly Gln Ala Asp Thr
 485 490 495
 Glu Ala Arg Lys Lys Glu Ile Cys Lys Arg Ser Tyr Asp Ile Leu Val
 500 505 510
 Asn Glu Val Gly Phe Pro Pro Glu Asp Ile Ile Phe Asp Pro Asn Ile
 515 520 525
 Phe Ala Val Ala Thr Gly Ile Glu Glu His Asn Asn Tyr Ala Val Asp
 530 535 540
 Phe Ile Asn Ala Cys Ala Tyr Ile Arg Asp Glu Leu Pro Tyr Ala Leu
 545 550 555 560
 Ser Ser Gly Gly Val Ser Asn Val Ser Phe Ser Phe Arg Gly Asn Asn
 565 570 575
 Pro Val Arg Glu Ala Ile His Ser Val Phe Leu Leu Tyr Ala Ile Arg
 580 585 590
 Ala Gly Leu Thr Met Gly Ile Val Asn Ala Gly Gln Leu Glu Ile Tyr
 595 600 605
 Asp Gln Ile Pro Gln Glu Leu Arg Asp Ala Val Glu Asp Val Ile Leu
 610 615 620
 Asn Arg Thr Pro Glu Gly Thr Asp Ala Leu Leu Ala Ile Ala Asp Lys
 625 630 635 640
 Tyr Lys Gly Asp Gly Ser Val Lys Glu Ala Glu Thr Glu Glu Trp Arg
 645 650 655
 Gly Trp Asp Val Asn Lys Arg Leu Glu His Ala Leu Val Lys Gly Ile
 660 665 670
 Thr Thr His Ile Val Glu Asp Thr Glu Glu Ser Arg Gln Ser Phe Ala
 675 680 685
 Arg Pro Ile Glu Val Ile Glu Gly Pro Leu Met Ser Gly Met Asn Ile
 690 695 700
 Val Gly Asp Leu Phe Gly Ala Gly Lys Met Phe Leu Pro Gln Val Val
 705 710 715 720
 Lys Ser Ala Arg Val Met Lys Gln Ala Val Ala His Leu Ile Pro Phe
 725 730 735

114

Ile Glu Leu Glu Lys Gly Asp Lys Pro Glu Ala Lys Gly Lys Ile Leu
 740 745 750
 Met Ala Thr Val Lys Gly Asp Val His Asp Ile Gly Lys Asn Ile Val
 755 760 765
 Gly Val Val Leu Gly Cys Asn Gly Tyr Asp Ile Val Asp Leu Gly Val
 770 775 780
 Met Val Pro Ala Glu Lys Ile Leu Gln Val Ala Lys Glu Gln Lys Cys
 785 790 795 800
 Asp Ile Ile Gly Leu Ser Gly Leu Ile Thr Pro Ser Leu Asp Glu Met
 805 810 815
 Val His Val Ala Arg Glu Met Gln Arg Gln Asp Phe His Leu Pro Leu
 820 825 830
 Met Ile Gly Gly Ala Thr Thr Ser Lys Ala His Thr Ala Val Lys Ile
 835 840 845
 Glu Pro Lys Tyr Ser Asn Asp Ala Val Val Tyr Val Thr Asp Ala Ser
 850 855 860
 Arg Ala Val Gly Val Ala Thr Gln Leu Leu Ser Lys Glu Leu Lys Ala
 865 870 875 880
 Gly Phe Val Gln Lys Thr Arg Glu Glu Tyr Ile Asp Val Arg Glu Arg
 885 890 895
 Thr Ala Asn Arg Ser Ala Arg Thr Glu Arg Leu Ser Tyr Ala Ala Ala
 900 905 910
 Ile Ala Lys Lys Pro Gln Phe Asp Trp Ala Thr Tyr Thr Pro Val Lys
 915 920 925
 Pro Thr Phe Thr Gly Thr Arg Val Leu Asp Asn Ile Asp Leu Asn Val
 930 935 940
 Leu Ala Glu Tyr Ile Asp Trp Thr Pro Phe Phe Ile Ser Trp Asp Leu
 945 950 955 960
 Ala Gly Lys Phe Pro Arg Ile Leu Glu Asp Glu Val Val Gly Glu Ala
 965 970 975
 Ala Thr Ala Leu Tyr Lys Asp Ala Arg Glu Met Leu Thr Lys Leu Ile
 980 985 990
 Asp Glu Lys Leu Ile Ser Ala Arg Ala Val Phe Gly Phe Trp Pro Ala
 995 1000 1005
 Asn Gln Val His Asp Asp Asp Ile Glu Leu Tyr Gly Asp Asp Gly Lys
 1010 1015 1020
 Pro Met Ala Arg Leu His His Leu Arg Gln Gln Ile Ile Lys Thr Asp
 1025 1030 1035 1040
 Gly Lys Pro Asn Phe Ser Leu Ala Asp Phe Val Ala Pro Lys Asp Ser
 1045 1050 1055
 Glu Val Thr Asp Tyr Val Gly Gly Phe Ile Thr Thr Ala Gly Ile Gly

115

1060 1065 1070
 Ala Glu Glu Val Ala Lys Ala Tyr Gln Asp Ala Gly Asp Asp Tyr Asn
 1075 1080 1085
 Ser Ile Met Val Lys Ala Leu Ala Asp Arg Leu Ala Glu Ala Cys Ala
 1090 1095 1100
 Glu Trp Leu His Gln Gln Val Arg Lys Glu His Trp Gly Tyr Ala Lys
 1105 1110 1115 1120
 Asp Glu Ala Leu Asp Asn Glu Ala Leu Ile Lys Glu Gln Tyr Ser Gly
 1125 1130 1135
 Ile Arg Pro Ala Pro Gly Tyr Pro Ala Cys Pro Asp His Thr Glu Lys
 1140 1145 1150
 Ala Thr Leu Phe Ala Leu Leu Asp Pro Glu Ala Gln Glu Met Arg Ala
 1155 1160 1165
 Gly Arg Ser Gly Val Phe Leu Thr Glu His Tyr Ala Met Phe Pro Ala
 1170 1175 1180
 Ala Ala Val Ser Gly Trp Tyr Phe Ala His Pro Gln Ala Gln Tyr Phe
 1185 1190 1195 1200
 Ala Val Gly Lys Val Asp Lys Asp Gln Val Gln Ser Tyr Thr Ser Arg
 1205 1210 1215
 Lys Gly Gln Glu Leu Ser Leu Thr Glu Arg Trp Leu Ala Pro Asn Leu
 1220 1225 1230
 Gly Tyr Asp Asn
 1235

 <210> 27
 <211> 3705
 <212> DNA
 <213> Pseudomonas aeruginosa

 <220>
 <221> CDS
 <222> (1)..(3702)
 <223> RPA01772

 <400> 27
 atg tcc agc ccg ctc acc gat cgc agc gcc cgc ctg caa gcc ctc cag 48
 Met Ser Ser Pro Leu Thr Asp Arg Ser Ala Arg Leu Gln Ala Leu Gln
 1 5 10 15
 cac gcc ctc agg gaa cgt atc ctg atc ctc gat ggc ggc atg ggc acc 96
 His Ala Leu Arg Glu Arg Ile Leu Ile Leu Asp Gly Gly Met Gly Thr
 20 25 30
 atg atc cag agc tac aag ctg gaa gag gcc gac tac cgc ggc gag cgc 144
 Met Ile Gln Ser Tyr Lys Leu Glu Glu Ala Asp Tyr Arg Gly Glu Arg
 35 40 45
 ttc gcc gac tgg ccg agc gac gtg aaa ggc aac aac gac ctc ttg ctg 192
 Phe Ala Asp Trp Pro Ser Asp Val Lys Gly Asn Asn Asp Leu Leu Leu
 50 55 60

116

| | |
|---|-----|
| ctg agc cgc ccg gac gtg atc cag gcc atc gag aag gcc tac ctc gac Leu Ser Arg Pro Asp Val Ile Gln Ala Ile Glu Lys Ala Tyr Leu Asp 65 70 75 80 | 240 |
| gcc ggc gcc gac atc ctc gag acc aac acc ttc aac gcc acc cag gtg Ala Gly Ala Asp Ile Leu Glu Thr Asn Thr Phe Asn Ala Thr Gln Val 85 90 95 | 288 |
| tcc cag gcc gac tac ggc atg cag tcg ctg gcc tac gaa ctc aac gtc Ser Gln Ala Asp Tyr Gly Met Gln Ser Leu Ala Tyr Glu Leu Asn Val 100 105 110 | 336 |
| gaa ggg gcg cgc ctg gcc cgc cag gtg gcg gac gcg aag acc gcc gag Glu Gly Ala Arg Leu Ala Arg Gln Val Ala Asp Ala Lys Thr Ala Glu 115 120 125 | 384 |
| acc ccg gac aag ccg cgt ttc gtc gcc ggc gtg ctc ggc ccg acc agc Thr Pro Asp Lys Pro Arg Phe Val Ala Gly Val Leu Gly Pro Thr Ser 130 135 140 | 432 |
| cgc acc tgc tcg att tcc ccg gac gtg aac aac ccc ggc tac cgc aac Arg Thr Cys Ser Ile Ser Pro Asp Val Asn Asn Pro Gly Tyr Arg Asn 145 150 155 160 | 480 |
| gtc acc ttc gac gaa ctg gtg gag aac tac gtc gag gcg acc cga ggc Val Thr Phe Asp Glu Leu Val Glu Asn Tyr Val Glu Ala Thr Arg Gly 165 170 175 | 528 |
| ctg atc gaa ggc ggc gcc gac ctg atc ctg atc gag acc atc ttc gac Leu Ile Glu Gly Gly Ala Asp Leu Ile Leu Ile Glu Thr Ile Phe Asp 180 185 190 | 576 |
| acc ctc aac gcc aag gcg gcg atc ttc gcc gtc cag ggc gtg ttc gag Thr Leu Asn Ala Lys Ala Ala Ile Phe Ala Val Gln Gly Val Phe Glu 195 200 205 | 624 |
| gaa ctc ggc gtg gag ctg ccg atc atg atc tcc gga acc atc acc gac Glu Leu Gly Val Glu Leu Pro Ile Met Ile Ser Gly Thr Ile Thr Asp 210 215 220 | 672 |
| gcc tcc ggc cgc acc ctg tcg ggc cag acc acc gag gcc ttc tgg aac Ala Ser Gly Arg Thr Leu Ser Gly Gln Thr Thr Glu Ala Phe Trp Asn 225 230 235 240 | 720 |
| tcg gtg ccg cat gcc ccg ccg atc tcg gta ggc ctg aac tgc gcc ctc Ser Val Arg His Ala Arg Pro Ile Ser Val Gly Leu Asn Cys Ala Leu 245 250 255 | 768 |
| ggc gcc aag gaa ttg ccg ccg tac atc gag gaa ctg tcg acc aag gcc Gly Ala Lys Glu Leu Arg Pro Tyr Ile Glu Glu Leu Ser Thr Lys Ala 260 265 270 | 816 |
| gac act cat gtc tcg gcc cac ccc aac gcc ggc ctg ccg aac gcc ttc Asp Thr His Val Ser Ala His Pro Asn Ala Gly Leu Pro Asn Ala Phe 275 280 285 | 864 |
| ggc gaa tac gac gaa tcg ccg gcg gaa atg gcc gtg gtg gtc gag gaa Gly Glu Tyr Asp Glu Ser Pro Ala Glu Met Ala Val Val Val Glu Glu 290 295 300 | 912 |
| ttc gcc gcc gcc ggc ttc ctc aat atc gtc ggc ggc tgc tgc ggc acc | 960 |

| Phe | Ala | Ala | Ala | Gly | Phe | Leu | Asn | Ile | Val | Gly | Gly | Cys | Cys | Gly | Thr | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| 305 | | | | | 310 | | | | | 315 | | | | | 320 | |
| acc | ccg | gcg | cac | atc | gag | gcg | atc | gcc | aag | gca | gtg | gcc | aag | tac | ccg | 1008 |
| Thr | Pro | Ala | His | Ile | Glu | Ala | Ile | Ala | Lys | Ala | Val | Ala | Lys | Tyr | Pro | |
| | | | | 325 | | | | | 330 | | | | | 335 | | |
| ccg | cgg | gcc | atc | ccg | gag | att | ccc | cgg | gcc | tgt | cgc | ctg | tcc | ggc | ctg | 1056 |
| Pro | Arg | Ala | Ile | Pro | Glu | Ile | Pro | Arg | Ala | Cys | Arg | Leu | Ser | Gly | Leu | |
| | | | | 340 | | | | 345 | | | | | 350 | | | |
| gag | ccg | ttc | acc | atc | gac | cgc | agc | tcg | ctg | ttc | gtc | aac | gtc | ggc | gag | 1104 |
| Glu | Pro | Phe | Thr | Ile | Asp | Arg | Ser | Ser | Leu | Phe | Val | Asn | Val | Gly | Glu | |
| | | | | 355 | | | 360 | | | | | 365 | | | | |
| cgc | acc | aac | atc | acc | ggc | tcg | gcc | aag | ttc | gcc | cgg | ctg | atc | cgc | gag | 1152 |
| Arg | Thr | Asn | Ile | Thr | Gly | Ser | Ala | Lys | Phe | Ala | Arg | Leu | Ile | Arg | Glu | |
| | | | | 370 | | 375 | | | | | 380 | | | | | |
| gaa | aac | tac | gcg | gaa | gct | ctc | gag | gtc | gcc | cag | cag | cag | gtg | gaa | gcc | 1200 |
| Glu | Asn | Tyr | Ala | Glu | Ala | Leu | Glu | Val | Ala | Gln | Gln | Gln | Val | Glu | Ala | |
| 385 | | | | | 390 | | | | | 395 | | | | | 400 | |
| ggc | gcc | cag | gtg | atc | gac | atc | aac | atg | gac | gaa | ggc | atg | ctg | gac | tcg | 1248 |
| Gly | Ala | Gln | Val | Ile | Asp | Ile | Asn | Met | Asp | Glu | Gly | Met | Leu | Asp | Ser | |
| | | | | 405 | | | | | 410 | | | | | 415 | | |
| aag | gcg | gcc | atg | gtc | acc | ttc | ctc | aac | ctg | atc | gcc | tcc | gag | ccc | gac | 1296 |
| Lys | Ala | Ala | Met | Val | Thr | Phe | Leu | Asn | Leu | Ile | Ala | Ser | Glu | Pro | Asp | |
| | | | | 420 | | | | 425 | | | | | 430 | | | |
| atc | tcg | cgc | gtg | ccg | atc | atg | atc | gac | tcc | tcc | aag | tgg | gaa | gtg | atc | 1344 |
| Ile | Ser | Arg | Val | Pro | Ile | Met | Ile | Asp | Ser | Ser | Lys | Trp | Glu | Val | Ile | |
| | | | | 435 | | | 440 | | | | | 445 | | | | |
| gag | gcc | ggc | ctg | aag | tgc | atc | cag | ggc | aag | ggc | atc | gtc | aac | tcg | atc | 1392 |
| Glu | Ala | Gly | Leu | Lys | Cys | Ile | Gln | Gly | Lys | Gly | Ile | Val | Asn | Ser | Ile | |
| | | | | 450 | | 455 | | | | | 460 | | | | | |
| tcg | atg | aag | gaa | ggc | gtc | gag | gcc | ttc | aag | cac | cat | gcc | cgc | ctg | tgc | 1440 |
| Ser | Met | Lys | Glu | Gly | Val | Glu | Ala | Phe | Lys | His | His | Ala | Arg | Leu | Cys | |
| 465 | | | | | 470 | | | | | 475 | | | | | 480 | |
| aag | cgc | tac | ggc | gcc | gcg | gtg | gtg | gtg | atg | gcc | ttc | gac | gag | gac | ggc | 1488 |
| Lys | Arg | Tyr | Gly | Ala | Ala | Val | Val | Val | Met | Ala | Phe | Asp | Glu | Asp | Gly | |
| | | | | 485 | | | | | 490 | | | | | 495 | | |
| cag | gcc | gac | acc | cag | gcg | cgc | aag | gaa | gaa | atc | tgc | aag | cgc | tcc | tac | 1536 |
| Gln | Ala | Asp | Thr | Gln | Ala | Arg | Lys | Glu | Glu | Ile | Cys | Lys | Arg | Ser | Tyr | |
| | | | | 500 | | | | 505 | | | | | 510 | | | |
| gac | atc | ctg | gtc | gac | gaa | gtc | ggc | ttc | cca | | | | | | | |

| | |
|---|------|
| ccc tac gcc ctg agc tcg ggc ggg gtg tcc aac gtg tcc ttc tcg ttc | 1728 |
| Pro Tyr Ala Leu Ser Ser Gly Gly Val Ser Asn Val Ser Phe Ser Phe | |
| 565 570 575 | |
| cgc ggc aac aac ccg gta cgc gag gcg atc cac tcg gtg ttc ctc tac | 1776 |
| Arg Gly Asn Asn Pro Val Arg Glu Ala Ile His Ser Val Phe Leu Tyr | |
| 580 585 590 | |
| tac gcg atc cgc aac ggc ctg acc atg ggc atc gtc aac gcc gcc cag | 1824 |
| Tyr Ala Ile Arg Asn Gly Leu Thr Met Gly Ile Val Asn Ala Gly Gln | |
| 595 600 605 | |
| ctg gaa atc tac gac gag att ccg aaa gcg ctg cgc gac cgg gtc gag | 1872 |
| Leu Glu Ile Tyr Asp Glu Ile Pro Lys Ala Leu Arg Asp Arg Val Glu | |
| 610 615 620 | |
| gac gtg gtg ctc aac cgc acg ccc gag gcc acc gag gcc ctg ctg gcg | 1920 |
| Asp Val Val Leu Asn Arg Thr Pro Glu Ala Thr Glu Ala Leu Leu Ala | |
| 625 630 635 640 | |
| atc gcc gac gac tac aag ggc ggc ggc gcg gtc aag gag gcc gag gac | 1968 |
| Ile Ala Asp Asp Tyr Lys Gly Gly Gly Ala Val Lys Glu Ala Glu Asp | |
| 645 650 655 | |
| gag gaa tgg cgc agc tac agc gtc gag aag cgc ctc gag cat gcg ctg | 2016 |
| Glu Glu Trp Arg Ser Tyr Ser Val Glu Lys Arg Leu Glu His Ala Leu | |
| 660 665 670 | |
| gtc aag ggc atc acc acc tgg atc gtc gag gac acc gag gaa tgc cgc | 2064 |
| Val Lys Gly Ile Thr Thr Trp Ile Val Glu Asp Thr Glu Glu Cys Arg | |
| 675 680 685 | |
| cag cag tgt gcg cgt ccc atc gag gtc atc gaa ggt ccg ctg atg tcc | 2112 |
| Gln Gln Cys Ala Arg Pro Ile Glu Val Ile Glu Gly Pro Leu Met Ser | |
| 690 695 700 | |
| ggg atg aac gtg gtc ggc gac ctg ttc ggc gcc ggc aag atg ttc ctc | 2160 |
| Gly Met Asn Val Val Gly Asp Leu Phe Gly Ala Gly Lys Met Phe Leu | |
| 705 710 715 720 | |
| ccg cag gtg gtc aag tcc gcg cga gtg atg aag cag gcg gtg gcc cac | 2208 |
| Pro Gln Val Val Lys Ser Ala Arg Val Met Lys Gln Ala Val Ala His | |
| 725 730 735 | |
| ctg att ccc ttc atc gag gcg gag aaa ggc gac aag ccg gaa gcc aag | 2256 |
| Leu Ile Pro Phe Ile Glu Ala Glu Lys Gly Asp Lys Pro Glu Ala Lys | |
| 740 745 750 | |
| ggc aag atc ctg atg gcc acg gtg aag ggc gac gtg cac gac atc ggc | 2304 |
| Gly Lys Ile Leu Met Ala Thr Val Lys Gly Asp Val His Asp Ile Gly | |
| 755 760 765 | |
| aag aac atc gtc ggc gtg gtg ctc ggc tgc aac ggc tat gac gtg gtc | 2352 |
| Lys Asn Ile Val Gly Val Leu Gly Cys Asn Gly Tyr Asp Val Val | |
| 770 775 780 | |
| gac ctc gcc gtg atg gtg ccg gcg gag aag atc ctg cag acc gcc atc | 2400 |
| Asp Leu Gly Val Met Val Pro Ala Glu Lys Ile Leu Gln Thr Ala Ile | |
| 785 790 795 800 | |
| gcc gag aaa tgc gac atc atc ggc ctg tct ggc ctg atc acg ccg tcg | 2448 |

119

| | |
|---|------|
| Ala Glu Lys Cys Asp Ile Ile Gly Leu Ser Gly Leu Ile Thr Pro Ser | |
| 805 810 815 | |
| ctg gac gag atg gtc cac gtc gcc aag gaa atg cag cgg cag aat ttc | 2496 |
| Leu Asp Glu Met Val His Val Ala Lys Glu Met Gln Arg Gln Asn Phe | |
| 820 825 830 | |
| cag ttg ccg ctg atg atc ggc gcc ggc act acc tcg aag gcg cat acc | 2544 |
| Gln Leu Pro Leu Met Ile Gly Gly Ala Thr Thr Ser Lys Ala His Thr | |
| 835 840 845 | |
| gcg gtg aag atc gat ccg cag tac agc aac gac gcg gtg gtc tac gtc | 2592 |
| Ala Val Lys Ile Asp Pro Gln Tyr Ser Asn Asp Ala Val Val Tyr Val | |
| 850 855 860 | |
| acc gac gcc tcg cgc gcg gta ggc gtg gcc acc agc ctg ctg tcc aag | 2640 |
| Thr Asp Ala Ser Arg Ala Val Gly Val Ala Thr Ser Leu Leu Ser Lys | |
| 865 870 875 880 | |
| gag ctg aag gcc gac tac gtg gcc cgc acc cgc gcc gac tac gcg gtg | 2688 |
| Glu Leu Lys Ala Asp Tyr Val Ala Arg Thr Arg Ala Asp Tyr Ala Val | |
| 885 890 895 | |
| gtc cgc gaa cgc acg gcc aac cgc agc gcc cgc acc gag cgg ctg agc | 2736 |
| Val Arg Glu Arg Thr Ala Asn Arg Ser Ala Arg Thr Glu Arg Leu Ser | |
| 900 905 910 | |
| tac gaa cag gcg atc gcc aac aag ccg gcg ttc gac tgg gcc ggc tac | 2784 |
| Tyr Glu Gln Ala Ile Ala Asn Lys Pro Ala Phe Asp Trp Ala Gly Tyr | |
| 915 920 925 | |
| cag gcg ccg acg cct tcc ttc acc ggc gtc agg gtg ctc gac gag atc | 2832 |
| Gln Ala Pro Thr Pro Ser Phe Thr Gly Val Arg Val Leu Asp Glu Ile | |
| 930 935 940 | |
| gac ctc gcg gtg ctc gcc gag tac atc gac tgg acg ccg ttc ttc att | 2880 |
| Asp Leu Ala Val Leu Ala Glu Tyr Ile Asp Trp Thr Pro Phe Phe Ile | |
| 945 950 955 960 | |
| tcc tgg gac ctg gcc ggc aag tac ccg cgc atc ctc acc gac gag gtg | 2928 |
| Ser Trp Asp Leu Ala Gly Lys Tyr Pro Arg Ile Leu Thr Asp Glu Val | |
| 965 970 975 | |
| gtc ggc gag gcc gcc acc tcg ttg ttc aac gac gcc cag gcg atg ctg | 2976 |
| Val Gly Glu Ala Ala Thr Ser Leu Phe Asn Asp Ala Gln Ala Met Leu | |
| 980 985 990 | |
| aag aag ctg atc gac gag aag ctg atc aag gcc cgc gcg gtg ttc ggc | 3024 |
| Lys Lys Leu Ile Asp Glu Lys Leu Ile Lys Ala Arg Ala Val Phe Gly | |
| 995 1000 1005 | |
| ttc tgg ccg gcc aac cag gtc gag cac gac gac ctg gag gtc tac ggc | 3072 |
| Phe Trp Pro Ala Asn Gln Val Glu His Asp Asp Leu Glu Val Tyr Gly | |
| 1010 1015 1020 | |
| gcc gat ggc gag acc ctc gcc acc ctg cac cac ctg cgg cag cag acg | 3120 |
| Ala Asp Gly Glu Thr Leu Ala Thr Leu His His Leu Arg Gln Gln Thr | |
| 1025 1030 1035 1040 | |
| atc aag ccg gac ggc aag ccg aac ctg tcg ctg gcc gat ttc gtc gcg | 3168 |
| Ile Lys Pro Asp Gly Lys Pro Asn Leu Ser Leu Ala Asp Phe Val Ala | |
| 1045 1050 1055 | |

120

ccg aag gaa agc ggc gtg cgc gac tac atc ggc ggc ttc atc acc acc 3216
 Pro Lys Glu Ser Gly Val Arg Asp Tyr Ile Gly Gly Phe Ile Thr Thr
 1060 1065 1070
 gcc ggg atc ggc gcc gag gaa gtg gcc aag gcg tac gaa gcc aag ggc 3264
 Ala Gly Ile Gly Ala Glu Glu Val Ala Lys Ala Tyr Glu Ala Lys Gly
 1075 1080 1085
 gac gac tac aac agc atc atg gtc aag gcg ctc gcc gac cgc ctc gcc 3312
 Asp Asp Tyr Asn Ser Ile Met Val Lys Ala Leu Ala Asp Arg Leu Ala
 1090 1095 1100
 gaa gcc tgc gcc gag tgg ctg cac gag cgg gtg cgc aag gag tac tgg 3360
 Glu Ala Cys Ala Glu Trp Leu His Glu Arg Val Arg Lys Glu Tyr Trp
 1105 1110 1115 1120
 ggc tac gcc cgc gac gaa cac ctc gac aac gag gcc ttg atc aag gag 3408
 Gly Tyr Ala Arg Asp Glu His Leu Asp Asn Glu Ala Leu Ile Lys Glu
 1125 1130 1135
 caa tac gtc ggc atc cgc ccg gca ccg ggc tac ccg gcc tgc ccc gac 3456
 Gln Tyr Val Gly Ile Arg Pro Ala Pro Gly Tyr Pro Ala Cys Pro Asp
 1140 1145 1150
 cat acc gag aaa ggc act ctg ttc gaa ctg ctc gat ccg cag ggc ctg 3504
 His Thr Glu Lys Gly Thr Leu Phe Glu Leu Leu Asp Pro Gln Gly Leu
 1155 1160 1165
 tcc ggc gtc agc ctg acc gag cac tac gcg atg ttc ccg gcc gcg gcg 3552
 Ser Gly Val Ser Leu Thr Glu His Tyr Ala Met Phe Pro Ala Ala Ala
 1170 1175 1180
 gtc agc ggt tgg tat ttc gcc cac ccg cag gcg cag tac ttc gcg gtc 3600
 Val Ser Gly Trp Tyr Phe Ala His Pro Gln Ala Gln Tyr Phe Ala Val
 1185 1190 1195 1200
 ggc aag atc gac aag gac cag gtg gaa cgc tac agc cag cgc aag ggc 3648
 Gly Lys Ile Asp Lys Asp Gln Val Glu Arg Tyr Ser Gln Arg Lys Gly
 1205 1210 1215
 cag gaa gcc agc gtc agc gag cgc tgg ctg gcg ccg aac ctt ggc tac 3696
 Gln Glu Ala Ser Val Ser Glu Arg Trp Leu Ala Pro Asn Leu Gly Tyr
 1220 1225 1230
 gat gac tga 3705
 Asp Asp

<210> 28

<211> 1234

<212> PRT

<213> Pseudomonas aeruginosa

<400> 28

Met Ser Ser Pro Leu Thr Asp Arg Ser Ala Arg Leu Gln Ala Leu Gln
 1 5 10 15

His Ala Leu Arg Glu Arg Ile Leu Ile Leu Asp Gly Gly Met Gly Thr
 20 25 30

121

Met Ile Gln Ser Tyr Lys Leu Glu Glu Ala Asp Tyr Arg Gly Glu Arg
 35 40 45
 Phe Ala Asp Trp Pro Ser Asp Val Lys Gly Asn Asn Asp Leu Leu Leu
 50 55 60
 Leu Ser Arg Pro Asp Val Ile Gln Ala Ile Glu Lys Ala Tyr Leu Asp
 65 70 75 80
 Ala Gly Ala Asp Ile Leu Glu Thr Asn Thr Phe Asn Ala Thr Gln Val
 85 90 95
 Ser Gln Ala Asp Tyr Gly Met Gln Ser Leu Ala Tyr Glu Leu Asn Val
 100 105 110
 Glu Gly Ala Arg Leu Ala Arg Gln Val Ala Asp Ala Lys Thr Ala Glu
 115 120 125
 Thr Pro Asp Lys Pro Arg Phe Val Ala Gly Val Leu Gly Pro Thr Ser
 130 135 140
 Arg Thr Cys Ser Ile Ser Pro Asp Val Asn Asn Pro Gly Tyr Arg Asn
 145 150 155 160
 Val Thr Phe Asp Glu Leu Val Glu Asn Tyr Val Glu Ala Thr Arg Gly
 165 170 175
 Leu Ile Glu Gly Gly Ala Asp Leu Ile Leu Ile Glu Thr Ile Phe Asp
 180 185 190
 Thr Leu Asn Ala Lys Ala Ala Ile Phe Ala Val Gln Gly Val Phe Glu
 195 200 205
 Glu Leu Gly Val Glu Leu Pro Ile Met Ile Ser Gly Thr Ile Thr Asp
 210 215 220
 Ala Ser Gly Arg Thr Leu Ser Gly Gln Thr Thr Glu Ala Phe Trp Asn
 225 230 235 240
 Ser Val Arg His Ala Arg Pro Ile Ser Val Gly Leu Asn Cys Ala Leu
 245 250 255
 Gly Ala Lys Glu Leu Arg Pro Tyr Ile Glu Glu Leu Ser Thr Lys Ala
 260 265 270
 Asp Thr His Val Ser Ala His Pro Asn Ala Gly Leu Pro Asn Ala Phe
 275 280 285
 Gly Glu Tyr Asp Glu Ser Pro Ala Glu Met Ala Val Val Val Glu Glu
 290 295 300
 Phe Ala Ala Ala Gly Phe Leu Asn Ile Val Gly Gly Cys Cys Gly Thr
 305 310 315 320
 Thr Pro Ala His Ile Glu Ala Ile Ala Lys Ala Val Ala Lys Tyr Pro
 325 330 335
 Pro Arg Ala Ile Pro Glu Ile Pro Arg Ala Cys Arg Leu Ser Gly Leu
 340 345 350
 Glu Pro Phe Thr Ile Asp Arg Ser Ser Leu Phe Val Asn Val Gly Glu
 355 360 365

122

Arg Thr Asn Ile Thr Gly Ser Ala Lys Phe Ala Arg Leu Ile Arg Glu
 370 375 380
 Glu Asn Tyr Ala Glu Ala Leu Glu Val Ala Gln Gln Gln Val Glu Ala
 385 390 395 400
 Gly Ala Gln Val Ile Asp Ile Asn Met Asp Glu Gly Met Leu Asp Ser
 405 410 415
 Lys Ala Ala Met Val Thr Phe Leu Asn Leu Ile Ala Ser Glu Pro Asp
 420 425 430
 Ile Ser Arg Val Pro Ile Met Ile Asp Ser Ser Lys Trp Glu Val Ile
 435 440 445
 Glu Ala Gly Leu Lys Cys Ile Gln Gly Lys Gly Ile Val Asn Ser Ile
 450 455 460
 Ser Met Lys Glu Gly Val Glu Ala Phe Lys His His Ala Arg Leu Cys
 465 470 475 480
 Lys Arg Tyr Gly Ala Ala Val Val Val Met Ala Phe Asp Glu Asp Gly
 485 490 495
 Gln Ala Asp Thr Gln Ala Arg Lys Glu Glu Ile Cys Lys Arg Ser Tyr
 500 505 510
 Asp Ile Leu Val Asp Glu Val Gly Phe Pro Pro Glu Asp Ile Ile Phe
 515 520 525
 Asp Ala Asn Ile Phe Ala Ile Ala Thr Gly Ile Glu Glu His Asn Asn
 530 535 540
 Tyr Ala Val Asp Phe Ile Asn Ala Cys Ala Tyr Ile Arg Asp Asn Leu
 545 550 555 560
 Pro Tyr Ala Leu Ser Ser Gly Gly Val Ser Asn Val Ser Phe Ser Phe
 565 570 575
 Arg Gly Asn Asn Pro Val Arg Glu Ala Ile His Ser Val Phe Leu Tyr
 580 585 590
 Tyr Ala Ile Arg Asn Gly Leu Thr Met Gly Ile Val Asn Ala Gly Gln
 595 600 605
 Leu Glu Ile Tyr Asp Glu Ile Pro Lys Ala Leu Arg Asp Arg Val Glu
 610 615 620
 Asp Val Val Leu Asn Arg Thr Pro Glu Ala Thr Glu Ala Leu Leu Ala
 625 630 635 640
 Ile Ala Asp Asp Tyr Lys Gly Gly Gly Ala Val Lys Glu Ala Glu Asp
 645 650 655
 Glu Glu Trp Arg Ser Tyr Ser Val Glu Lys Arg Leu Glu His Ala Leu
 660 665 670
 Val Lys Gly Ile Thr Thr Trp Ile Val Glu Asp Thr Glu Glu Cys Arg
 675 680 685
 Gln Gln Cys Ala Arg Pro Ile Glu Val Ile Glu Gly Pro Leu Met Ser

123

| | | |
|---|------|-------------|
| 690 | 695 | 700 |
| Gly Met Asn Val Val Gly Asp Leu Phe Gly Ala Gly Lys Met Phe Leu | | |
| 705 | 710 | 715 720 |
| Pro Gln Val Val Lys Ser Ala Arg Val Met Lys Gln Ala Val Ala His | | |
| | 725 | 730 735 |
| Leu Ile Pro Phe Ile Glu Ala Glu Lys Gly Asp Lys Pro Glu Ala Lys | | |
| | 740 | 745 750 |
| Gly Lys Ile Leu Met Ala Thr Val Lys Gly Asp Val His Asp Ile Gly | | |
| | 755 | 760 765 |
| Lys Asn Ile Val Gly Val Val Leu Gly Cys Asn Gly Tyr Asp Val Val | | |
| | 770 | 775 780 |
| Asp Leu Gly Val Met Val Pro Ala Glu Lys Ile Leu Gln Thr Ala Ile | | |
| | 785 | 790 795 800 |
| Ala Glu Lys Cys Asp Ile Ile Gly Leu Ser Gly Leu Ile Thr Pro Ser | | |
| | 805 | 810 815 |
| Leu Asp Glu Met Val His Val Ala Lys Glu Met Gln Arg Gln Asn Phe | | |
| | 820 | 825 830 |
| Gln Leu Pro Leu Met Ile Gly Gly Ala Thr Thr Ser Lys Ala His Thr | | |
| | 835 | 840 845 |
| Ala Val Lys Ile Asp Pro Gln Tyr Ser Asn Asp Ala Val Val Tyr Val | | |
| | 850 | 855 860 |
| Thr Asp Ala Ser Arg Ala Val Gly Val Ala Thr Ser Leu Leu Ser Lys | | |
| | 865 | 870 875 880 |
| Glu Leu Lys Ala Asp Tyr Val Ala Arg Thr Arg Ala Asp Tyr Ala Val | | |
| | 885 | 890 895 |
| Val Arg Glu Arg Thr Ala Asn Arg Ser Ala Arg Thr Glu Arg Leu Ser | | |
| | 900 | 905 910 |
| Tyr Glu Gln Ala Ile Ala Asn Lys Pro Ala Phe Asp Trp Ala Gly Tyr | | |
| | 915 | 920 925 |
| Gln Ala Pro Thr Pro Ser Phe Thr Gly Val Arg Val Leu Asp Glu Ile | | |
| | 930 | 935 940 |
| Asp Leu Ala Val Leu Ala Glu Tyr Ile Asp Trp Thr Pro Phe Phe Ile | | |
| | 945 | 950 955 960 |
| Ser Trp Asp Leu Ala Gly Lys Tyr Pro Arg Ile Leu Thr Asp Glu Val | | |
| | 965 | 970 975 |
| Val Gly Glu Ala Ala Thr Ser Leu Phe Asn Asp Ala Gln Ala Met Leu | | |
| | 980 | 985 990 |
| Lys Lys Leu Ile Asp Glu Lys Leu Ile Lys Ala Arg Ala Val Phe Gly | | |
| | 995 | 1000 1005 |
| Phe Trp Pro Ala Asn Gln Val Glu His Asp Asp Leu Glu Val Tyr Gly | | |
| | 1010 | 1015 1020 |

124

Ala Asp Gly Glu Thr Leu Ala Thr Leu His His Leu Arg Gln Gln Thr
 1025 1030 1035 1040

Ile Lys Pro Asp Gly Lys Pro Asn Leu Ser Leu Ala Asp Phe Val Ala
 1045 1050 1055

Pro Lys Glu Ser Gly Val Arg Asp Tyr Ile Gly Gly Phe Ile Thr Thr
 1060 1065 1070

Ala Gly Ile Gly Ala Glu Glu Val Ala Lys Ala Tyr Glu Ala Lys Gly
 1075 1080 1085

Asp Asp Tyr Asn Ser Ile Met Val Lys Ala Leu Ala Asp Arg Leu Ala
 1090 1095 1100

Glu Ala Cys Ala Glu Trp Leu His Glu Arg Val Arg Lys Glu Tyr Trp
 1105 1110 1115 1120

Gly Tyr Ala Arg Asp Glu His Leu Asp Asn Glu Ala Leu Ile Lys Glu
 1125 1130 1135

Gln Tyr Val Gly Ile Arg Pro Ala Pro Gly Tyr Pro Ala Cys Pro Asp
 1140 1145 1150

His Thr Glu Lys Gly Thr Leu Phe Glu Leu Leu Asp Pro Gln Gly Leu
 1155 1160 1165

Ser Gly Val Ser Leu Thr Glu His Tyr Ala Met Phe Pro Ala Ala Ala
 1170 1175 1180

Val Ser Gly Trp Tyr Phe Ala His Pro Gln Ala Gln Tyr Phe Ala Val
 1185 1190 1195 1200

Gly Lys Ile Asp Lys Asp Gln Val Glu Arg Tyr Ser Gln Arg Lys Gly
 1205 1210 1215

Gln Glu Ala Ser Val Ser Glu Arg Trp Leu Ala Pro Asn Leu Gly Tyr
 1220 1225 1230

Asp Asp

<210> 29
 <211> 3714
 <212> DNA
 <213> Nitrosomas europeae

<220>
 <221> CDS
 <222> (1) .. (3711)
 <223> RNE01732

<400> 29
 atg aca atg cat gaa cgt gct gat ttg ctg aaa cgg ttg ctt gcc gag 48
 Met Thr Met His Glu Arg Ala Asp Leu Leu Lys Arg Leu Leu Ala Glu
 1 5 10 15

cgt atc ctg atg ctc gac ggt gcc atg ggt acg atg atc cag agc tac 96
 Arg Ile Leu Met Leu Asp Gly Ala Met Gly Thr Met Ile Gln Ser Tyr
 20 25 30

125

| | |
|---|-----|
| aaa ctg acc gag tcg gat tat cgg ggg gaa cgt ttt gcc gat ttt ccg | 144 |
| Lys Leu Thr Glu Ser Asp Tyr Arg Gly Glu Arg Phe Ala Asp Phe Pro | |
| 35 40 45 | |
| cat gat ctc aaa ggc aac aat gat ctg ctc tgc ctg acc aga ccg gaa | 192 |
| His Asp Leu Lys Gly Asn Asn Asp Leu Leu Cys Leu Thr Arg Pro Glu | |
| 50 55 60 | |
| gtc atc cgc tcc att cat cgt gct tac ctc gaa gcc ggg tcg gat atc | 240 |
| Val Ile Arg Ser Ile His Arg Ala Tyr Leu Glu Ala Gly Ser Asp Ile | |
| 65 70 75 80 | |
| atc gag acc aac acg ttc aac tcg aat gcg ccg tcg atg gcg gac tac | 288 |
| Ile Glu Thr Asn Thr Phe Asn Ser Asn Ala Pro Ser Met Ala Asp Tyr | |
| 85 90 95 | |
| cac atg cag gat ctg gtg tat gaa ctg aat gtg gcg ggt gcg cgc ctg | 336 |
| His Met Gln Asp Leu Val Tyr Glu Leu Asn Val Ala Gly Ala Arg Leu | |
| 100 105 110 | |
| gcg tgt gag gaa gcg cgg gca atg gaa acg cag caa cct gac cgg ccc | 384 |
| Ala Cys Glu Glu Ala Arg Ala Met Glu Thr Gln Gln Pro Asp Arg Pro | |
| 115 120 125 | |
| cgt ttc gtt gcc ggt gtg atc ggg cct acc acc aaa acg gct tca ctc | 432 |
| Arg Phe Val Ala Gly Val Ile Gly Pro Thr Thr Lys Thr Ala Ser Leu | |
| 130 135 140 | |
| tca ccg gat gtc aat gat cct gga ttc cgg gcc att acc ttc gat gat | 480 |
| Ser Pro Asp Val Asn Asp Pro Gly Phe Arg Ala Ile Thr Phe Asp Asp | |
| 145 150 155 160 | |
| ctg gtg gaa agc tat acc gag tcg gtg cgc ggg ctg atc gac gga ggc | 528 |
| Leu Val Glu Ser Tyr Thr Glu Ser Val Arg Gly Leu Ile Asp Gly Gly | |
| 165 170 175 | |
| gcg gat att ctg ctg gtc gaa acc att ttt gac acc ttg aat gcc aaa | 576 |
| Ala Asp Ile Leu Leu Val Glu Thr Ile Phe Asp Thr Leu Asn Ala Lys | |
| 180 185 190 | |
| gcc gca ttg ttt gcc atc gat cag tat ttc gaa acg cat gga tta cgt | 624 |
| Ala Ala Leu Phe Ala Ile Asp Gln Tyr Phe Glu Thr His Gly Leu Arg | |
| 195 200 205 | |
| ctg ccg gtg atg ata tcg gtc acg att acc gat gct tcg gga cgt aat | 672 |
| Leu Pro Val Met Ile Ser Val Thr Ile Thr Asp Ala Ser Gly Arg Asn | |
| 210 215 220 | |
| ctt tcc ggg cag aca ccg gaa gct ttc tgg aat tcg gta cgg cat gca | 720 |
| Leu Ser Gly Gln Thr Pro Glu Ala Phe Trp Asn Ser Val Arg His Ala | |
| 225 230 235 240 | |
| cgt ccg ctt tcg gtg gga atc aac tgc gcg ttg ggt gcg gag ttg atg | 768 |
| Arg Pro Leu Ser Val Gly Ile Asn Cys Ala Leu Gly Ala Glu Leu Met | |
| 245 250 255 | |
| cgc ccc tac gtg gaa gag ttg tcc aat gtg gct gag gtt ttc acc agc | 816 |
| Arg Pro Tyr Val Glu Glu Leu Ser Asn Val Ala Glu Val Phe Thr Ser | |
| 260 265 270 | |
| gcc cat ccc aat gcc ggc ttg cct aat ccc ttg gcg gaa acc ggt tat | 864 |
| Ala His Pro Asn Ala Gly Leu Pro Asn Pro Leu Ala Glu Thr Gly Tyr | |

126

| 275 | 280 | 285 | |
|-------------------------|---------------------|-------------------------|------|
| gac gaa acg ccg gaa tat | acc gcc cgt ctg atc | aag gat ttt gcg caa | 912 |
| Asp Glu Thr Pro Glu Tyr | Thr Ala Arg Leu Ile | Lys Asp Phe Ala Gln | |
| 290 | 295 | 300 | |
| tcc ggg ttc gtc aac att | gtc gcc ggc tgc tgt | ggc act aca ccg aaa | 960 |
| Ser Gly Phe Val Asn Ile | Val Gly Gly Cys Cys | Gly Thr Thr Pro Lys | |
| 305 | 310 | 315 320 | |
| cat atc gcg gcc att gca | gaa gcg gta cgg gac | atc cct ccg cgc cca | 1008 |
| His Ile Ala Ala Ile | Ala Glu Ala Val Arg | Asp Ile Pro Pro Arg Pro | |
| 325 | 330 | 335 | |
| ctg ccc gat att cct aaa | aaa ctg agg ctt tcc | ggc ctc gag ccg ctc | 1056 |
| Leu Pro Asp Ile Pro Lys | Lys Leu Arg Leu Ser | Gly Leu Glu Pro Leu | |
| 340 | 345 | 350 | |
| aat atc gat gaa cat tcc | ctg ttc gta aac gtg | ggg gaa cgt acc aat | 1104 |
| Asn Ile Asp Glu His Ser | Leu Phe Val Asn Val | Gly Glu Arg Thr Asn | |
| 355 | 360 | 365 | |
| gtc acc ggc tcc aag gca | ttt gcc cgg ctg att | ctc aat ggc ggt tat | 1152 |
| Val Thr Gly Ser Lys Ala | Phe Ala Arg Leu Ile | Leu Asn Gly Gly Tyr | |
| 370 | 375 | 380 | |
| gct gaa ggg ctg gtg atc | gcg cgc agc cag gtg | gag aac ggc gca caa | 1200 |
| Ala Glu Gly Leu Val Ile | Ala Arg Ser Gln Val | Glu Asn Gly Ala Gln | |
| 385 | 390 | 395 400 | |
| atc atc gat atc aac atg | gat gaa gcg atg ctg | gat tca cag aag gcg | 1248 |
| Ile Ile Asp Ile Asn Met | Asp Glu Ala Met Leu | Asp Ser Gln Lys Ala | |
| 405 | 410 | 415 | |
| atg gtg acc ttt ctg aat | ctg ctc gct gcc gaa | ccg gat atc agc cgg | 1296 |
| Met Val Thr Phe Leu Asn | Leu Leu Ala Glu Pro | Asp Ile Ser Arg | |
| 420 | 425 | 430 | |
| ctg ccg atc atg ctc gat | tcc agc aaa tgg tgc | gtg atc gaa gcc gga | 1344 |
| Leu Pro Ile Met Leu Asp | Ser Ser Lys Trp Ser | Val Ile Glu Ala Gly | |
| 435 | 440 | 445 | |
| ctg aaa tgt gtc cag ggt | aag gcg gtc atc aat | tcc atc agc ctc aag | 1392 |
| Leu Lys Cys Val Gln Gly | Lys Ala Val Ile Asn | Ser Ile Ser Leu Lys | |
| 450 | 455 | 460 | |
| gaa ggt gaa gcg gag ttt | tta cat cat gcc agg | ctg gcg cgt cgt tat | 1440 |
| Glu Gly Glu Ala Glu Phe | Leu His His Ala Arg | Leu Ala Arg Arg Tyr | |
| 465 | 470 | 475 480 | |
| ggg gcc gcg gtg att gtc | atg gct ttc gac gaa | acc ggg cag gcc gat | 1488 |
| Gly Ala Ala Val Ile Val | Met Ala Phe Asp Glu | Thr Gly Gln Ala Asp | |
| 485 | 490 | 495 | |
| acc ttg cag cgc aag gtg | gaa atc tgc acg cgt | tgt tac cat aca ctg | 1536 |
| Thr Leu Gln Arg Lys Val | Glu Ile Cys Thr Arg | Cys Tyr His Thr Leu | |
| 500 | 505 | 510 | |
| att gaa cag gcc gat ttc | cca ccc gag gat atc | att ttc gac ccc aat | 1584 |
| Ile Glu Gln Ala Asp Phe | Pro Pro Glu Asp Ile | Ile Phe Asp Pro Asn | |
| 515 | 520 | 525 | |

127

| | |
|---|------|
| att ttt gcc att gct acg ggt atc gaa gaa cac agt aac tat gca gtg Ile Phe Ala Ile Ala Thr Gly Ile Glu Glu His Ser Asn Tyr Ala Val 530 535 540 | 1632 |
| gat ttt atc gag gcg aca cac gtc atc cgg caa acg ctg cct tat gcc Asp Phe Ile Glu Ala Thr His Val Ile Arg Gln Thr Leu Pro Tyr Ala 545 550 555 560 | 1680 |
| aaa gtc agc ggg ggt gtt tcc aat gtt tcc ttc tcg ttc cgg ggt aac Lys Val Ser Gly Gly Val Ser Asn Val Ser Phe Ser Phe Arg Gly Asn 565 570 575 | 1728 |
| gaa ccg atc cgc gaa gcc att cat acc gca ttc ctg tat cac gcg gtc Glu Pro Ile Arg Glu Ala Ile His Thr Ala Phe Leu Tyr His Ala Val 580 585 590 | 1776 |
| aag gca ggc atg acc atg ggt atc gtc aac gca ggt cag ctt ggg gtt Lys Ala Gly Met Thr Met Gly Ile Val Asn Ala Gly Gln Leu Gly Val 595 600 605 | 1824 |
| tat tcc gac att ccg ccc gat ctg ctg gaa cat gtc gag gat gta ctg Tyr Ser Asp Ile Pro Pro Asp Leu Leu Glu His Val Glu Asp Val Leu 610 615 620 | 1872 |
| ctg aac cgg cgg cct gat gca acc gaa cgt ctg gtg gag ttt gcg gaa Leu Asn Arg Arg Pro Asp Ala Thr Glu Arg Leu Val Glu Phe Ala Glu 625 630 635 640 | 1920 |
| cat ttc aag gga cag aaa aag gag cag atc gaa gat ctg tcc tgg cgt His Phe Lys Gly Gln Lys Lys Glu Gln Ile Glu Asp Leu Ser Trp Arg 645 650 655 | 1968 |
| gat gaa ccg gtg cgg cag cgc ctg att cat gca ctg gtc agg ggt atc Asp Glu Pro Val Arg Gln Arg Leu Ile His Ala Leu Val Arg Gly Ile 660 665 670 | 2016 |
| agc acc tac atc gtc gag gat acc gag ctc gtc cgg cag gag atc gac Ser Thr Tyr Ile Val Glu Asp Thr Glu Leu Val Arg Gln Glu Ile Asp 675 680 685 | 2064 |
| agc cag gga ggc aag ccg atc gag gtg atc gaa ggc ccg ctc atg gac Ser Gln Gly Gly Lys Pro Ile Glu Val Ile Glu Gly Pro Leu Met Asp 690 695 700 | 2112 |
| ggc atg aat gta gtg ggg gat ctg ttt ggc gca ggc aag atg ttt ctg Gly Met Asn Val Val Gly Asp Leu Phe Gly Ala Gly Lys Met Phe Leu 705 710 715 720 | 2160 |
| cca cag gtg gtc aag tcg gca cgg gtg atg aag cag gcg gtt gcc tat Pro Gln Val Val Lys Ser Ala Arg Val Met Lys Gln Ala Val Ala Tyr 725 730 735 | 2208 |
| ctg ttg ccg tac atc gag gca gag aaa aaa att tcc ggc gac agc aag Leu Leu Pro Tyr Ile Glu Ala Glu Lys Lys Ile Ser Gly Asp Ser Lys 740 745 750 | 2256 |
| ccc aag ggc aag gtg gtg atc gct acc gtc aaa ggg gat gtg cat gat Pro Lys Gly Lys Val Val Ile Ala Thr Val Lys Gly Asp Val His Asp 755 760 765 | 2304 |
| att ggc aag aat atc gtt tcc gtc gtg ttg cag tgt aat aac ttt gaa Ile Gly Lys Asn Ile Val Ser Val Val Leu Gln Cys Asn Asn Phe Glu | 2352 |

128

| 770 | 775 | 780 | |
|---|-----|-----|------|
| gtc atc aac atg ggg gtg atg gtc ccc agt gca cag att ctg gaa aca Val Ile Asn Met Gly Val Met Val Pro Ser Ala Gln Ile Leu Glu Thr 785 790 795 800 | | | 2400 |
| gca cgc cgt gaa cag gtc gat atg atc ggt ctg tcc ggc ctg atc acc Ala Arg Arg Glu Gln Val Asp Met Ile Gly Leu Ser Gly Leu Ile Thr 805 810 815 | | | 2448 |
| cct tcg ctg gaa gaa atg gcg cat gtt gcc cgg gaa atg gag cgt gaa Pro Ser Leu Glu Glu Met Ala His Val Ala Arg Glu Met Glu Arg Glu 820 825 830 | | | 2496 |
| caa ttc acc gtt ccg ctg ctg atc ggt ggc gcc acc act tcg cgg atg Gln Phe Thr Val Pro Leu Leu Ile Gly Gly Ala Thr Thr Ser Arg Met 835 840 845 | | | 2544 |
| cat acg gca gtc aaa atc gca ccc cat tac ggt ggg gtg acc gta tgg His Thr Ala Val Lys Ile Ala Pro His Tyr Gly Gly Val Thr Val Trp 850 855 860 | | | 2592 |
| gtg ccg gat gcc agc cgg gca gtc ggg gtg tgc agc aat ctg atg tca Val Pro Asp Ala Ser Arg Ala Val Gly Val Cys Ser Asn Leu Met Ser 865 870 875 880 | | | 2640 |
| cag gat ctg cgt gat gac tat gtc cgg cag gtc aag gcc gag cag gag Gln Asp Leu Arg Asp Asp Tyr Val Arg Gln Val Lys Ala Glu Gln Glu 885 890 895 | | | 2688 |
| aag agc cgg gtg cag cac cgc aac aag aaa ggg cca tcc aag ctc ctc Lys Ser Arg Val Gln His Arg Asn Lys Lys Gly Pro Ser Lys Leu Leu 900 905 910 | | | 2736 |
| act ttc gag gaa gcc cgg gcc aac gca ctc aag acg gat tgg gct cgt Thr Phe Glu Glu Ala Arg Ala Asn Ala Leu Lys Thr Asp Trp Ala Arg 915 920 925 | | | 2784 |
| tat act cca cca gct ccg gat ttc ctg ggg ttg cgc acc ctc aac aac Tyr Thr Pro Pro Ala Pro Asp Phe Leu Gly Leu Arg Thr Leu Asn Asn 930 935 940 | | | 2832 |
| tat ccg ctg gaa aca ctg gtg ccg cac atc gac tgg aca cct ttc ttc Tyr Pro Leu Glu Thr Leu Val Pro His Ile Asp Trp Thr Pro Phe Phe 945 950 955 960 | | | 2880 |
| cag gca tgg gaa ctg cac ggg cgc tat cct gcc atc ctg cag gat gaa Gln Ala Trp Glu Leu His Gly Arg Tyr Pro Ala Ile Leu Gln Asp Glu 965 970 975 | | | 2928 |
| ctc gtc ggg gaa gca gcc agc aat ctg ttt cgc gat gcc cag aat atg Leu Val Gly Glu Ala Ala Ser Asn Leu Phe Arg Asp Ala Gln Asn Met 980 985 990 | | | 2976 |
| ctc aga aaa atc gtc gag caa aaa tgg ctc acc gcc aac gcc gtt atc Leu Arg Lys Ile Val Glu Gln Lys Trp Leu Thr Ala Asn Ala Val Ile 995 1000 1005 | | | 3024 |
| ggc ctg ttc ccg gcc aat acc gtc aat gga gat gat atc gag att tat Gly Leu Phe Pro Ala Asn Thr Val Asn Gly Asp Asp Ile Glu Ile Tyr 1010 1015 1020 | | | 3072 |

129

gct gac cgt agt cgc agt cag gtg atc atg acc tgg cac acc ttg cgg 3120
 Ala Asp Arg Ser Arg Ser Gln Val Ile Met Thr Trp His Thr Leu Arg
 1025 1030 1035 1040
 cag cag acg gcc aaa ccg gca ggg cgt ccc aat ctg gca ctg gct gat 3168
 Gln Gln Thr Ala Lys Pro Ala Gly Arg Pro Asn Leu Ala Leu Ala Asp
 1045 1050 1055
 ttc att gcg ccg cgt gaa acc gga ctg gac gat acc atc ggt ttg ttt 3216
 Phe Ile Ala Pro Arg Glu Thr Gly Leu Asp Asp Thr Ile Gly Leu Phe
 1060 1065 1070
 gcc gtc agc gcc ggt ttc ggt atc gat gaa cgc ata cgc gct ttt gaa 3264
 Ala Val Ser Ala Gly Phe Gly Ile Asp Glu Arg Ile Arg Ala Phe Glu
 1075 1080 1085
 gct gca aac gat gat tac agt gcc atc atc ctg aaa gca ctg gct gat 3312
 Ala Ala Asn Asp Asp Tyr Ser Ala Ile Ile Leu Lys Ala Leu Ala Asp
 1090 1095 1100
 cgt ctg gct gaa gcg ttt gca gaa cac atg cat gca cgg gtg cgg cga 3360
 Arg Leu Ala Glu Ala Phe Ala Glu His Met His Ala Arg Val Arg Arg
 1105 1110 1115 1120
 gaa ttc tgg ggc tat gtg aaa gat gag agt ctg gac aat gaa cag ttg 3408
 Glu Phe Trp Gly Tyr Val Lys Asp Glu Ser Leu Asp Asn Glu Gln Leu
 1125 1130 1135
 atc gac gag caa tac ctg gga atc cgt cca gca cca ggt tat cct gcc 3456
 Ile Asp Glu Gln Tyr Leu Gly Ile Arg Pro Ala Pro Gly Tyr Pro Ala
 1140 1145 1150
 tgc cct gat cat acc gaa aag ggg cca ttg ttc gct ctg ctg gaa gcg 3504
 Cys Pro Asp His Thr Glu Lys Gly Pro Leu Phe Ala Leu Leu Glu Ala
 1155 1160 1165
 gaa aaa cgc agc gga atc gtc ata acg gaa tca ttt gcc atg gtg ccg 3552
 Glu Lys Arg Ser Gly Ile Val Ile Thr Glu Ser Phe Ala Met Val Pro
 1170 1175 1180
 act gca gca gta tcc ggc ttc tat ctc tct tac cct gaa tcc agc tat 3600
 Thr Ala Ala Val Ser Gly Phe Tyr Leu Ser Tyr Pro Glu Ser Ser Tyr
 1185 1190 1195 1200
 ttt gct gtt gga aaa atc gga aaa gat cag gtc gag gat tat gca aga 3648
 Phe Ala Val Gly Lys Ile Gly Lys Asp Gln Val Glu Asp Tyr Ala Arg
 1205 1210 1215
 cgc aaa ggg tgg acg ctg gaa gaa gca gaa agg tgg ctt gcg cct gtc 3696
 Arg Lys Gly Trp Thr Leu Glu Glu Ala Glu Arg Trp Leu Ala Pro Val
 1220 1225 1230
 ttg gcg tat gag cgt taa 3714
 Leu Ala Tyr Glu Arg
 1235

<210> 30

<211> 1237

<212> PRT

<213> Nitrosomas europaeae

130

<400> 30

Met Thr Met His Glu Arg Ala Asp Leu Leu Lys Arg Leu Leu Ala Glu
 1 5 10 15
 Arg Ile Leu Met Leu Asp Gly Ala Met Gly Thr Met Ile Gln Ser Tyr
 20 25 30
 Lys Leu Thr Glu Ser Asp Tyr Arg Gly Glu Arg Phe Ala Asp Phe Pro
 35 40 45
 His Asp Leu Lys Gly Asn Asn Asp Leu Leu Cys Leu Thr Arg Pro Glu
 50 55 60
 Val Ile Arg Ser Ile His Arg Ala Tyr Leu Glu Ala Gly Ser Asp Ile
 65 70 75 80
 Ile Glu Thr Asn Thr Phe Asn Ser Asn Ala Pro Ser Met Ala Asp Tyr
 85 90 95
 His Met Gln Asp Leu Val Tyr Glu Leu Asn Val Ala Gly Ala Arg Leu
 100 105 110
 Ala Cys Glu Glu Ala Arg Ala Met Glu Thr Gln Gln Pro Asp Arg Pro
 115 120 125
 Arg Phe Val Ala Gly Val Ile Gly Pro Thr Thr Lys Thr Ala Ser Leu
 130 135 140
 Ser Pro Asp Val Asn Asp Pro Gly Phe Arg Ala Ile Thr Phe Asp Asp
 145 150 155 160
 Leu Val Glu Ser Tyr Thr Glu Ser Val Arg Gly Leu Ile Asp Gly Gly
 165 170 175
 Ala Asp Ile Leu Leu Val Glu Thr Ile Phe Asp Thr Leu Asn Ala Lys
 180 185 190
 Ala Ala Leu Phe Ala Ile Asp Gln Tyr Phe Glu Thr His Gly Leu Arg
 195 200 205
 Leu Pro Val Met Ile Ser Val Thr Ile Thr Asp Ala Ser Gly Arg Asn
 210 215 220
 Leu Ser Gly Gln Thr Pro Glu Ala Phe Trp Asn Ser Val Arg His Ala
 225 230 235 240
 Arg Pro Leu Ser Val Gly Ile Asn Cys Ala Leu Gly Ala Glu Leu Met
 245 250 255
 Arg Pro Tyr Val Glu Glu Leu Ser Asn Val Ala Glu Val Phe Thr Ser
 260 265 270
 Ala His Pro Asn Ala Gly Leu Pro Asn Pro Leu Ala Glu Thr Gly Tyr
 275 280 285
 Asp Glu Thr Pro Glu Tyr Thr Ala Arg Leu Ile Lys Asp Phe Ala Gln
 290 295 300
 Ser Gly Phe Val Asn Ile Val Gly Gly Cys Cys Gly Thr Thr Pro Lys
 305 310 315 320
 His Ile Ala Ala Ile Ala Glu Ala Val Arg Asp Ile Pro Pro Arg Pro

131

325

330

335

Leu Pro Asp Ile Pro Lys Lys Leu Arg Leu Ser Gly Leu Glu Pro Leu
 340 345 350
 Asn Ile Asp Glu His Ser Leu Phe Val Asn Val Gly Glu Arg Thr Asn
 355 360 365
 Val Thr Gly Ser Lys Ala Phe Ala Arg Leu Ile Leu Asn Gly Gly Tyr
 370 375 380
 Ala Glu Gly Leu Val Ile Ala Arg Ser Gln Val Glu Asn Gly Ala Gln
 385 390 395 400
 Ile Ile Asp Ile Asn Met Asp Glu Ala Met Leu Asp Ser Gln Lys Ala
 405 410 415
 Met Val Thr Phe Leu Asn Leu Leu Ala Ala Glu Pro Asp Ile Ser Arg
 420 425 430
 Leu Pro Ile Met Leu Asp Ser Ser Lys Trp Ser Val Ile Glu Ala Gly
 435 440 445
 Leu Lys Cys Val Gln Gly Lys Ala Val Ile Asn Ser Ile Ser Leu Lys
 450 455 460
 Glu Gly Glu Ala Glu Phe Leu His His Ala Arg Leu Ala Arg Arg Tyr
 465 470 475 480
 Gly Ala Ala Val Ile Val Met Ala Phe Asp Glu Thr Gly Gln Ala Asp
 485 490 495
 Thr Leu Gln Arg Lys Val Glu Ile Cys Thr Arg Cys Tyr His Thr Leu
 500 505 510
 Ile Glu Gln Ala Asp Phe Pro Pro Glu Asp Ile Ile Phe Asp Pro Asn
 515 520 525
 Ile Phe Ala Ile Ala Thr Gly Ile Glu Glu His Ser Asn Tyr Ala Val
 530 535 540
 Asp Phe Ile Glu Ala Thr His Val Ile Arg Gln Thr Leu Pro Tyr Ala
 545 550 555 560
 Lys Val Ser Gly Gly Val Ser Asn Val Ser Phe Ser Phe Arg Gly Asn
 565 570 575
 Glu Pro Ile Arg Glu Ala Ile His Thr Ala Phe Leu Tyr His Ala Val
 580 585 590
 Lys Ala Gly Met Thr Met Gly Ile Val Asn Ala Gly Gln Leu Gly Val
 595 600 605
 Tyr Ser Asp Ile Pro Pro Asp Leu Leu Glu His Val Glu Asp Val Leu
 610 615 620
 Leu Asn Arg Arg Pro Asp Ala Thr Glu Arg Leu Val Glu Phe Ala Glu
 625 630 635 640
 His Phe Lys Gly Gln Lys Lys Glu Gln Ile Glu Asp Leu Ser Trp Arg
 645 650 655

132

Asp Glu Pro Val Arg Gln Arg Leu Ile His Ala Leu Val Arg Gly Ile
 660 665 670

Ser Thr Tyr Ile Val Glu Asp Thr Glu Leu Val Arg Gln Glu Ile Asp
 675 680 685

Ser Gln Gly Gly Lys Pro Ile Glu Val Ile Glu Gly Pro Leu Met Asp
 690 695 700

Gly Met Asn Val Val Gly Asp Leu Phe Gly Ala Gly Lys Met Phe Leu
 705 710 715 720

Pro Gln Val Val Lys Ser Ala Arg Val Met Lys Gln Ala Val Ala Tyr
 725 730 735

Leu Leu Pro Tyr Ile Glu Ala Glu Lys Lys Ile Ser Gly Asp Ser Lys
 740 745 750

Pro Lys Gly Lys Val Val Ile Ala Thr Val Lys Gly Asp Val His Asp
 755 760 765

Ile Gly Lys Asn Ile Val Ser Val Val Leu Gln Cys Asn Asn Phe Glu
 770 775 780

Val Ile Asn Met Gly Val Met Val Pro Ser Ala Gln Ile Leu Glu Thr
 785 790 795 800

Ala Arg Arg Glu Gln Val Asp Met Ile Gly Leu Ser Gly Leu Ile Thr
 805 810 815

Pro Ser Leu Glu Glu Met Ala His Val Ala Arg Glu Met Glu Arg Glu
 820 825 830

Gln Phe Thr Val Pro Leu Leu Ile Gly Gly Ala Thr Thr Ser Arg Met
 835 840 845

His Thr Ala Val Lys Ile Ala Pro His Tyr Gly Gly Val Thr Val Trp
 850 855 860

Val Pro Asp Ala Ser Arg Ala Val Gly Val Cys Ser Asn Leu Met Ser
 865 870 875 880

Gln Asp Leu Arg Asp Asp Tyr Val Arg Gln Val Lys Ala Glu Gln Glu
 885 890 895

Lys Ser Arg Val Gln His Arg Asn Lys Lys Gly Pro Ser Lys Leu Leu
 900 905 910

Thr Phe Glu Glu Ala Arg Ala Asn Ala Leu Lys Thr Asp Trp Ala Arg
 915 920 925

Tyr Thr Pro Pro Ala Pro Asp Phe Leu Gly Leu Arg Thr Leu Asn Asn
 930 935 940

Tyr Pro Leu Glu Thr Leu Val Pro His Ile Asp Trp Thr Pro Phe Phe
 945 950 955 960

Gln Ala Trp Glu Leu His Gly Arg Tyr Pro Ala Ile Leu Gln Asp Glu
 965 970 975

Leu Val Gly Glu Ala Ala Ser Asn Leu Phe Arg Asp Ala Gln Asn Met
 980 985 990

133

Leu Arg Lys Ile Val Glu Gln Lys Trp Leu Thr Ala Asn Ala Val Ile
 995 1000 1005
 Gly Leu Phe Pro Ala Asn Thr Val Asn Gly Asp Asp Ile Glu Ile Tyr
 1010 1015 1020
 Ala Asp Arg Ser Arg Ser Gln Val Ile Met Thr Trp His Thr Leu Arg
 1025 1030 1035 1040
 Gln Gln Thr Ala Lys Pro Ala Gly Arg Pro Asn Leu Ala Leu Ala Asp
 1045 1050 1055
 Phe Ile Ala Pro Arg Glu Thr Gly Leu Asp Asp Thr Ile Gly Leu Phe
 1060 1065 1070
 Ala Val Ser Ala Gly Phe Gly Ile Asp Glu Arg Ile Arg Ala Phe Glu
 1075 1080 1085
 Ala Ala Asn Asp Asp Tyr Ser Ala Ile Ile Leu Lys Ala Leu Ala Asp
 1090 1095 1100
 Arg Leu Ala Glu Ala Phe Ala Glu His Met His Ala Arg Val Arg Arg
 1105 1110 1115 1120
 Glu Phe Trp Gly Tyr Val Lys Asp Glu Ser Leu Asp Asn Glu Gln Leu
 1125 1130 1135
 Ile Asp Glu Gln Tyr Leu Gly Ile Arg Pro Ala Pro Gly Tyr Pro Ala
 1140 1145 1150
 Cys Pro Asp His Thr Glu Lys Gly Pro Leu Phe Ala Leu Leu Glu Ala
 1155 1160 1165
 Glu Lys Arg Ser Gly Ile Val Ile Thr Glu Ser Phe Ala Met Val Pro
 1170 1175 1180
 Thr Ala Ala Val Ser Gly Phe Tyr Leu Ser Tyr Pro Glu Ser Ser Tyr
 1185 1190 1195 1200
 Phe Ala Val Gly Lys Ile Gly Lys Asp Gln Val Glu Asp Tyr Ala Arg
 1205 1210 1215
 Arg Lys Gly Trp Thr Leu Glu Glu Ala Glu Arg Trp Leu Ala Pro Val
 1220 1225 1230
 Leu Ala Tyr Glu Arg
 1235

<210> 31
 <211> 3774
 <212> DNA
 <213> Bordetella pertussis

<220>
 <221> CDS
 <222> (1)..(3771)
 <223> RBP00104

<220>
 <221> unsure

134

<222> 205 .. 205

<223> All occurrences of n indicate any nucleotide

<220>

<221> unsure

<222> 277 .. 277

<223> All occurrences of n indicate any nucleotide

<400> 31

| | |
|---|-----|
| gtg cct tat ccc cgt atc ccc ttc ccg ctg tcc gcc tac acg cat ggc | 48 |
| Val Pro Tyr Pro Arg Ile Pro Phe Pro Leu Ser Ala Tyr Thr His Gly | |
| 1 5 10 15 | |
| ggc gag ttc gtc cgc caa ctg gac aag cgc atc ctg atc ctg gat ggt | 96 |
| Gly Glu Phe Val Arg Gln Leu Asp Lys Arg Ile Leu Ile Leu Asp Gly | |
| 20 25 30 | |
| gcc atg ggc acg atg atc cag cgc tac aag ctg ggc gag gcc gat ttc | 144 |
| Ala Met Gly Thr Met Ile Gln Arg Tyr Lys Leu Gly Glu Ala Asp Phe | |
| 35 40 45 | |
| cgt ggc gag cgc ttc gcc gag cac cac aag gat ctc aag ggc gac aac | 192 |
| Arg Gly Glu Arg Phe Ala Glu His His Lys Asp Leu Lys Gly Asp Asn | |
| 50 55 60 | |
| gaa ctg ctg tcg ntg gtg cgc ccg gac gtg atc gcg gaa atc cac cgg | 240 |
| Glu Leu Leu Ser Xaa Val Arg Pro Asp Val Ile Ala Glu Ile His Arg | |
| 65 70 75 80 | |
| cag tac ctc gag gcc ggc gcc gac gtg atc gag acc nac acc ttc ggc | 288 |
| Gln Tyr Leu Glu Ala Gly Ala Asp Val Ile Glu Thr Xaa Thr Phe Gly | |
| 85 90 95 | |
| gcc acg tcg atc gcc cag ggc gat tac gac ctg ccg gag ctg gcc tac | 336 |
| Ala Thr Ser Ile Ala Gln Gly Asp Tyr Asp Leu Pro Glu Leu Ala Tyr | |
| 100 105 110 | |
| gag atg aac ctg gag tcg gcc cgc ctg gcg cgc gcc gcc tgc gac gcc | 384 |
| Glu Met Asn Leu Glu Ser Ala Arg Leu Ala Arg Ala Ala Cys Asp Ala | |
| 115 120 125 | |
| tac agc acg ccc gag cat ccg cgc ttc gtg gcc ggg gcg ctg ggg ccg | 432 |
| Tyr Ser Thr Pro Glu His Pro Arg Phe Val Ala Gly Ala Leu Gly Pro | |
| 130 135 140 | |
| cag ccc aag acc gcg tcc atc tcg ccc gac gtc aac gac ccg ggg gcg | 480 |
| Gln Pro Lys Thr Ala Ser Ile Ser Pro Asp Val Asn Asp Pro Gly Ala | |
| 145 150 155 160 | |
| cgc aac gtc acc ttc gac gag ctg cgc gcg gcc tat gtc gag cag ctc | 528 |
| Arg Asn Val Thr Phe Asp Glu Leu Arg Ala Ala Tyr Val Glu Gln Leu | |
| 165 170 175 | |
| aat ggc ctg ctc gac ggc ggc atc gac atc gtc ctg atc gaa acc atc | 576 |
| Asn Gly Leu Leu Asp Gly Gly Ile Asp Ile Val Leu Ile Glu Thr Ile | |
| 180 185 190 | |
| ttc gat acg ctc aac gcc aag gcg gcc atc ttc gcc gtc gag gaa gcg | 624 |
| Phe Asp Thr Leu Asn Ala Lys Ala Ala Ile Phe Ala Val Glu Glu Ala | |
| 195 200 205 | |
| ttc gag gcg cgc ggc gtg cgc ctg ccg gtg atg att tcg ggc acc gtg | 672 |

| Phe | Glu | Ala | Arg | Gly | Val | Arg | Leu | Pro | Val | Met | Ile | Ser | Gly | Thr | Val | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| 210 | | | | | | 215 | | | | | 220 | | | | | |
| acc | gat | gcg | tcg | ggc | cgc | atc | ctg | tcc | ggc | cag | acc | gtc | gag | gcg | ttc | 720 |
| Thr | Asp | Ala | Ser | Gly | Arg | Ile | Leu | Ser | Gly | Gln | Thr | Val | Glu | Ala | Phe | |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 | |
| tgg | aac | tcg | gtg | cgc | cat | gcg | cgg | ccg | gtc | acc | atc | ggc | ctg | aac | tgc | 768 |
| Trp | Asn | Ser | Val | Arg | His | Ala | Arg | Pro | Val | Thr | Ile | Gly | Leu | Asn | Cys | |
| | | | | 245 | | | | | 250 | | | | | 255 | | |
| gcg | ctg | ggc | gcg | gcg | ctg | atg | cgt | ccg | tat | gtg | gcc | gag | ctg | tcc | aag | 816 |
| Ala | Leu | Gly | Ala | Ala | Leu | Met | Arg | Pro | Tyr | Val | Ala | Glu | Leu | Ser | Lys | |
| | | | 260 | | | | | 265 | | | | | 270 | | | |
| atc | tgc | gac | acc | tat | gtg | tgc | gtc | tat | ccc | aac | gcc | ggc | ctg | ccc | aat | 864 |
| Ile | Cys | Asp | Thr | Tyr | Val | Cys | Val | Tyr | Pro | Asn | Ala | Gly | Leu | Pro | Asn | |
| | | 275 | | | | | 280 | | | | | 285 | | | | |
| ccc | atg | gcc | gag | acg | ggc | ttt | gac | gaa | acg | ccg | gcc | gat | acc | tcg | gcc | 912 |
| Pro | Met | Ala | Glu | Thr | Gly | Phe | Asp | Glu | Thr | Pro | Ala | Asp | Thr | Ser | Ala | |
| | | 290 | | | | 295 | | | | | 300 | | | | | |
| ctg | ctg | gaa | gag | ttc | gcc | cag | gcc | ggg | ctg | gtc | aac | atg | gcc | ggc | ggc | 960 |
| Leu | Leu | Glu | Glu | Phe | Ala | Gln | Ala | Gly | Leu | Val | Asn | Met | Ala | Gly | Gly | |
| 305 | | | | | 310 | | | | | 315 | | | | | 320 | |
| tgt | tgc | ggc | acc | acg | ccc | gag | cac | atc | cgc | gcc | atc | gcc | ggc | aag | gtg | 1008 |
| Cys | Cys | Gly | Thr | Thr | Pro | Glu | His | Ile | Arg | Ala | Ile | Ala | Gly | Lys | Val | |
| | | | | 325 | | | | | 330 | | | | | 335 | | |
| gcc | gcg | ctg | acg | ccg | cgc | gcg | gtg | ccc | gag | gtg | ccg | gtc | aag | acc | cgc | 1056 |
| Ala | Ala | Leu | Thr | Pro | Arg | Ala | Val | Pro | Glu | Val | Pro | Val | Lys | Thr | Arg | |
| | | | 340 | | | | | 345 | | | | | 350 | | | |
| ctg | tcg | ggc | ctg | gag | gcg | ctc | aac | atc | gac | gac | gag | act | ctg | ttc | gtc | 1104 |
| Leu | Ser | Gly | Leu | Glu | Ala | Leu | Asn | Ile | Asp | Asp | Glu | Thr | Leu | Phe | Val | |
| | | 355 | | | | | 360 | | | | | 365 | | | | |
| aac | gtg | ggc | gag | cgc | acc | aac | gtg | acg | ggc | agc | aag | atg | ttc | gcc | cgc | 1152 |
| Asn | Val | Gly | Glu | Arg | Thr | Asn | Val | Thr | Gly | Ser | Lys | Met | Phe | Ala | Arg | |
| | | 370 | | | | 375 | | | | | 380 | | | | | |
| ctg | gtc | cgc | gag | gag | aaa | tac | gac | gag | gcg | ctg | gcc | gtg | gcg | cgc | cag | 1200 |
| Leu | Val | Arg | Glu | Glu | Lys | Tyr | Asp | Glu | Ala | Leu | Ala | Val | Ala | Arg | Gln | |
| 385 | | | | | 390 | | | | | 395 | | | | | 400 | |
| cag | gtc | gag | aac | ggg | gcc | cag | atc | atc | gac | gtc | aac | atg | gac | gag | gcg | 1248 |
| Gln | Val | Glu | Asn | Gly | Ala | Gln | Ile | Ile | Asp | Val | Asn | Met | Asp | Glu | Ala | |
| | | | | 405 | | | | | 410 | | | | | 415 | | |
| atg | ctg | gac | tcg | gtg | gcc | tgt | atg | cac | c | | | | | | | |

| Val | Ala | Ala | Arg | Gly | Arg | Thr | Ile | Glu | Val | Ile | Glu | Gly | Pro | Leu | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-------|-----|-----|-----|------|
| 705 | | | | | | | | | | | | | | | 720 | |
| atg | gac | ggc | atg | aac | gtg | gtc | ggc | gac | ctg | ttc | ggc | gcg | ggc | aag | atg | 2208 |
| Met | Asp | Gly | Met | Asn | Val | Val | Gly | Asp | Leu | Phe | Gly | Ala | Gly | Lys | Met | |
| | | | | 725 | | | | | 730 | | | | | 735 | | |
| ttc | ctg | ccg | caa | gtg | gtg | aag | tgc | gcg | cgc | gtg | atg | aag | cag | gcg | gtg | 2256 |
| Phe | Leu | Pro | Gln | Val | Val | Lys | Ser | Ala | Arg | Val | Met | Lys | Gln | Ala | Val | |
| | | | 740 | | | | | 745 | | | | | 750 | | | |
| gcg | cac | ctg | att | ccc | ttc | atc | gag | gag | gaa | aag | cgc | cag | atc | gcg | gcc | 2304 |
| Ala | His | Leu | Ile | Pro | Phe | Ile | Glu | Glu | Glu | Lys | Arg | Gln | Ile | Ala | Ala | |
| | | 755 | | | | | 760 | | | | | 765 | | | | |
| gcg | ggc | ggc | gat | gtg | cgc | gcc | aag | ggc | aag | atc | gtg | atc | gcc | acc | gtc | 2352 |
| Ala | Gly | Gly | Asp | Val | Arg | Ala | Lys | Gly | Lys | Ile | Val | Ile | Ala | Thr | Val | |
| | 770 | | | | | 775 | | | | | 780 | | | | | |
| aag | ggc | gac | gtg | cac | gac | atc | ggc | aag | aac | atc | gtg | tgc | gtg | gtc | ttg | 2400 |
| Lys | Gly | Asp | Val | His | Asp | Ile | Gly | Lys | Asn | Ile | Val | Ser | Val | Val | Leu | |
| 785 | | | | | 790 | | | | | 795 | | | | | 800 | |
| cag | tgc | aat | aac | ttc | gaa | gtc | gtg | aac | atg | ggc | gtg | atg | gtg | ccg | tgc | 2448 |
| Gln | Cys | Asn | Asn | Phe | Glu | Val | Val | Asn | Met | Gly | Val | Met | Val | Pro | Cys | |
| | | | | 805 | | | | | 810 | | | | | 815 | | |
| gcc | cag | atc | ctg | cag | aag | gcc | aag | gac | gag | aac | gcc | gac | atg | atc | ggc | 2496 |
| Ala | Gln | Ile | Leu | Gln | Lys | Ala | Lys | Asp | Glu | Asn | Ala | Asp | Met | Ile | Gly | |
| | | | 820 | | | | | 825 | | | | | 830 | | | |
| ctg | tcc | ggc | ctg | atc | acg | ccc | agc | ctc | gaa | gag | atg | gcc | tac | gtg | gct | 2544 |
| Leu | Ser | Gly | Leu | Ile | Thr | Pro | Ser | Leu | Glu | Glu | Met | Ala | Tyr | Val | Ala | |
| | | 835 | | | | | 840 | | | | | 845 | | | | |
| tca | gaa | atg | cag | cgc | gac | ccc | tat | ttc | cgc | gag | cgc | gcc | atg | ccg | ctg | 2592 |
| Ser | Glu | Met | Gln | Arg | Asp | Pro | Tyr | Phe | Arg | Glu | Arg | Ala | Met | Pro | Leu | |
| | 850 | | | | | 855 | | | | | 860 | | | | | |
| atg | ata | ggc | ggg | gcg | acc | acc | agc | cgg | gtc | cat | acg | gcg | gtc | aag | atc | 2640 |
| Met | Ile | Gly | Gly | Ala | Thr | Thr | Ser | Arg | Val | His | Thr | Ala | Val | Lys | Ile | |
| 865 | | | | | 870 | | | | | 875 | | | | 880 | | |
| gcg | ccc | aac | tac | gac | ggt | ccg | gtg | atc | tac | gtg | ccc | gat | gcc | agc | cgt | 2688 |
| Ala | Pro | Asn | Tyr | Asp | Gly | Pro | Val | Ile | Tyr | Val | Pro | Asp | Ala | Ser | Arg | |
| | | | | 885 | | | | | 890 | | | | | 895 | | |
| tgc | gtc | ggc | gtg | gcg | acc | agc | ctc | atg | tcc | gac | cag | gcc | ccg | gcc | tat | 2736 |
| Ser | Val | Gly | Val | Ala | Thr | Ser | Leu | Met | Ser | Asp | Gln | Ala | Pro | Ala | Tyr | |
| | | | 900 | | | | | 905 | | | | | 910 | | | |
| ttg | gcg | gag | ctg | gcg | cag | gag | tac | gag | gat | gtg | cgc | cgc</ | | | | |

138

ctg ggc cgg cgc gcc ttc aag agc tac gac ctg gcc gag atc gcg cgc 2928
 Leu Gly Arg Arg Ala Phe Lys Ser Tyr Asp Leu Ala Glu Ile Ala Arg
 965 970 975

tat atc gac tgg ggg ccg ttc ttc cag acg tgg agc ctg ttc ggc ccg 2976
 Tyr Ile Asp Trp Gly Pro Phe Phe Gln Thr Trp Ser Leu Phe Gly Pro
 980 985 990

ttc ccc gcc atc ctg gac gac aag gtg gtg ggc gag cag gcg cgc aag 3024
 Phe Pro Ala Ile Leu Asp Asp Lys Val Val Gly Glu Gln Ala Arg Lys
 995 1000 1005

gtc tac gag gaa ggc cag gcc atg ctc aag cgc atc atc gac ggg cgc 3072
 Val Tyr Glu Glu Gly Gln Ala Met Leu Lys Arg Ile Ile Asp Gly Arg
 1010 1015 1020

tgg ctg acc gcc agc ggc gtg gtc ggc ttc tat ccg gcc aac cgc gtc 3120
 Trp Leu Thr Ala Ser Gly Val Val Gly Phe Tyr Pro Ala Asn Arg Val
 1025 1030 1035 1040

aat gac gaa gac atc gag gtc tac gcg gac gag acg cgc agc gag atg 3168
 Asn Asp Glu Asp Ile Glu Val Tyr Ala Asp Glu Thr Arg Ser Glu Met
 1045 1050 1055

ctg ttc acc tac cgc aac ctg cgc cag cag ggc gtc aag cgc gaa ggc 3216
 Leu Phe Thr Tyr Arg Asn Leu Arg Gln Gln Gly Val Lys Arg Glu Gly
 1060 1065 1070

gtc agc aac aag tgc ctg gcc gac tac atc gcg ccg cgc gac agc ggc 3264
 Val Ser Asn Lys Cys Leu Ala Asp Tyr Ile Ala Pro Arg Asp Ser Gly
 1075 1080 1085

ctg ctc gac tac atc ggc atg ttc gcc gtg acc gcg ggc ctg ggc atc 3312
 Leu Leu Asp Tyr Ile Gly Met Phe Ala Val Thr Ala Gly Leu Gly Ile
 1090 1095 1100

gag aag aaa gag gcc gag ttc cag gcg gcg ctg gac gac tac tcc agc 3360
 Glu Lys Lys Glu Ala Glu Phe Gln Ala Ala Leu Asp Asp Tyr Ser Ser
 1105 1110 1115 1120

atc atg ctg aag tcg ctg gcc gac cgg ctg gcc gag gcg ttc gcc gaa 3408
 Ile Met Leu Lys Ser Leu Ala Asp Arg Leu Ala Glu Ala Phe Ala Glu
 1125 1130 1135

tgc atg cac gcg cgc gtg cgc cgc gac ctg tgg ggc tac gcg gcg gac 3456
 Cys Met His Ala Arg Val Arg Arg Asp Leu Trp Gly Tyr Ala Ala Asp
 1140 1145 1150

gag gcg ctg tcc aac gat gag ctg atc gcc gag aag tac agc ggc atc 3504
 Glu Ala Leu Ser Asn Asp Glu Leu Ile Ala Glu Lys Tyr Ser Gly Ile
 1155 1160 1165

cgg ccg gcg ccc ggc tat ccg gcc tgc ccg gag cac gtg gtc aag acg 3552
 Arg Pro Ala Pro Gly Tyr Pro Ala Cys Pro Glu His Val Val Lys Thr
 1170 1175 1180

gac ctg ttc cgc gtg ctg gac gcc gcc gac gtc gga atg gag ctg acc 3600
 Asp Leu Phe Arg Val Leu Asp Ala Ala Asp Val Gly Met Glu Leu Thr
 1185 1190 1195 1200

gac agc tac gcc atg ttc ccg gcc tcc agc gtc tcg ggg ttc tat ttc 3648

139

Asp Ser Tyr Ala Met Phe Pro Ala Ser Ser Val Ser Gly Phe Tyr Phe
 1205 1210 1215

agc cac ccc gag tcg cag tat ttc aac gtg ggc aac atc ggc gcc gac 3696
 Ser His Pro Glu Ser Gln Tyr Phe Asn Val Gly Asn Ile Gly Ala Asp
 1220 1225 1230

cag ctg gcc gac tac gtg gcg cgc agc ggc cgc gcc gaa gag gac gtg 3744
 Gln Leu Ala Asp Tyr Val Ala Arg Ser Gly Arg Ala Glu Glu Asp Val
 1235 1240 1245

cgc cgc acc ctg gcg ccg aac ctg ggc tag 3774
 Arg Arg Thr Leu Ala Pro Asn Leu Gly
 1250 1255

<210> 32

<211> 1257

<212> PRT

<213> Bordetella pertussis

<220>

<221> unsure

<222> 69 .. 69

<223> All occurrences of Xaa indicate any amino acid

<220>

<221> unsure

<222> 93 .. 93

<223> All occurrences of Xaa indicate any amino acid

<400> 32

Val Pro Tyr Pro Arg Ile Pro Phe Pro Leu Ser Ala Tyr Thr His Gly
 1 5 10 15

Gly Glu Phe Val Arg Gln Leu Asp Lys Arg Ile Leu Ile Leu Asp Gly
 20 25 30

Ala Met Gly Thr Met Ile Gln Arg Tyr Lys Leu Gly Glu Ala Asp Phe
 35 40 45

Arg Gly Glu Arg Phe Ala Glu His His Lys Asp Leu Lys Gly Asp Asn
 50 55 60

Glu Leu Leu Ser Xaa Val Arg Pro Asp Val Ile Ala Glu Ile His Arg
 65 70 75 80

Gln Tyr Leu Glu Ala Gly Ala Asp Val Ile Glu Thr Xaa Thr Phe Gly
 85 90 95

Ala Thr Ser Ile Ala Gln Gly Asp Tyr Asp Leu Pro Glu Leu Ala Tyr
 100 105 110

Glu Met Asn Leu Glu Ser Ala Arg Leu Ala Arg Ala Ala Cys Asp Ala
 115 120 125

Tyr Ser Thr Pro Glu His Pro Arg Phe Val Ala Gly Ala Leu Gly Pro
 130 135 140

Gln Pro Lys Thr Ala Ser Ile Ser Pro Asp Val Asn Asp Pro Gly Ala
 145 150 155 160

140

Arg Asn Val Thr Phe Asp Glu Leu Arg Ala Ala Tyr Val Glu Gln Leu
 165 170 175
 Asn Gly Leu Leu Asp Gly Gly Ile Asp Ile Val Leu Ile Glu Thr Ile
 180 185 190
 Phe Asp Thr Leu Asn Ala Lys Ala Ala Ile Phe Ala Val Glu Glu Ala
 195 200 205
 Phe Glu Ala Arg Gly Val Arg Leu Pro Val Met Ile Ser Gly Thr Val
 210 215 220
 Thr Asp Ala Ser Gly Arg Ile Leu Ser Gly Gln Thr Val Glu Ala Phe
 225 230 235 240
 Trp Asn Ser Val Arg His Ala Arg Pro Val Thr Ile Gly Leu Asn Cys
 245 250 255
 Ala Leu Gly Ala Ala Leu Met Arg Pro Tyr Val Ala Glu Leu Ser Lys
 260 265 270
 Ile Cys Asp Thr Tyr Val Cys Val Tyr Pro Asn Ala Gly Leu Pro Asn
 275 280 285
 Pro Met Ala Glu Thr Gly Phe Asp Glu Thr Pro Ala Asp Thr Ser Ala
 290 295 300
 Leu Leu Glu Glu Phe Ala Gln Ala Gly Leu Val Asn Met Ala Gly Gly
 305 310 315 320
 Cys Cys Gly Thr Thr Pro Glu His Ile Arg Ala Ile Ala Gly Lys Val
 325 330 335
 Ala Ala Leu Thr Pro Arg Ala Val Pro Glu Val Pro Val Lys Thr Arg
 340 345 350
 Leu Ser Gly Leu Glu Ala Leu Asn Ile Asp Asp Glu Thr Leu Phe Val
 355 360 365
 Asn Val Gly Glu Arg Thr Asn Val Thr Gly Ser Lys Met Phe Ala Arg
 370 375 380
 Leu Val Arg Glu Glu Lys Tyr Asp Glu Ala Leu Ala Val Ala Arg Gln
 385 390 395 400
 Gln Val Glu Asn Gly Ala Gln Ile Ile Asp Val Asn Met Asp Glu Ala
 405 410 415
 Met Leu Asp Ser Val Ala Cys Met His Arg Phe Leu Asn Leu Ile Ala
 420 425 430
 Ser Glu Pro Asp Ile Ala Arg Val Pro Val Met Ile Asp Ser Ser Lys
 435 440 445
 Trp Glu Val Ile Glu Thr Gly Leu Lys Cys Val Gln Gly Lys Ala Val
 450 455 460
 Val Asn Ser Ile Ser Met Lys Glu Gly Glu Glu Pro Phe Arg His His
 465 470 475 480
 Ala Arg Leu Cys Arg Arg Tyr Gly Ala Ala Met Val Val Met Ala Phe
 485 490 495

141

Asp Glu Gln Gly Gln Ala Asp Ser Leu Glu Arg Arg Lys Glu Ile Cys
 500 505 510

Gly Arg Ala Tyr Arg Ile Leu Val Glu Glu Glu Gly Phe Pro Pro Glu
 515 520 525

Asp Ile Ile Phe Asp Pro Asn Val Phe Ala Val Ala Thr Gly Ile Asp
 530 535 540

Glu His Asn His Tyr Ala Val Asp Phe Ile Glu Gly Ala Arg Trp Ile
 545 550 555 560

Arg Ala Asn Leu Pro His Ala Arg Ile Ser Gly Gly Ile Ser Asn Val
 565 570 575

Ser Phe Ser Phe Arg Gly Asn Glu Pro Met Arg Glu Ala Ile His Thr
 580 585 590

Val Phe Leu Tyr Tyr Ala Ile Glu Ala Gly Leu Thr Met Gly Ile Val
 595 600 605

Asn Ala Gly Gln Leu Gly Val Tyr Ala Asp Leu Ala Pro His Leu Arg
 610 615 620

Asp Leu Val Glu Asp Val Ile Leu Asp Arg Pro Glu Pro Val Gly Arg
 625 630 635 640

Ser Asp Ser Ala Asp Glu Arg Ser Pro Thr Glu Arg Leu Val Gln Phe
 645 650 655

Ala Glu Thr Val Lys Gly Ser Gly Ala Lys Lys Glu Glu Asp Leu Thr
 660 665 670

Trp Arg Thr Gly Ser Val Glu Gln Arg Leu Ala His Ala Leu Val His
 675 680 685

Gly Ile Thr Thr Phe Ile Val Glu Asp Thr Glu Glu Val Arg Gln Gln
 690 695 700

Val Ala Ala Arg Gly Gly Arg Thr Ile Glu Val Ile Glu Gly Pro Leu
 705 710 715 720

Met Asp Gly Met Asn Val Val Gly Asp Leu Phe Gly Ala Gly Lys Met
 725 730 735

Phe Leu Pro Gln Val Val Lys Ser Ala Arg Val Met Lys Gln Ala Val
 740 745 750

Ala His Leu Ile Pro Phe Ile Glu Glu Glu Lys Arg Gln Ile Ala Ala
 755 760 765

Ala Gly Gly Asp Val Arg Ala Lys Gly Lys Ile Val Ile Ala Thr Val
 770 775 780

Lys Gly Asp Val His Asp Ile Gly Lys Asn Ile Val Ser Val Val Leu
 785 790 795 800

Gln Cys Asn Asn Phe Glu Val Val Asn Met Gly Val Met Val Pro Cys
 805 810 815

Ala Gln Ile Leu Gln Lys Ala Lys Asp Glu Asn Ala Asp Met Ile Gly

142

| | | |
|---|------|------|
| 820 | 825 | 830 |
| Leu Ser Gly Leu Ile Thr Pro Ser Leu Glu Glu Met Ala Tyr Val Ala | | |
| 835 | 840 | 845 |
| Ser Glu Met Gln Arg Asp Pro Tyr Phe Arg Glu Arg Ala Met Pro Leu | | |
| 850 | 855 | 860 |
| Met Ile Gly Gly Ala Thr Thr Ser Arg Val His Thr Ala Val Lys Ile | | |
| 865 | 870 | 875 |
| | | 880 |
| Ala Pro Asn Tyr Asp Gly Pro Val Ile Tyr Val Pro Asp Ala Ser Arg | | |
| 885 | 890 | 895 |
| Ser Val Gly Val Ala Thr Ser Leu Met Ser Asp Gln Ala Pro Ala Tyr | | |
| 900 | 905 | 910 |
| Leu Ala Glu Leu Ala Gln Glu Tyr Glu Asp Val Arg Arg Cys His Ala | | |
| 915 | 920 | 925 |
| Asn Arg Lys Ala Val Pro Leu Val Ser Leu Ala Glu Ala Arg Ala Ala | | |
| 930 | 935 | 940 |
| Arg Pro Gln Ile Asp Trp Ser Gly Tyr Gln Pro Pro Arg Pro Lys Phe | | |
| 945 | 950 | 955 |
| | | 960 |
| Leu Gly Arg Arg Ala Phe Lys Ser Tyr Asp Leu Ala Glu Ile Ala Arg | | |
| 965 | 970 | 975 |
| Tyr Ile Asp Trp Gly Pro Phe Phe Gln Thr Trp Ser Leu Phe Gly Pro | | |
| 980 | 985 | 990 |
| Phe Pro Ala Ile Leu Asp Asp Lys Val Val Gly Glu Gln Ala Arg Lys | | |
| 995 | 1000 | 1005 |
| Val Tyr Glu Glu Gly Gln Ala Met Leu Lys Arg Ile Ile Asp Gly Arg | | |
| 1010 | 1015 | 1020 |
| Trp Leu Thr Ala Ser Gly Val Val Gly Phe Tyr Pro Ala Asn Arg Val | | |
| 1025 | 1030 | 1035 |
| | | 1040 |
| Asn Asp Glu Asp Ile Glu Val Tyr Ala Asp Glu Thr Arg Ser Glu Met | | |
| 1045 | 1050 | 1055 |
| Leu Phe Thr Tyr Arg Asn Leu Arg Gln Gln Gly Val Lys Arg Glu Gly | | |
| 1060 | 1065 | 1070 |
| Val Ser Asn Lys Cys Leu Ala Asp Tyr Ile Ala Pro Arg Asp Ser Gly | | |
| 1075 | 1080 | 1085 |
| Leu Leu Asp Tyr Ile Gly Met Phe Ala Val Thr Ala Gly Leu Gly Ile | | |
| 1090 | 1095 | 1100 |
| Glu Lys Lys Glu Ala Glu Phe Gln Ala Ala Leu Asp Asp Tyr Ser Ser | | |
| 1105 | 1110 | 1115 |
| | | 1120 |
| Ile Met Leu Lys Ser Leu Ala Asp Arg Leu Ala Glu Ala Phe Ala Glu | | |
| 1125 | 1130 | 1135 |
| Cys Met His Ala Arg Val Arg Arg Asp Leu Trp Gly Tyr Ala Ala Asp | | |
| 1140 | 1145 | 1150 |

143

Glu Ala Leu Ser Asn Asp Glu Leu Ile Ala Glu Lys Tyr Ser Gly Ile
 1155 1160 1165

Arg Pro Ala Pro Gly Tyr Pro Ala Cys Pro Glu His Val Val Lys Thr
 1170 1175 1180

Asp Leu Phe Arg Val Leu Asp Ala Ala Asp Val Gly Met Glu Leu Thr
 1185 1190 1195 1200

Asp Ser Tyr Ala Met Phe Pro Ala Ser Ser Val Ser Gly Phe Tyr Phe
 1205 1210 1215

Ser His Pro Glu Ser Gln Tyr Phe Asn Val Gly Asn Ile Gly Ala Asp
 1220 1225 1230

Gln Leu Ala Asp Tyr Val Ala Arg Ser Gly Arg Ala Glu Glu Asp Val
 1235 1240 1245

Arg Arg Thr Leu Ala Pro Asn Leu Gly
 1250 1255

<210> 33

<211> 3645

<212> DNA

<213> Chlorobium tepidum

<220>

<221> CDS

<222> (1)..(3642)

<223> RCL00420

<400> 33

gtg ctc gac ggg gcc atg ggc acc atg atc cag agg cat ggc ctc gac 48
 Val Leu Asp Gly Ala Met Gly Thr Met Ile Gln Arg His Gly Leu Asp
 1 5 10 15

gaa cag gac tac cgg ggc gag cgt ttc gct tcg cat gac cat ccg ctg 96
 Glu Gln Asp Tyr Arg Gly Glu Arg Phe Ala Ser His Asp His Pro Leu
 20 25 30

aag ggc aac aac gac ctt ctt gtc atc acc cgg ccc gac atc atc cgt 144
 Lys Gly Asn Asn Asp Leu Leu Val Ile Thr Arg Pro Asp Ile Ile Arg
 35 40 45

tcg atc cac tgc gac ttc ctc gac gcg ggt gcg gac atc atc gag acc 192
 Ser Ile His Cys Asp Phe Leu Asp Ala Gly Ala Asp Ile Ile Glu Thr
 50 55 60

tgc acc ttc aac gcc aac ccg atc tcg cag tcg gac tac cag ttg cag 240
 Cys Thr Phe Asn Ala Asn Pro Ile Ser Gln Ser Asp Tyr Gln Leu Gln
 65 70 75 80

gac ttg acc cgc gag ctg aac gtg gcg gcg gca aag ata gcc cgc tcg 288
 Asp Leu Thr Arg Glu Leu Asn Val Ala Ala Lys Ile Ala Arg Ser
 85 90 95

gca gcg gac gag ttc acc gca aag act ccc gac aag ccg cgt ttc gtg 336
 Ala Ala Asp Glu Phe Thr Ala Lys Thr Pro Asp Lys Pro Arg Phe Val
 100 105 110

gcc ggt tcc atc gga ccg acc aac aag acg ctc tcg ctc tcg ccg gac 384

144

| | |
|---|------|
| Ala Gly Ser Ile Gly Pro Thr Asn Lys Thr Leu Ser Leu Ser Pro Asp | |
| 115 120 125 | |
| gtg aac aac ccc ggc ttc cgc gcc gtc acc ttc cag gag atg gtc gat | 432 |
| Val Asn Asn Pro Gly Phe Arg Ala Val Thr Phe Gln Glu Met Val Asp | |
| 130 135 140 | |
| aac tac act gcc cag ctc gaa ggc ttg cac gag ggc ggt gtc gat ctc | 480 |
| Asn Tyr Thr Ala Gln Leu Glu Gly Leu His Glu Gly Gly Val Asp Leu | |
| 145 150 155 160 | |
| ttg ctc gtc gag acg gtg ttc gac aca ctg aac tgc aag gcg gcg ctc | 528 |
| Leu Leu Val Glu Thr Val Phe Asp Thr Leu Asn Cys Lys Ala Ala Leu | |
| 165 170 175 | |
| tac gct atc gag gag tac gcg gtg aaa acc ggc tgg cag gtg ccc gtg | 576 |
| Tyr Ala Ile Glu Glu Tyr Ala Val Lys Thr Gly Trp Gln Val Pro Val | |
| 180 185 190 | |
| atg gtc tcc ggc acg gtg gtg gac gcg agc ggc cgc acc ctc tcc ggc | 624 |
| Met Val Ser Gly Thr Val Val Asp Ala Ser Gly Arg Thr Leu Ser Gly | |
| 195 200 205 | |
| caa acc acc gag gcg ttc tgg att tcg att tcg cac atg ccg agt ctg | 672 |
| Gln Thr Thr Glu Ala Phe Trp Ile Ser Ile Ser His Met Pro Ser Leu | |
| 210 215 220 | |
| ctc tcg gtc ggc ctg aac tgc gca ctc ggc tcc aag cag atg cgc ccc | 720 |
| Leu Ser Val Gly Leu Asn Cys Ala Leu Gly Ser Lys Gln Met Arg Pro | |
| 225 230 235 240 | |
| ttc atc gag gcg ctc tcg aac atc gcc gaa agc tac gtc agc gtc tat | 768 |
| Phe Ile Glu Ala Leu Ser Asn Ile Ala Glu Ser Tyr Val Ser Val Tyr | |
| 245 250 255 | |
| ccc aac gcg ggc ctg ccg aat gag ttc ggc gag tac gac gac tcc ccc | 816 |
| Pro Asn Ala Gly Leu Pro Asn Glu Phe Gly Glu Tyr Asp Asp Ser Pro | |
| 260 265 270 | |
| gag tac atg gcc gcg cag atc gcg ggc ttc gcc gaa tca ggc ttc gtg | 864 |
| Glu Tyr Met Ala Ala Gln Ile Ala Gly Phe Ala Glu Ser Gly Phe Val | |
| 275 280 285 | |
| aac atc gtc ggc ggc tgc tgc ggc acc acg ccg acg cac atc cgc gcc | 912 |
| Asn Ile Val Gly Gly Cys Cys Gly Thr Thr Pro Thr His Ile Arg Ala | |
| 290 295 300 | |
| att gcc gaa gcg gtc aag act ctc ccg ccg aga aag cgc ccc gcc aac | 960 |
| Ile Ala Glu Ala Val Lys Thr Leu Pro Pro Arg Lys Arg Pro Ala Asn | |
| 305 310 315 320 | |
| aag cac gtg ctg agg ctc tcc ggc ctc gaa ccg ctc gtg gtt gac gaa | 1008 |
| Lys His Val Leu Arg Leu Ser Gly Leu Glu Pro Leu Val Val Asp Glu | |
| 325 330 335 | |
| acc acc ggc ttc atc aac gtc ggc gag cgc acc aac gtc acc ggt tcg | 1056 |
| Thr Thr Gly Phe Ile Asn Val Gly Glu Arg Thr Asn Val Thr Gly Ser | |
| 340 345 350 | |
| cgc aag ttc gcc cgc ctc atc aag gag gcc aat tac gac gaa gcg ctc | 1104 |
| Arg Lys Phe Ala Arg Leu Ile Lys Glu Ala Asn Tyr Asp Glu Ala Leu | |
| 355 360 365 | |

145

| | |
|---|------|
| tcc att gcc cgc cag cag gtc gag aac ggc gcg cag gtg atc gac gtg Ser Ile Ala Arg Gln Gln Val Glu Asn Gly Ala Gln Val Ile Asp Val 370 375 380 | 1152 |
| aac ctc gac gaa gga atg ctc gac tcc gaa aag gtg atc gtc gaa ttc Asn Leu Asp Glu Gly Met Leu Asp Ser Glu Lys Val Ile Val Glu Phe 385 390 395 400 | 1200 |
| ctg aac ctc atc gcc tcc gag cct gag atc gcc aag gtg ccg gtg atg Leu Asn Leu Ile Ala Ser Glu Pro Glu Ile Ala Lys Val Pro Val Met 405 410 415 | 1248 |
| atc gac tcg tcg aaa tgg tcg gtc atc gaa aac ggc ctg cgc tgc acc Ile Asp Ser Ser Lys Trp Ser Val Ile Glu Asn Gly Leu Arg Cys Thr 420 425 430 | 1296 |
| cag ggc aag agc atc gtc aac tcg atc agc ctc aag gag ggc gag gag Gln Gly Lys Ser Ile Val Asn Ser Ile Ser Leu Lys Glu Gly Glu Glu 435 440 445 | 1344 |
| ctg ttc aag gag cgc gct cgc aag atc atg caa tac ggc gcg gcg gcg Leu Phe Lys Glu Arg Ala Arg Lys Ile Met Gln Tyr Gly Ala Ala Ala 450 455 460 | 1392 |
| gtg gtc atg gcc ttc gac gag cag ggc cag gcc gac agc ctg cac cgc Val Val Met Ala Phe Asp Glu Gln Gly Gln Ala Asp Ser Leu His Arg 465 470 475 480 | 1440 |
| cgc atc gag att tgc agc cgc gcc tac aaa att ctc acc gaa gag gtg Arg Ile Glu Ile Cys Ser Arg Ala Tyr Lys Ile Leu Thr Glu Glu Val 485 490 495 | 1488 |
| ggc ttc ccg ccg gag gac atc atc ttt gac ccg aac gtg ctg acc gtg Gly Phe Pro Pro Glu Asp Ile Ile Phe Asp Pro Asn Val Leu Thr Val 500 505 510 | 1536 |
| gcc acc ggc atc gac gag cac aac aac tac gcg ctc gac ttc atc gaa Ala Thr Gly Ile Asp Glu His Asn Asn Tyr Ala Leu Asp Phe Ile Glu 515 520 525 | 1584 |
| agc gtg cgc tgg atc aag cag aac ctg ccg cac gcg aag gtc tcc ggc Ser Val Arg Trp Ile Lys Gln Asn Leu Pro His Ala Lys Val Ser Gly 530 535 540 | 1632 |
| ggc atc agc aac gtt tcg ttc tcc ttc cgc ggc aac gag ccg gtg cgc Gly Ile Ser Asn Val Ser Phe Ser Phe Arg Gly Asn Glu Pro Val Arg 545 550 555 560 | 1680 |
| gag gcg atg cac acc gcg ttc ctc tac cac gcc atc cac gcc ggt ctc Glu Ala Met His Thr Ala Phe Leu Tyr His Ala Ile His Ala Gly Leu 565 570 575 | 1728 |
| gac atg ggc atc gtc aac gcc gcc cag ctt ggc atc tac gaa gag atc Asp Met Gly Ile Val Asn Ala Ala Gln Leu Gly Ile Tyr Glu Glu Ile 580 585 590 | 1776 |
| gac ccg gag ctt ctt gtc tat gtc gag gac gtg ctg ctg aac cgc cgc Asp Pro Glu Leu Leu Val Tyr Val Glu Asp Val Leu Leu Asn Arg Arg 595 600 605 | 1824 |
| gac gac gcc acc gag cgg ctc gtg gcg ttc gct gaa acg atc cgc gac | 1872 |

146

| | |
|---|------|
| Asp Asp Ala Thr Glu Arg Leu Val Ala Phe Ala Glu Thr Ile Arg Asp 610 615 620 | |
| ggc ggc gaa aag gcc gag gcc aag aac gcc gaa tgg cgc aac gcc ccg Gly Gly Glu Lys Ala Glu Ala Lys Asn Ala Glu Trp Arg Asn Ala Pro 625 630 635 640 | 1920 |
| gtc gag gag cgg ctg aaa cac gcg ctc gtc aag ggc atc gtt gac tac Val Glu Glu Arg Leu Lys His Ala Leu Val Lys Gly Ile Val Asp Tyr 645 650 655 | 1968 |
| atc gac gag gac acc gaa gag gcc cgc cag ctc tac ccg agt ccg ctg Ile Asp Glu Asp Thr Glu Glu Ala Arg Gln Leu Tyr Pro Ser Pro Leu 660 665 670 | 2016 |
| gag gtg atc gag ggg ccg ctc atg aac ggc atg aac cac gtc ggc gac Glu Val Ile Glu Gly Pro Leu Met Asn Gly Met Asn His Val Gly Asp 675 680 685 | 2064 |
| ctc ttc gcc gaa ggc aag atg ttc ctg cca cag gtg gtc aaa agc gcc Leu Phe Ala Glu Gly Lys Met Phe Leu Pro Gln Val Val Lys Ser Ala 690 695 700 | 2112 |
| cgc gtc atg aag cgc tcg gta gct gcg ctg att ccc tat atc gag gag Arg Val Met Lys Arg Ser Val Ala Ala Leu Ile Pro Tyr Ile Glu Glu 705 710 715 720 | 2160 |
| gag aag tcg aaa aac tgc gac acg agc gcc aaa gcc aag gtg ctg ctc Glu Lys Ser Lys Asn Cys Asp Thr Ser Ala Lys Ala Lys Val Leu Leu 725 730 735 | 2208 |
| gcc acg gtg aag ggc gac gtg cac gac atc ggc aag aac atc gtg tcg Ala Thr Val Lys Gly Asp Val His Asp Ile Gly Lys Asn Ile Val Ser 740 745 750 | 2256 |
| gtg gtg ctt gcc tgc aac aac ttc gac gtg atc gac atc ggc gtc atg Val Val Leu Ala Cys Asn Asn Phe Asp Val Ile Asp Ile Gly Val Met 755 760 765 | 2304 |
| atg cca tgc gac aag att ctc gaa gcg ctg gca gaa cac aag ccc gac Met Pro Cys Asp Lys Ile Leu Glu Ala Leu Ala Glu His Lys Pro Asp 770 775 780 | 2352 |
| gtg ctc ggc ctc tcc ggc ctc atc acc ccg tcg ctc gaa gag atg gcg Val Leu Gly Leu Ser Gly Leu Ile Thr Pro Ser Leu Glu Glu Met Ala 785 790 795 800 | 2400 |
| cac gtg gcc aaa gag atg gag cgg ctc ggc atg aac att ccg ctc atc His Val Ala Lys Glu Met Glu Arg Leu Gly Met Asn Ile Pro Leu Ile 805 810 815 | 2448 |
| atc ggc ggc gcg acc acc tcg aag gtg cac acg gcg gtg aaa ctc gcg Ile Gly Gly Ala Thr Thr Ser Lys Val His Thr Ala Val Lys Leu Ala 820 825 830 | 2496 |
| ccc tgc tac ccc agc ggc gcg gta gta cac gtg ctc gac gcc tcg cgc Pro Cys Tyr Pro Ser Gly Ala Val Val His Val Leu Asp Ala Ser Arg 835 840 845 | 2544 |
| agc gtg ccg gtg gtc agc aac ctc tgc aac ccc gcc cag cgc gac agc Ser Val Pro Val Val Ser Asn Leu Cys Asn Pro Ala Gln Arg Asp Ser 850 855 860 | 2592 |

147

| | |
|---|------|
| tat atc gcg gcg ctg aag gat gag cag gag gcg atg cgc aag agc cac Tyr Ile Ala Ala Leu Lys Asp Glu Gln Glu Ala Met Arg Lys Ser His 865 870 875 880 | 2640 |
| gcc gag cgc atg gcg gca aaa aag tac gtc tcg ctc gac gcc gcc cgc Ala Glu Arg Met Ala Ala Lys Lys Tyr Val Ser Leu Asp Ala Ala Arg 885 890 895 | 2688 |
| gac aac cgc ctc acc att gac tgg gag gcc gaa acc atc gac aag ccc Asp Asn Arg Leu Thr Ile Asp Trp Glu Ala Glu Thr Ile Asp Lys Pro 900 905 910 | 2736 |
| gcc cag act gcc gtc acc gtg ctg gag gat gtc acc gtc gcc gcg ctc Ala Gln Thr Gly Val Thr Val Leu Glu Asp Val Thr Val Gly Ala Leu 915 920 925 | 2784 |
| cgc ccg tat atc gac tgg gca mcc ttc ttc tgg agc tgg gag ctg cac Arg Pro Tyr Ile Asp Trp Ala Xaa Phe Phe Trp Ser Trp Glu Leu His 930 935 940 | 2832 |
| ggc gtc tat ccg cag att ctg gag gat gaa aag gtc gcc gag gag gca Gly Val Tyr Pro Gln Ile Leu Glu Asp Glu Lys Val Gly Glu Glu Ala 945 950 955 960 | 2880 |
| acc aaa ctc ttc aac gac gcc acc gct ctg ctc gac cgg atc gac agc Thr Lys Leu Phe Asn Asp Ala Thr Ala Leu Leu Asp Arg Ile Asp Ser 965 970 975 | 2928 |
| gaa aag ctg ctc gcc atc aaa gcc gtg gcg gcc atc ttc ccg gcc aac Glu Lys Leu Leu Gly Ile Lys Gly Val Ala Gly Ile Phe Pro Ala Asn 980 985 990 | 2976 |
| agc atc gcc gac gac atc ttc gtc tat gcg gat gac gag cgc tcg ata Ser Ile Gly Asp Asp Ile Phe Val Tyr Ala Asp Asp Glu Arg Ser Ile 995 1000 1005 | 3024 |
| atc cgc acc gtg ctg cac acc ctg cgc cag caa gcc gaa aag cac gcc Ile Arg Thr Val Leu His Thr Leu Arg Gln Gln Gly Glu Lys His Gly 1010 1015 1020 | 3072 |
| gaa gcg aac ctc gcg ctg gcg gac ttc gtg gcc ccg cgc gaa agc gcc Glu Ala Asn Leu Ala Leu Ala Asp Phe Val Ala Pro Arg Glu Ser Gly 1025 1030 1035 1040 | 3120 |
| gtc aac gac tgg atc gcc tgc ttc acc gta acc gcc gga ctc gcc atc Val Asn Asp Trp Ile Gly Cys Phe Thr Val Thr Ala Gly Leu Gly Ile 1045 1050 1055 | 3168 |
| cag aat ttg ctc gac gag ttc aca gca gag aac gac gac tac cac cgc Gln Asn Leu Leu Asp Glu Phe Thr Ala Glu Asn Asp Asp Tyr His Arg 1060 1065 1070 | 3216 |
| atc atg aca cag gcg ctc gcc gac cga ctg gcc gaa gcg ttc gca gag Ile Met Thr Gln Ala Leu Ala Asp Arg Leu Ala Glu Ala Phe Ala Glu 1075 1080 1085 | 3264 |
| atg ctg cac gaa aag gtg cgc cgc gaa ctc tgg gcc tac gcg ccc gcc Met Leu His Glu Lys Val Arg Arg Glu Leu Trp Gly Tyr Ala Pro Gly 1090 1095 1100 | 3312 |
| gaa atc ctc gcc aac gaa gag ctg atc gcc gaa aag tac cga gcc atc | 3360 |

148

Glu Ile Leu Gly Asn Glu Glu Leu Ile Ala Glu Lys Tyr Arg Gly Ile
 1105 1110 1115 1120

cgc ccc gcc ccc ggc tac ccc gcc tgc ccg gat cac acc gaa aag gca 3408
 Arg Pro Ala Pro Gly Tyr Pro Ala Cys Pro Asp His Thr Glu Lys Ala
 1125 1130 1135

atc atc ttc gac ctg ctc aac gct gaa gcg gcc acc ggc gtc acg ctg 3456
 Ile Ile Phe Asp Leu Leu Asn Ala Glu Ala Ala Thr Gly Val Thr Leu
 1140 1145 1150

acg gaa act ttc gcg atg aac ccc gca gcc tca gtc tgc ggc ctc tac 3504
 Thr Glu Thr Phe Ala Met Asn Pro Ala Ala Ser Val Cys Gly Leu Tyr
 1155 1160 1165

ttc gcc aac ccg gcc tcg aaa tac ttc gta ctc ggc aag att ggt aag 3552
 Phe Ala Asn Pro Ala Ser Lys Tyr Phe Val Leu Gly Lys Ile Gly Lys
 1170 1175 1180

gat cag gtc gaa gac tac gcc aac cgc aaa ggg ctg gaa gta gca gaa 3600
 Asp Gln Val Glu Asp Tyr Ala Asn Arg Lys Gly Leu Glu Val Ala Glu
 1185 1190 1195 1200

gcc gag aag tgg ctc gcg ccc tcg ctg aac tac gat cca gcg 3642
 Ala Glu Lys Trp Leu Ala Pro Ser Leu Asn Tyr Asp Pro Ala
 1205 1210

taa 3645

<210> 34
 <211> 1214
 <212> PRT
 <213> Chlorobium tepidum

<220>
 <221> unsure
 <222> 936 .. 936
 <223> All occurrences of Xaa indicate any amino acid

<400> 34
 Val Leu Asp Gly Ala Met Gly Thr Met Ile Gln Arg His Gly Leu Asp
 1 5 10 15
 Glu Gln Asp Tyr Arg Gly Glu Arg Phe Ala Ser His Asp His Pro Leu
 20 25 30
 Lys Gly Asn Asn Asp Leu Leu Val Ile Thr Arg Pro Asp Ile Ile Arg
 35 40 45
 Ser Ile His Cys Asp Phe Leu Asp Ala Gly Ala Asp Ile Ile Glu Thr
 50 55 60
 Cys Thr Phe Asn Ala Asn Pro Ile Ser Gln Ser Asp Tyr Gln Leu Gln
 65 70 75 80
 Asp Leu Thr Arg Glu Leu Asn Val Ala Ala Lys Ile Ala Arg Ser
 85 90 95
 Ala Ala Asp Glu Phe Thr Ala Lys Thr Pro Asp Lys Pro Arg Phe Val
 100 105 110

149

Ala Gly Ser Ile Gly Pro Thr Asn Lys Thr Leu Ser Leu Ser Pro Asp
 115 120 125

Val Asn Asn Pro Gly Phe Arg Ala Val Thr Phe Gln Glu Met Val Asp
 130 135 140

Asn Tyr Thr Ala Gln Leu Glu Gly Leu His Glu Gly Gly Val Asp Leu
 145 150 155 160

Leu Leu Val Glu Thr Val Phe Asp Thr Leu Asn Cys Lys Ala Ala Leu
 165 170 175

Tyr Ala Ile Glu Glu Tyr Ala Val Lys Thr Gly Trp Gln Val Pro Val
 180 185 190

Met Val Ser Gly Thr Val Val Asp Ala Ser Gly Arg Thr Leu Ser Gly
 195 200 205

Gln Thr Thr Glu Ala Phe Trp Ile Ser Ile Ser His Met Pro Ser Leu
 210 215 220

Leu Ser Val Gly Leu Asn Cys Ala Leu Gly Ser Lys Gln Met Arg Pro
 225 230 235 240

Phe Ile Glu Ala Leu Ser Asn Ile Ala Glu Ser Tyr Val Ser Val Tyr
 245 250 255

Pro Asn Ala Gly Leu Pro Asn Glu Phe Gly Glu Tyr Asp Asp Ser Pro
 260 265 270

Glu Tyr Met Ala Ala Gln Ile Ala Gly Phe Ala Glu Ser Gly Phe Val
 275 280 285

Asn Ile Val Gly Gly Cys Cys Gly Thr Thr Pro Thr His Ile Arg Ala
 290 295 300

Ile Ala Glu Ala Val Lys Thr Leu Pro Pro Arg Lys Arg Pro Ala Asn
 305 310 315 320

Lys His Val Leu Arg Leu Ser Gly Leu Glu Pro Leu Val Val Asp Glu
 325 330 335

Thr Thr Gly Phe Ile Asn Val Gly Glu Arg Thr Asn Val Thr Gly Ser
 340 345 350

Arg Lys Phe Ala Arg Leu Ile Lys Glu Ala Asn Tyr Asp Glu Ala Leu
 355 360 365

Ser Ile Ala Arg Gln Gln Val Glu Asn Gly Ala Gln Val Ile Asp Val
 370 375 380

Asn Leu Asp Glu Gly Met Leu Asp Ser Glu Lys Val Ile Val Glu Phe
 385 390 395 400

Leu Asn Leu Ile Ala Ser Glu Pro Glu Ile Ala Lys Val Pro Val Met
 405 410 415

Ile Asp Ser Ser Lys Trp Ser Val Ile Glu Asn Gly Leu Arg Cys Thr
 420 425 430

Gln Gly Lys Ser Ile Val Asn Ser Ile Ser Leu Lys Glu Gly Glu Glu
 435 440 445

150

Leu Phe Lys Glu Arg Ala Arg Lys Ile Met Gln Tyr Gly Ala Ala Ala
 450 455 460
 Val Val Met Ala Phe Asp Glu Gln Gly Gln Ala Asp Ser Leu His Arg
 465 470 475 480
 Arg Ile Glu Ile Cys Ser Arg Ala Tyr Lys Ile Leu Thr Glu Glu Val
 485 490 495
 Gly Phe Pro Pro Glu Asp Ile Ile Phe Asp Pro Asn Val Leu Thr Val
 500 505 510
 Ala Thr Gly Ile Asp Glu His Asn Asn Tyr Ala Leu Asp Phe Ile Glu
 515 520 525
 Ser Val Arg Trp Ile Lys Gln Asn Leu Pro His Ala Lys Val Ser Gly
 530 535 540
 Gly Ile Ser Asn Val Ser Phe Ser Phe Arg Gly Asn Glu Pro Val Arg
 545 550 555 560
 Glu Ala Met His Thr Ala Phe Leu Tyr His Ala Ile His Ala Gly Leu
 565 570 575
 Asp Met Gly Ile Val Asn Ala Ala Gln Leu Gly Ile Tyr Glu Glu Ile
 580 585 590
 Asp Pro Glu Leu Leu Val Tyr Val Glu Asp Val Leu Leu Asn Arg Arg
 595 600 605
 Asp Asp Ala Thr Glu Arg Leu Val Ala Phe Ala Glu Thr Ile Arg Asp
 610 615 620
 Gly Gly Glu Lys Ala Glu Ala Lys Asn Ala Glu Trp Arg Asn Ala Pro
 625 630 635 640
 Val Glu Glu Arg Leu Lys His Ala Leu Val Lys Gly Ile Val Asp Tyr
 645 650 655
 Ile Asp Glu Asp Thr Glu Glu Ala Arg Gln Leu Tyr Pro Ser Pro Leu
 660 665 670
 Glu Val Ile Glu Gly Pro Leu Met Asn Gly Met Asn His Val Gly Asp
 675 680 685
 Leu Phe Ala Glu Gly Lys Met Phe Leu Pro Gln Val Val Lys Ser Ala
 690 695 700
 Arg Val Met Lys Arg Ser Val Ala Ala Leu Ile Pro Tyr Ile Glu Glu
 705 710 715 720
 Glu Lys Ser Lys Asn Cys Asp Thr Ser Ala Lys Ala Lys Val Leu Leu
 725 730 735
 Ala Thr Val Lys Gly Asp Val His Asp Ile Gly Lys Asn Ile Val Ser
 740 745 750
 Val Val Leu Ala Cys Asn Asn Phe Asp Val Ile Asp Ile Gly Val Met
 755 760 765
 Met Pro Cys Asp Lys Ile Leu Glu Ala Leu Ala Glu His Lys Pro Asp

151

770 775 780
 Val Leu Gly Leu Ser Gly Leu Ile Thr Pro Ser Leu Glu Glu Met Ala
 785 790 795 800
 His Val Ala Lys Glu Met Glu Arg Leu Gly Met Asn Ile Pro Leu Ile
 805 810 815
 Ile Gly Gly Ala Thr Thr Ser Lys Val His Thr Ala Val Lys Leu Ala
 820 825 830
 Pro Cys Tyr Pro Ser Gly Ala Val Val His Val Leu Asp Ala Ser Arg
 835 840 845
 Ser Val Pro Val Val Ser Asn Leu Cys Asn Pro Ala Gln Arg Asp Ser
 850 855 860
 Tyr Ile Ala Ala Leu Lys Asp Glu Gln Glu Ala Met Arg Lys Ser His
 865 870 875 880
 Ala Glu Arg Met Ala Ala Lys Lys Tyr Val Ser Leu Asp Ala Ala Arg
 885 890 895
 Asp Asn Arg Leu Thr Ile Asp Trp Glu Ala Glu Thr Ile Asp Lys Pro
 900 905 910
 Ala Gln Thr Gly Val Thr Val Leu Glu Asp Val Thr Val Gly Ala Leu
 915 920 925
 Arg Pro Tyr Ile Asp Trp Ala Xaa Phe Phe Trp Ser Trp Glu Leu His
 930 935 940
 Gly Val Tyr Pro Gln Ile Leu Glu Asp Glu Lys Val Gly Glu Glu Ala
 945 950 955 960
 Thr Lys Leu Phe Asn Asp Ala Thr Ala Leu Leu Asp Arg Ile Asp Ser
 965 970 975
 Glu Lys Leu Leu Gly Ile Lys Gly Val Ala Gly Ile Phe Pro Ala Asn
 980 985 990
 Ser Ile Gly Asp Asp Ile Phe Val Tyr Ala Asp Asp Glu Arg Ser Ile
 995 1000 1005
 Ile Arg Thr Val Leu His Thr Leu Arg Gln Gln Gly Glu Lys His Gly
 1010 1015 1020
 Glu Ala Asn Leu Ala Leu Ala Asp Phe Val Ala Pro Arg Glu Ser Gly
 1025 1030 1035 1040
 Val Asn Asp Trp Ile Gly Cys Phe Thr Val Thr Ala Gly Leu Gly Ile
 1045 1050 1055
 Gln Asn Leu Leu Asp Glu Phe Thr Ala Glu Asn Asp Asp Tyr His Arg
 1060 1065 1070
 Ile Met Thr Gln Ala Leu Ala Asp Arg Leu Ala Glu Ala Phe Ala Glu
 1075 1080 1085
 Met Leu His Glu Lys Val Arg Arg Glu Leu Trp Gly Tyr Ala Pro Gly
 1090 1095 1100

152

Glu Ile Leu Gly Asn Glu Glu Leu Ile Ala Glu Lys Tyr Arg Gly Ile
 1105 1110 1115 1120

Arg Pro Ala Pro Gly Tyr Pro Ala Cys Pro Asp His Thr Glu Lys Ala
 1125 1130 1135

Ile Ile Phe Asp Leu Leu Asn Ala Glu Ala Ala Thr Gly Val Thr Leu
 1140 1145 1150

Thr Glu Thr Phe Ala Met Asn Pro Ala Ala Ser Val Cys Gly Leu Tyr
 1155 1160 1165

Phe Ala Asn Pro Ala Ser Lys Tyr Phe Val Leu Gly Lys Ile Gly Lys
 1170 1175 1180

Asp Gln Val Glu Asp Tyr Ala Asn Arg Lys Gly Leu Glu Val Ala Glu
 1185 1190 1195 1200

Ala Glu Lys Trp Leu Ala Pro Ser Leu Asn Tyr Asp Pro Ala
 1205 1210

<210> 35

<211> 3777

<212> DNA

<213> Deinococcus radiodurans

<220>

<221> CDS

<222> (1)..(3774)

<223> RDR02645

<400> 35

atg agc cat cac cca gaa gcg tgc gct tcc gcc aat ccg tcc atc aac 48
 Met Ser His His Pro Glu Ala Ser Ala Ser Ala Asn Pro Ser Ile Asn
 1 5 10 15

cat caa ccg tcc acc atc acc gag gcc gcc cgc cag cgc atc ctg att 96
 His Gln Pro Ser Thr Ile Thr Glu Ala Ala Arg Gln Arg Ile Leu Ile
 20 25 30

ctc gac ggc gcc tgg ggt acg cag ctt cag cga gcc aac ctc acc gaa 144
 Leu Asp Gly Ala Trp Gly Thr Gln Leu Gln Arg Ala Asn Leu Thr Glu
 35 40 45

gcg gac ttc cgc tgg gac gaa gcc gac ccc acg cgg atg tac cgg ggc 192
 Ala Asp Phe Arg Trp Asp Glu Ala Asp Pro Thr Arg Met Tyr Arg Gly
 50 55 60

aac ttc gac ctg ctg caa ctg acc aag cct gac gtg att cgc gcc gtg 240
 Asn Phe Asp Leu Leu Gln Leu Thr Lys Pro Asp Val Ile Arg Ala Val
 65 70 75 80

cac cgc gcc tat ttc gag gcc gga gcg gac atc gcc agc acc aat acc 288
 His Arg Ala Tyr Phe Glu Ala Gly Ala Asp Ile Ala Ser Thr Asn Thr
 85 90 95

ttc aac tcc acg acc atc tgc cag gcg gat tac ggc acc gag gca ctg 336
 Phe Asn Ser Thr Thr Ile Ser Gln Ala Asp Tyr Gly Thr Glu Ala Leu
 100 105 110

gcc tac gcc atg aac cgc gag ggg gca agg ctg gcc cgc gaa gtc gcc 384

153

| | |
|---|------|
| Ala Tyr Ala Met Asn Arg Glu Gly Ala Arg Leu Ala Arg Glu Val Ala | |
| 115 120 125 | |
| gac gag ttc gag gcg cgc gac ggc aaa aag cgc tgg gtg gcg ggg agt | 432 |
| Asp Glu Phe Glu Ala Arg Asp Gly Lys Lys Arg Trp Val Ala Gly Ser | |
| 130 135 140 | |
| gtc ggt ccc acc aac cgc acc gcg acc ctt tct ccc gac gtg gag cgg | 480 |
| Val Gly Pro Thr Asn Arg Thr Ala Thr Leu Ser Pro Asp Val Glu Arg | |
| 145 150 155 160 | |
| ccc gag ttc cgc aac gtg acc tac gac gac ctc gtg gcg gcg tac tcg | 528 |
| Pro Glu Phe Arg Asn Val Thr Tyr Asp Asp Leu Val Ala Ala Tyr Ser | |
| 165 170 175 | |
| gag gcc atc acc ggg ttg atg gaa ggt ggc gcg gac ctg ctg ctc att | 576 |
| Glu Ala Ile Thr Gly Leu Met Glu Gly Gly Ala Asp Leu Leu Leu Ile | |
| 180 185 190 | |
| gaa acg gtg ttt gac acg ctg aac gcc aaa gcc gcg ctg ttt gcc gcg | 624 |
| Glu Thr Val Phe Asp Thr Leu Asn Ala Lys Ala Ala Leu Phe Ala Ala | |
| 195 200 205 | |
| cag gac gtg ttc gcg gcg cag ggg cgc gag ctg ccg gtc atg ctc tcg | 672 |
| Gln Asp Val Phe Ala Ala Gln Gly Arg Glu Leu Pro Val Met Leu Ser | |
| 210 215 220 | |
| ggc acc atc acc gac gcc tcg ggc cgc acg ctg agc ggg cag acg ccc | 720 |
| Gly Thr Ile Thr Asp Ala Ser Gly Arg Thr Leu Ser Gly Gln Thr Pro | |
| 225 230 235 240 | |
| gaa gcc ttc gcg gtg agc acc gag cac gcc ggc ctc ttt tcg ctg ggc | 768 |
| Glu Ala Phe Ala Val Ser Thr Glu His Ala Gly Leu Phe Ser Leu Gly | |
| 245 250 255 | |
| ctg aac tgc gcg ctg ggc gcc gac ctg ctg cgg ccc cac ctg cgc gca | 816 |
| Leu Asn Cys Ala Leu Gly Ala Asp Leu Leu Arg Pro His Leu Arg Ala | |
| 260 265 270 | |
| att gcg gcg aac acg gag gcg ctg gtg tcg gtt cac ccc aac gcg ggc | 864 |
| Ile Ala Ala Asn Thr Glu Ala Leu Val Ser Val His Pro Asn Ala Gly | |
| 275 280 285 | |
| ctc ccc aac gcc ttc ggg gaa tac gac gaa acg ccc gaa cac acg gcg | 912 |
| Leu Pro Asn Ala Phe Gly Glu Tyr Asp Glu Thr Pro Glu His Thr Ala | |
| 290 295 300 | |
| gcg gtg ctg gcc gac ttc gcc cgc gag ggg ctg gtc aac atc gtg ggc | 960 |
| Ala Val Leu Ala Asp Phe Ala Arg Glu Gly Leu Val Asn Ile Val Gly | |
| 305 310 315 320 | |
| ggc tgc tgc ggc acc aca ccc gag cac atc aaa gcg att gcg gag gcg | 1008 |
| Gly Cys Cys Gly Thr Thr Pro Glu His Ile Lys Ala Ile Ala Glu Ala | |
| 325 330 335 | |
| gtg aag gac att ccc ccg cgc cag gcg ctg caa ctg ccg cct tac ctg | 1056 |
| Val Lys Asp Ile Pro Pro Arg Gln Ala Leu Gln Leu Pro Pro Tyr Leu | |
| 340 345 350 | |
| cgc ctc agc ggc ctc gaa gcc ttc acc ctg acg ccg gaa acc aac ttc | 1104 |
| Arg Leu Ser Gly Leu Glu Ala Phe Thr Leu Thr Pro Glu Thr Asn Phe | |
| 355 360 365 | |

154

| | |
|---|------|
| gtc aac gtg ggc gag cgc acc aac gtg acc ggc agt ccc aag ttc agc Val Asn Val Gly Glu Arg Thr Asn Val Thr Gly Ser Pro Lys Phe Ser 370 375 380 | 1152 |
| aag gcg att ctg gcc ggc gac tac gac gca ggg ctc aag att gcc cgc Lys Ala Ile Leu Ala Gly Asp Tyr Asp Ala Gly Leu Lys Ile Ala Arg 385 390 395 400 | 1200 |
| cag cag gtg acg aac ggc gcg caa atc gtg gac atc aac ttc gac gag Gln Gln Val Thr Asn Gly Ala Gln Ile Val Asp Ile Asn Phe Asp Glu 405 410 415 | 1248 |
| ggg atg ctc gac ggc gaa gga gcg atg gtc aag ttc ctc aac ctg ctc Gly Met Leu Asp Gly Glu Gly Ala Met Val Lys Phe Leu Asn Leu Leu 420 425 430 | 1296 |
| gcc ggg gag ccg gac atc tcg cgc gtg ccc ctg atg ctc gac tcg tcc Ala Gly Glu Pro Asp Ile Ser Arg Val Pro Leu Met Leu Asp Ser Ser 435 440 445 | 1344 |
| aag tgg gag att ctg gaa gcg ggg ctg cgg cgg gtg cag ggc aag gca Lys Trp Glu Ile Leu Glu Ala Gly Leu Arg Arg Val Gln Gly Lys Ala 450 455 460 | 1392 |
| gtc gtc aac tcc atc tcg ctc aag gac ggc gag gcc agg ttt ctg gaa Val Val Asn Ser Ile Ser Leu Lys Asp Gly Glu Ala Arg Phe Leu Glu 465 470 475 480 | 1440 |
| cgc gcc cgg ctg ctg cgg cgc tac ggg gcg gcg gcg gtg gtc atg gcc Arg Ala Arg Leu Leu Arg Arg Tyr Gly Ala Ala Ala Val Val Met Ala 485 490 495 | 1488 |
| ttc gac gaa cag gga cag gcc gac aac ctc gcc cga cgc cgg gag att Phe Asp Glu Gln Gly Gln Ala Asp Asn Leu Ala Arg Arg Arg Glu Ile 500 505 510 | 1536 |
| ctg ggc cgc gcg tat agg ctg ctg acc gag cag gcg gac ttt ccg ccg Leu Gly Arg Ala Tyr Arg Leu Leu Thr Glu Gln Ala Asp Phe Pro Pro 515 520 525 | 1584 |
| cag gac atc att ttc gac ccc aac gtg ctg acc gtt gcc acc ggc atc Gln Asp Ile Ile Phe Asp Pro Asn Val Leu Thr Val Ala Thr Gly Ile 530 535 540 | 1632 |
| gag gaa cac gac cgc tac gcg ctg gac ttt atc gag gcg acg cgc tgg Glu Glu His Asp Arg Tyr Ala Leu Asp Phe Ile Glu Ala Thr Arg Trp 545 550 555 560 | 1680 |
| att aaa gaa aac ctg ccg gcg gcg aag gtg tcg ggc ggg att tcc aac Ile Lys Glu Asn Leu Pro Ala Ala Lys Val Ser Gly Gly Ile Ser Asn 565 570 575 | 1728 |
| gtc tcg ttc agc ttc cgg ggc aac aac cac gtg cgc gag gcg atg cac Val Ser Phe Ser Phe Arg Gly Asn Asn His Val Arg Glu Ala Met His 580 585 590 | 1776 |
| gcg gtg ttt ctg tac cac gcc atc cgc gcc ggg ctg gac atg ggc atc Ala Val Phe Leu Tyr His Ala Ile Arg Ala Gly Leu Asp Met Gly Ile 595 600 605 | 1824 |
| gtg aac gcg ggg atg ctg gcg gtg tac gag gac atc gag ccg gag ctg | 1872 |

155

| | | | |
|---|-----|-----|----------|
| Val Asn Ala Gly Met Leu Ala Val Tyr Glu Asp Ile Glu Pro Glu Leu 610 | 615 | 620 | |
| cgc gag gcc gtc gag gac gtc att ctg gct cgc cgt ccg gac gcc acc Arg Glu Ala Val Glu Asp Val Ile Leu Ala Arg Arg Pro Asp Ala Thr 625 | 630 | 635 | 640 1920 |
| gag cgt ttg ctg acg ctg gcc gac cgc tac aag gac atc aag cgc gaa Glu Arg Leu Leu Thr Leu Ala Asp Arg Tyr Lys Asp Ile Lys Arg Glu 645 | 650 | 655 | 1968 |
| agt gcc gcc cag agc gcc tgg cgc gac ctg ccg gtg cag gaa cgg ctg Ser Ala Ala Gln Ser Ala Trp Arg Asp Leu Pro Val Gln Glu Arg Leu 660 | 665 | 670 | 2016 |
| cgg cac gca ctg gtg cag ggc gtc gcc gac cac gtg gat gag gac gcc Arg His Ala Leu Val Gln Gly Val Ala Asp His Val Asp Glu Asp Ala 675 | 680 | 685 | 2064 |
| gag gcc gcc tat cag gaa ctc ggc agc ccg ctg gcc gtc atc gaa ggc Glu Ala Ala Tyr Gln Glu Leu Gly Ser Pro Leu Ala Val Ile Glu Gly 690 | 695 | 700 | 2112 |
| ccg ctg atg gac ggc atg aac gtg gtg ggc gac ctc ttc ggc gcg ggg Pro Leu Met Asp Gly Met Asn Val Val Gly Asp Leu Phe Gly Ala Gly 705 | 710 | 715 | 720 2160 |
| aaa atg ttc ctg ccg cag gtg gtc aaa tcc gcc cgc gtg atg aaa aag Lys Met Phe Leu Pro Gln Val Val Lys Ser Ala Arg Val Met Lys Lys 725 | 730 | 735 | 2208 |
| gca gtg gcc tac ctc acg ccc tat ctg gaa gcg gag aag gcg gaa agc Ala Val Ala Tyr Leu Thr Pro Tyr Leu Glu Ala Glu Lys Ala Glu Ser 740 | 745 | 750 | 2256 |
| tcc agc aag ggc aag gta ctg ctg gcg acc gtc aag ggc gat gtg cac Ser Ser Lys Gly Lys Val Leu Leu Ala Thr Val Lys Gly Asp Val His 755 | 760 | 765 | 2304 |
| gac atc ggc aag aac atc gtg ggc gtg gtg ctc gcc tgc aac ggc tat Asp Ile Gly Lys Asn Ile Val Gly Val Val Leu Ala Cys Asn Gly Tyr 770 | 775 | 780 | 2352 |
| cag gtg acc gac ctc ggc gtg atg gtg ccg ggc gag aag att ctg gac Gln Val Thr Asp Leu Gly Val Met Val Pro Gly Glu Lys Ile Leu Asp 785 | 790 | 795 | 800 2400 |
| gaa gcc gag cgg ctc ggt gcc gac gtg atc ggt ctg agc ggg ctg att Glu Ala Glu Arg Leu Gly Ala Asp Val Ile Gly Leu Ser Gly Leu Ile 805 | 810 | 815 | 2448 |
| acg cct tcc tta gac gaa atg gtg aac gtg gcc cgc gag atg acg cgc Thr Pro Ser Leu Asp Glu Met Val Asn Val Ala Arg Glu Met Thr Arg 820 | 825 | 830 | 2496 |
| cgg ggc gtg aaa act cca ctg ctg atc ggc ggc gcg acg acc agc cgg Arg Gly Val Lys Thr Pro Leu Leu Ile Gly Gly Ala Thr Thr Ser Arg 835 | 840 | 845 | 2544 |
| gcg cac acg gcg gtc aag att gac ccg gcc tac gac ggg acg gta gtg Ala His Thr Ala Val Lys Ile Asp Pro Ala Tyr Asp Gly Thr Val Val 850 | 855 | 860 | 2592 |

156

| | |
|---|------|
| cac gtg ctg gac gcc agc cgc gcc gtg acc gtg acc aac gac ctg ctg His Val Leu Asp Ala Ser Arg Ala Val Thr Val Thr Asn Asp Leu Leu 865 870 875 880 | 2640 |
| acc gac gag gcc gcc tac gct ggg cgc gtg cag gcc gag tat gac acc Thr Asp Glu Ala Ala Tyr Ala Gly Arg Val Gln Gly Glu Tyr Asp Thr 885 890 895 | 2688 |
| ttg cgc gag cgc cac ggc gag cgg cag gtg cgg ctg att gcg ctg gca Leu Arg Glu Arg His Gly Glu Arg Gln Val Arg Leu Ile Ala Leu Ala 900 905 910 | 2736 |
| gaa gcc cgc gcc cgc gcc ccg caa ctg agt gcc gcc gtg ccc ccc gcg Glu Ala Arg Ala Arg Ala Pro Gln Leu Ser Ala Ala Val Pro Pro Ala 915 920 925 | 2784 |
| ccg cac gat ctg ggc cgt cag gtg gtc gaa cag ccc att gcc gag ctg Pro His Asp Leu Gly Arg Gln Val Val Glu Gln Pro Ile Ala Glu Leu 930 935 940 | 2832 |
| ctg ccc ttc atc gac tgg acg ccc ttt ttc atc gcc tgg gag atg aag Leu Pro Phe Ile Asp Trp Thr Pro Phe Phe Ile Ala Trp Glu Met Lys 945 950 955 960 | 2880 |
| ggc atc tac ccg ggc atc ctg acc gac cct ctg cgt ggc gag gag gcc Gly Ile Tyr Pro Gly Ile Leu Thr Asp Pro Leu Arg Gly Glu Glu Ala 965 970 975 | 2928 |
| cgc aag ctg ttt gcc gac gcg cag gcg ctg ctg gag cag gtt atc gcc Arg Lys Leu Phe Ala Asp Ala Gln Ala Leu Leu Glu Gln Val Ile Ala 980 985 990 | 2976 |
| gac gcc tcg ctg cgg gcg cgc gcc gtc atc ggg ctg tgg ccc gcg cac Asp Gly Ser Leu Arg Ala Arg Gly Val Ile Gly Leu Trp Pro Ala His 995 1000 1005 | 3024 |
| ggc gac gac atc gtg ctg gac gat gcg gcg atg ggg cgt gcc gag acg Gly Asp Asp Ile Val Leu Asp Asp Ala Ala Met Gly Arg Gly Glu Thr 1010 1015 1020 | 3072 |
| ctg gat ttc gag acg cac gaa ctc gcc gcc ggg cgc gag ccg ctg ccg Leu Asp Phe Glu Thr His Glu Leu Ala Ala Gly Arg Glu Pro Leu Pro 1025 1030 1035 1040 | 3120 |
| aac atg ccg cgc ctg cac acg ctg cgg cag cag cgc gac cag acc acg Asn Met Pro Arg Leu His Thr Leu Arg Gln Gln Arg Asp Gln Thr Thr 1045 1050 1055 | 3168 |
| ccg aac act gcg ctg gct gac ttt gtg gcg gaa gga gcc gac cac atc Pro Asn Thr Ala Leu Ala Asp Phe Val Ala Glu Gly Gly Asp His Ile 1060 1065 1070 | 3216 |
| ggc gcc ttc gcc acg gcc atc ttc ggc gcc gag gag ttg gcg cag cag Gly Ala Phe Ala Thr Ala Ile Phe Gly Ala Glu Glu Leu Ala Gln Gln 1075 1080 1085 | 3264 |
| ttc gag gcg cag cac gac gac tac aac tcg att ctg gtc aag gcg gtg Phe Glu Ala Gln His Asp Asp Tyr Asn Ser Ile Leu Val Lys Ala Val 1090 1095 1100 | 3312 |
| gcc gac cga ctg gcc gag gcc ttt gcc gag aag ctg cac cgc gac gtg | 3360 |

157

Ala Asp Arg Leu Ala Glu Ala Phe Ala Glu Lys Leu His Arg Asp Val
 1105 1110 1115 1120

cgc gtg cgg cac tgg ggt tac gcc gag ggc gag gcg ctc gac aac acc 3408
 Arg Val Arg His Trp Gly Tyr Ala Glu Gly Glu Ala Leu Asp Asn Thr
 1125 1130 1135

gac ctc atc aag gag cgc tat cag ggc atc cgc cct gcg ccc ggc tac 3456
 Asp Leu Ile Lys Glu Arg Tyr Gln Gly Ile Arg Pro Ala Pro Gly Tyr
 1140 1145 1150

ccc gcg cag ccc gac cac acc gag aaa cgc acc ctg ttt gag ctg ctg 3504
 Pro Ala Gln Pro Asp His Thr Glu Lys Arg Thr Leu Phe Glu Leu Leu
 1155 1160 1165

gac gcg gaa agc atc ggc ctg cgc ctc acc gag tcg tgt gcc atg acc 3552
 Asp Ala Glu Ser Ile Gly Leu Arg Leu Thr Glu Ser Cys Ala Met Thr
 1170 1175 1180

ccg gcg gcg gcg gtg tcg ggg ctg tac ttc gcg cat ccg gag gcc cgt 3600
 Pro Ala Ala Val Ser Gly Leu Tyr Phe Ala His Pro Glu Ala Arg
 1185 1190 1195 1200

tat ttc gca gtg ggc cgc atc ggg cgc gac cag gtg gag aac tac gcc 3648
 Tyr Phe Ala Val Gly Arg Ile Gly Arg Asp Gln Val Glu Asn Tyr Ala
 1205 1210 1215

gcc cgt aag ggt tgg act gtg cag gaa gcc gag cgc tgg ctg ggg ccg 3696
 Ala Arg Lys Gly Trp Thr Val Gln Glu Ala Glu Arg Trp Leu Gly Pro
 1220 1225 1230

ctg ctg gcg tac agc gcc ggg ccg ggg cca gaa gca agc cag aaa gcc 3744
 Leu Leu Ala Tyr Ser Ala Gly Pro Glu Ala Ser Gln Lys Ala
 1235 1240 1245

ctc ggc gca gag ctg aca gga gcg caa tcg tga 3777
 Leu Gly Ala Glu Leu Thr Gly Ala Gln Ser
 1250 1255

<210> 36

<211> 1258

<212> PRT

<213> Deinococcus radiodurans

<400> 36

Met Ser His His Pro Glu Ala Ser Ala Ser Ala Asn Pro Ser Ile Asn
 1 5 10 15

His Gln Pro Ser Thr Ile Thr Glu Ala Ala Arg Gln Arg Ile Leu Ile
 20 25 30

Leu Asp Gly Ala Trp Gly Thr Gln Leu Gln Arg Ala Asn Leu Thr Glu
 35 40 45

Ala Asp Phe Arg Trp Asp Glu Ala Asp Pro Thr Arg Met Tyr Arg Gly
 50 55 60

Asn Phe Asp Leu Leu Gln Leu Thr Lys Pro Asp Val Ile Arg Ala Val
 65 70 75 80

His Arg Ala Tyr Phe Glu Ala Gly Ala Asp Ile Ala Ser Thr Asn Thr

158

| 85 | 90 | 95 |
|--|-----|-----|
| Phe Asn Ser Thr Thr Ile Ser Gln Ala Asp Tyr Gly Thr Glu Ala Leu 100 | 105 | 110 |
| Ala Tyr Ala Met Asn Arg Glu Gly Ala Arg Leu Ala Arg Glu Val Ala 115 | 120 | 125 |
| Asp Glu Phe Glu Ala Arg Asp Gly Lys Lys Arg Trp Val Ala Gly Ser 130 | 135 | 140 |
| Val Gly Pro Thr Asn Arg Thr Ala Thr Leu Ser Pro Asp Val Glu Arg 145 | 150 | 155 |
| Pro Glu Phe Arg Asn Val Thr Tyr Asp Asp Leu Val Ala Ala Tyr Ser 165 | 170 | 175 |
| Glu Ala Ile Thr Gly Leu Met Glu Gly Gly Ala Asp Leu Leu Leu Ile 180 | 185 | 190 |
| Glu Thr Val Phe Asp Thr Leu Asn Ala Lys Ala Ala Leu Phe Ala Ala 195 | 200 | 205 |
| Gln Asp Val Phe Ala Ala Gln Gly Arg Glu Leu Pro Val Met Leu Ser 210 | 215 | 220 |
| Gly Thr Ile Thr Asp Ala Ser Gly Arg Thr Leu Ser Gly Gln Thr Pro 225 | 230 | 235 |
| Glu Ala Phe Ala Val Ser Thr Glu His Ala Gly Leu Phe Ser Leu Gly 245 | 250 | 255 |
| Leu Asn Cys Ala Leu Gly Ala Asp Leu Leu Arg Pro His Leu Arg Ala 260 | 265 | 270 |
| Ile Ala Ala Asn Thr Glu Ala Leu Val Ser Val His Pro Asn Ala Gly 275 | 280 | 285 |
| Leu Pro Asn Ala Phe Gly Glu Tyr Asp Glu Thr Pro Glu His Thr Ala 290 | 295 | 300 |
| Ala Val Leu Ala Asp Phe Ala Arg Glu Gly Leu Val Asn Ile Val Gly 305 | 310 | 315 |
| Gly Cys Cys Gly Thr Thr Pro Glu His Ile Lys Ala Ile Ala Glu Ala 325 | 330 | 335 |
| Val Lys Asp Ile Pro Pro Arg Gln Ala Leu Gln Leu Pro Pro Tyr Leu 340 | 345 | 350 |
| Arg Leu Ser Gly Leu Glu Ala Phe Thr Leu Thr Pro Glu Thr Asn Phe 355 | 360 | 365 |
| Val Asn Val Gly Glu Arg Thr Asn Val Thr Gly Ser Pro Lys Phe Ser 370 | 375 | 380 |
| Lys Ala Ile Leu Ala Gly Asp Tyr Asp Ala Gly Leu Lys Ile Ala Arg 385 | 390 | 395 |
| Gln Gln Val Thr Asn Gly Ala Gln Ile Val Asp Ile Asn Phe Asp Glu 405 | 410 | 415 |

159

Gly Met Leu Asp Gly Glu Gly Ala Met Val Lys Phe Leu Asn Leu Leu
 420 425 430
 Ala Gly Glu Pro Asp Ile Ser Arg Val Pro Leu Met Leu Asp Ser Ser
 435 440 445
 Lys Trp Glu Ile Leu Glu Ala Gly Leu Arg Arg Val Gln Gly Lys Ala
 450 455 460
 Val Val Asn Ser Ile Ser Leu Lys Asp Gly Glu Ala Arg Phe Leu Glu
 465 470 475 480
 Arg Ala Arg Leu Leu Arg Arg Tyr Gly Ala Ala Val Val Met Ala
 485 490 495
 Phe Asp Glu Gln Gly Gln Ala Asp Asn Leu Ala Arg Arg Arg Glu Ile
 500 505 510
 Leu Gly Arg Ala Tyr Arg Leu Leu Thr Glu Gln Ala Asp Phe Pro Pro
 515 520 525
 Gln Asp Ile Ile Phe Asp Pro Asn Val Leu Thr Val Ala Thr Gly Ile
 530 535 540
 Glu Glu His Asp Arg Tyr Ala Leu Asp Phe Ile Glu Ala Thr Arg Trp
 545 550 555 560
 Ile Lys Glu Asn Leu Pro Ala Ala Lys Val Ser Gly Gly Ile Ser Asn
 565 570 575
 Val Ser Phe Ser Phe Arg Gly Asn Asn His Val Arg Glu Ala Met His
 580 585 590
 Ala Val Phe Leu Tyr His Ala Ile Arg Ala Gly Leu Asp Met Gly Ile
 595 600 605
 Val Asn Ala Gly Met Leu Ala Val Tyr Glu Asp Ile Glu Pro Glu Leu
 610 615 620
 Arg Glu Ala Val Glu Asp Val Ile Leu Ala Arg Arg Pro Asp Ala Thr
 625 630 635 640
 Glu Arg Leu Leu Thr Leu Ala Asp Arg Tyr Lys Asp Ile Lys Arg Glu
 645 650 655
 Ser Ala Ala Gln Ser Ala Trp Arg Asp Leu Pro Val Gln Glu Arg Leu
 660 665 670
 Arg His Ala Leu Val Gln Gly Val Ala Asp His Val Asp Glu Asp Ala
 675 680 685
 Glu Ala Ala Tyr Gln Glu Leu Gly Ser Pro Leu Ala Val Ile Glu Gly
 690 695 700
 Pro Leu Met Asp Gly Met Asn Val Val Gly Asp Leu Phe Gly Ala Gly
 705 710 715 720
 Lys Met Phe Leu Pro Gln Val Val Lys Ser Ala Arg Val Met Lys Lys
 725 730 735
 Ala Val Ala Tyr Leu Thr Pro Tyr Leu Glu Ala Glu Lys Ala Glu Ser
 740 745 750

160

Ser Ser Lys Gly Lys Val Leu Leu Ala Thr Val Lys Gly Asp Val His
 755 760 765
 Asp Ile Gly Lys Asn Ile Val Gly Val Val Leu Ala Cys Asn Gly Tyr
 770 775 780
 Gln Val Thr Asp Leu Gly Val Met Val Pro Gly Glu Lys Ile Leu Asp
 785 790 795 800
 Glu Ala Glu Arg Leu Gly Ala Asp Val Ile Gly Leu Ser Gly Leu Ile
 805 810 815
 Thr Pro Ser Leu Asp Glu Met Val Asn Val Ala Arg Glu Met Thr Arg
 820 825 830
 Arg Gly Val Lys Thr Pro Leu Leu Ile Gly Gly Ala Thr Thr Ser Arg
 835 840 845
 Ala His Thr Ala Val Lys Ile Asp Pro Ala Tyr Asp Gly Thr Val Val
 850 855 860
 His Val Leu Asp Ala Ser Arg Ala Val Thr Val Thr Asn Asp Leu Leu
 865 870 875 880
 Thr Asp Glu Ala Ala Tyr Ala Gly Arg Val Gln Gly Glu Tyr Asp Thr
 885 890 895
 Leu Arg Glu Arg His Gly Glu Arg Gln Val Arg Leu Ile Ala Leu Ala
 900 905 910
 Glu Ala Arg Ala Arg Ala Pro Gln Leu Ser Ala Ala Val Pro Pro Ala
 915 920 925
 Pro His Asp Leu Gly Arg Gln Val Val Glu Gln Pro Ile Ala Glu Leu
 930 935 940
 Leu Pro Phe Ile Asp Trp Thr Pro Phe Phe Ile Ala Trp Glu Met Lys
 945 950 955 960
 Gly Ile Tyr Pro Gly Ile Leu Thr Asp Pro Leu Arg Gly Glu Glu Ala
 965 970 975
 Arg Lys Leu Phe Ala Asp Ala Gln Ala Leu Leu Glu Gln Val Ile Ala
 980 985 990
 Asp Gly Ser Leu Arg Ala Arg Gly Val Ile Gly Leu Trp Pro Ala His
 995 1000 1005
 Gly Asp Asp Ile Val Leu Asp Asp Ala Ala Met Gly Arg Gly Glu Thr
 1010 1015 1020
 Leu Asp Phe Glu Thr His Glu Leu Ala Ala Gly Arg Glu Pro Leu Pro
 1025 1030 1035 1040
 Asn Met Pro Arg Leu His Thr Leu Arg Gln Gln Arg Asp Gln Thr Thr
 1045 1050 1055
 Pro Asn Thr Ala Leu Ala Asp Phe Val Ala Glu Gly Gly Asp His Ile
 1060 1065 1070
 Gly Ala Phe Ala Thr Ala Ile Phe Gly Ala Glu Glu Leu Ala Gln Gln

161

1075 1080 1085
 Phe Glu Ala Gln His Asp Asp Tyr Asn Ser Ile Leu Val Lys Ala Val
 1090 1095 1100
 Ala Asp Arg Leu Ala Glu Ala Phe Ala Glu Lys Leu His Arg Asp Val
 1105 1110 1115 1120
 Arg Val Arg His Trp Gly Tyr Ala Glu Gly Glu Ala Leu Asp Asn Thr
 1125 1130 1135
 Asp Leu Ile Lys Glu Arg Tyr Gln Gly Ile Arg Pro Ala Pro Gly Tyr
 1140 1145 1150
 Pro Ala Gln Pro Asp His Thr Glu Lys Arg Thr Leu Phe Glu Leu Leu
 1155 1160 1165
 Asp Ala Glu Ser Ile Gly Leu Arg Leu Thr Glu Ser Cys Ala Met Thr
 1170 1175 1180
 Pro Ala Ala Ala Val Ser Gly Leu Tyr Phe Ala His Pro Glu Ala Arg
 1185 1190 1195 1200
 Tyr Phe Ala Val Gly Arg Ile Gly Arg Asp Gln Val Glu Asn Tyr Ala
 1205 1210 1215
 Ala Arg Lys Gly Trp Thr Val Gln Glu Ala Glu Arg Trp Leu Gly Pro
 1220 1225 1230
 Leu Leu Ala Tyr Ser Ala Gly Pro Gly Pro Glu Ala Ser Gln Lys Ala
 1235 1240 1245
 Leu Gly Ala Glu Leu Thr Gly Ala Gln Ser
 1250 1255

 <210> 37
 <211> 3642
 <212> DNA
 <213> Clostridium acetobutylicum

 <220>
 <221> CDS
 <222> (1) .. (3639)
 <223> RCA01265

 <400> 37
 ctt atg aat tct tca cta aag aat ttg tta aat aac aaa att tta gtt 48
 Leu Met Asn Ser Ser Leu Lys Asn Leu Leu Asn Asn Lys Ile Leu Val
 1 5 10 15
 tta gat ggt gct atg gga aca tgt att caa tcc ttt aat cta gat gaa 96
 Leu Asp Gly Ala Met Gly Thr Cys Ile Gln Ser Phe Asn Leu Asp Glu
 20 25 30
 ggc gac ttt aaa ggt tcc tta tct tgt aca tgt cat tcc aat caa aaa 144
 Gly Asp Phe Lys Gly Ser Leu Ser Cys Thr Cys His Ser Asn Gln Lys
 35 40 45
 gga aac aat gat gtt tta aat tta acc aag cca gaa ata ata aaa gaa 192
 Gly Asn Asn Asp Val Leu Asn Leu Thr Lys Pro Glu Ile Ile Lys Glu
 50 55 60

162

atc cac aag aga tac ctt gaa gct ggc gca gat ata ata gaa aca aac 240
 Ile His Lys Arg Tyr Leu Glu Ala Gly Ala Asp Ile Ile Glu Thr Asn
 65 70 75 80

act ttt aac gct act gaa ata tca caa aaa gat tat aat atg caa gat 288
 Thr Phe Asn Ala Thr Glu Ile Ser Gln Lys Asp Tyr Asn Met Gln Asp
 85 90 95

aaa ata tat gat att aat ttt aag ggg gca aaa ctc gca aag gaa gct 336
 Lys Ile Tyr Asp Ile Asn Phe Lys Gly Ala Lys Leu Ala Lys Glu Ala
 100 105 110

tgt act tac tac aca aaa cta aat cct aat aag cct aga ttt gct gct 384
 Cys Thr Tyr Tyr Thr Lys Leu Asn Pro Asn Lys Pro Arg Phe Ala Ala
 115 120 125

ggt tct att ggg cct aca aat aga act gct tct cta tct cca gat gtt 432
 Gly Ser Ile Gly Pro Thr Asn Arg Thr Ala Ser Leu Ser Pro Asp Val
 130 135 140

gaa aat cct ggt ttt aga aat gta acc ttt gat gag cta tgt aat gcc 480
 Glu Asn Pro Gly Phe Arg Asn Val Thr Phe Asp Glu Leu Cys Asn Ala
 145 150 155 160

tat aaa cat caa ata gag gct cta ata gat gga ggt gta gac ctt ctt 528
 Tyr Lys His Gln Ile Glu Ala Leu Ile Asp Gly Gly Val Asp Leu Leu
 165 170 175

tta att gaa act ata ttt gat act tta aac gct aga gca gca atc ttt 576
 Leu Ile Glu Thr Ile Phe Asp Thr Leu Asn Ala Arg Ala Ala Ile Phe
 180 185 190

gca gca gaa aca gta ttt gaa aat aaa aaa ata aaa ctt cct att ata 624
 Ala Ala Glu Thr Val Phe Glu Asn Lys Lys Ile Lys Leu Pro Ile Ile
 195 200 205

att tca ggg aca ata gct gat aaa agt gga aga ata tta tcc ggt caa 672
 Ile Ser Gly Thr Ile Ala Asp Lys Ser Gly Arg Ile Leu Ser Gly Gln
 210 215 220

act ctt gac gct ttt gca gaa agt tta aaa aac gaa aat ata att gct 720
 Thr Leu Asp Ala Phe Ala Glu Ser Leu Lys Asn Glu Asn Ile Ile Ala
 225 230 235 240

ata ggg ctt aat tgt tcc ttt ggt gct gaa gaa ctt ata cct ttt ata 768
 Ile Gly Leu Asn Cys Ser Phe Gly Ala Glu Glu Leu Ile Pro Phe Ile
 245 250 255

aaa aga ctc tct gaa aca caa aat aga tat ata tcc ttt cat cca aac 816
 Lys Arg Leu Ser Glu Thr Gln Asn Arg Tyr Ile Ser Phe His Pro Asn
 260 265 270

gca gga ctt cca aac tcc ctt ggt gaa tat gaa gaa ctg cca gag gaa 864
 Ala Gly Leu Pro Asn Ser Leu Gly Glu Tyr Glu Glu Leu Pro Glu Glu
 275 280 285

act gct agc att gta aaa aaa tta gca ctt gaa gga cat tta aat ata 912
 Thr Ala Ser Ile Val Lys Lys Leu Ala Leu Glu Gly His Leu Asn Ile
 290 295 300

gtt gga ggc tgc tgt ggc act aca cca gaa cat ata aga gca ata agc 960

| | | | | | | | | | | | | | | | | | | |
|---|--|--|--|--|-----|--|--|-----|-----|-----|--|--|--|--|--|--|------|--|
| 163 | | | | | | | | | | | | | | | | | | |
| Val Gly Gly Cys Cys Gly Thr Thr Pro Glu His Ile Arg Ala Ile Ser | | | | | | | | | | | | | | | | | | |
| 305 | | | | | 310 | | | | | 315 | | | | | | | 320 | |
| agc gta gtt aaa ggc att tct cca aga aaa gtt cca aac ttg gaa ccc | | | | | | | | | | | | | | | | | 1008 | |
| Ser Val Val Lys Gly Ile Ser Pro Arg Lys Val Pro Asn Leu Glu Pro | | | | | 325 | | | | 330 | | | | | | | | 335 | |
| aaa aca att tac agc gga cta gaa aac ata aaa att gat aag aac agt | | | | | | | | | | | | | | | | | 1056 | |
| Lys Thr Ile Tyr Ser Gly Leu Glu Asn Ile Lys Ile Asp Lys Asn Ser | | | | | 340 | | | 345 | | | | | | | | | 350 | |
| aac ttc ata aat ata ggc gaa aga aca aat gta gcg ggc tca aga aaa | | | | | | | | | | | | | | | | | 1104 | |
| Asn Phe Ile Asn Ile Gly Glu Arg Thr Asn Val Ala Gly Ser Arg Lys | | | | | 355 | | | 360 | | | | | | | | | 365 | |
| ttc gca agg ctt ata cgt gaa aaa aat tat gag gag gct cta acc att | | | | | | | | | | | | | | | | | 1152 | |
| Phe Ala Arg Leu Ile Arg Glu Lys Asn Tyr Glu Glu Ala Leu Thr Ile | | | | | 370 | | | 375 | | | | | | | | | 380 | |
| gca aga cat cag gtt gaa aat ggt gcc caa att ata gat ata aat ttt | | | | | | | | | | | | | | | | | 1200 | |
| Ala Arg His Gln Val Glu Asn Gly Ala Gln Ile Ile Asp Ile Asn Phe | | | | | 385 | | | | | 395 | | | | | | | 400 | |
| gat gat gca ctt tta gat gct cgc tct gaa atg gaa aca ttt tta aga | | | | | | | | | | | | | | | | | 1248 | |
| Asp Asp Ala Leu Leu Asp Ala Arg Ser Glu Met Glu Thr Phe Leu Arg | | | | | 405 | | | | 410 | | | | | | | | 415 | |
| ctt att gca agt gaa cct gaa ata tca aaa gtt cca gtt atg ata gac | | | | | | | | | | | | | | | | | 1296 | |
| Leu Ile Ala Ser Glu Pro Glu Ile Ser Lys Val Pro Val Met Ile Asp | | | | | 420 | | | 425 | | | | | | | | | 430 | |
| tcc tct aat ttt gaa gtt tta aaa gtt gga tta aag tct att caa ggt | | | | | | | | | | | | | | | | | 1344 | |
| Ser Ser Asn Phe Glu Val Leu Lys Val Gly Leu Lys Ser Ile Gln Gly | | | | | 435 | | | 440 | | | | | | | | | 445 | |
| aaa gcc ata gta aat tcc ata agt ctt aag gtt gga gaa gaa aag ttc | | | | | | | | | | | | | | | | | 1392 | |
| Lys Ala Ile Val Asn Ser Ile Ser Leu Lys Val Gly Glu Glu Lys Phe | | | | | 450 | | | 455 | | | | | | | | | 460 | |
| att gaa gag gca aaa ttt ata aag aac ttt ggc gct ggc gta gtt gta | | | | | | | | | | | | | | | | | 1440 | |
| Ile Glu Glu Ala Lys Phe Ile Lys Asn Phe Gly Ala Gly Val Val Val | | | | | 465 | | | | | 475 | | | | | | | 480 | |
| atg gcc ttt gac gaa gaa ggt caa gca gct act tat gaa aga aaa att | | | | | | | | | | | | | | | | | 1488 | |
| Met Ala Phe Asp Glu Glu Gly Gln Ala Ala Thr Tyr Glu Arg Lys Ile | | | | | 485 | | | | 490 | | | | | | | | 495 | |
| gaa atc tgc aag aga gct tat act att ctc aca gaa aaa gtt gag ttt | | | | | | | | | | | | | | | | | 1536 | |
| Glu Ile Cys Lys Arg Ala Tyr Thr Ile Leu Thr Glu Lys Val Glu Phe | | | | | 500 | | | 505 | | | | | | | | | 510 | |
| cca cct gaa aat ata ata ttt gat cca aat ata cta tct ata gcg aca | | | | | | | | | | | | | | | | | 1584 | |
| Pro Pro Glu Asn Ile Ile Phe Asp Pro Asn Ile Leu Ser Ile Ala Thr | | | | | 515 | | | 520 | | | | | | | | | 525 | |
| gga att gaa gaa cat gac aac tat gca gtt aat tac ata aaa gct gtt | | | | | | | | | | | | | | | | | 1632 | |
| Gly Ile Glu Glu His Asp Asn Tyr Ala Val Asn Tyr Ile Lys Ala Val | | | | | 530 | | | 535 | | | | | | | | | 540 | |
| aaa tgg ata aaa gag aat cta cca tac gct aaa gtc agc ggt gga gtt | | | | | | | | | | | | | | | | | 1680 | |
| Lys Trp Ile Lys Glu Asn Leu Pro Tyr Ala Lys Val Ser Gly Gly Val | | | | | | | | | | | | | | | | | | |

164

| | |
|---|------|
| agc aac ctc tcc ttt tct ttt agg ggt aat gac gca ata aga aga gct Ser Asn Leu Ser Phe Ser Phe Arg Gly Asn Asp Ala Ile Arg Arg Ala 565 570 575 | 1728 |
| atg cat tct gtt ttc ctt tac cat gca ata aac gct gga atg gat atg Met His Ser Val Phe Leu Tyr His Ala Ile Asn Ala Gly Met Asp Met 580 585 590 | 1776 |
| ggt att gtt aat cca gca atg att gat tta tat gac gat ata gat aag Gly Ile Val Asn Pro Ala Met Ile Asp Leu Tyr Asp Asp Ile Asp Lys 595 600 605 | 1824 |
| gat ctt ctc gaa aag gtt gag aat gtt gta cta aat aaa tca tct aac Asp Leu Leu Glu Lys Val Glu Asn Val Val Leu Asn Lys Ser Ser Asn 610 615 620 | 1872 |
| gct tct gaa tca tta cta gaa ttt gct caa acg tat aaa aag acg act Ala Ser Glu Ser Leu Leu Glu Phe Ala Gln Thr Tyr Lys Lys Thr Thr 625 630 635 640 | 1920 |
| gaa acc tta gaa aag cac gag gat gaa tgg cga caa aaa agc cca agt Glu Thr Leu Glu Lys His Glu Asp Glu Trp Arg Gln Lys Ser Pro Ser 645 650 655 | 1968 |
| gaa agg ttg agt tat gct tta gtt aaa gga aat gtt gaa ttt att gaa Glu Arg Leu Ser Tyr Ala Leu Val Lys Gly Asn Val Glu Phe Ile Glu 660 665 670 | 2016 |
| gaa gat ata gaa gaa gca aga aaa gag tat aca aat gca ctt gaa att Glu Asp Ile Glu Glu Ala Arg Lys Glu Tyr Thr Asn Ala Leu Glu Ile 675 680 685 | 2064 |
| ata gag gtt cct tta atg aat gga atg aaa aaa gtg ggt aaa ctt ttt Ile Glu Val Pro Leu Met Asn Gly Met Lys Lys Val Gly Lys Leu Phe 690 695 700 | 2112 |
| gga gag gga aaa atg ttt ctt cct caa gta gta aaa agt gct aga gtt Gly Glu Gly Lys Met Phe Leu Pro Gln Val Val Lys Ser Ala Arg Val 705 710 715 720 | 2160 |
| atg aaa aag gct gtt gaa tgt ctt ctt ccc tat ata aac gaa gaa aag Met Lys Lys Ala Val Glu Cys Leu Leu Pro Tyr Ile Asn Glu Glu Lys 725 730 735 | 2208 |
| tct aaa aat cac aat aaa agt gct ggt aag gtt gta ttt gca act gtt Ser Lys Asn His Asn Lys Ser Ala Gly Lys Val Val Phe Ala Thr Val 740 745 750 | 2256 |
| aaa ggc gat gtt cat gac ata ggc aaa aat atc gta tct gta gtt ctt Lys Gly Asp Val His Asp Ile Gly Lys Asn Ile Val Ser Val Val Leu 755 760 765 | 2304 |
| tcc tgc aac aat ttt gaa gtt ata gat tta gga gta atg gtt ccc cct Ser Cys Asn Asn Phe Glu Val Ile Asp Leu Gly Val Met Val Pro Pro 770 775 780 | 2352 |
| gaa acc ata ctt gaa acg gca aaa cgt gaa aat gca gat atc att gct Glu Thr Ile Leu Glu Thr Ala Lys Arg Glu Asn Ala Asp Ile Ile Ala 785 790 795 800 | 2400 |
| tta agt ggt tta att aca cct tct ctt aat gaa atg gct tat gta gct | 2448 |

165

| | |
|---|------|
| Leu Ser Gly Leu Ile Thr Pro Ser Leu Asn Glu Met Ala Tyr Val Ala | |
| 805 810 815 | |
| gaa gaa atg aaa agg ctt aat ttt gat ata cca ctt atg gtg ggt ggt | 2496 |
| Glu Glu Met Lys Arg Leu Asn Phe Asp Ile Pro Leu Met Val Gly Gly | |
| 820 825 830 | |
| gct gct acc tca aaa act cac aca gct tta aaa cta gct acg aaa tat | 2544 |
| Ala Ala Thr Ser Lys Thr His Thr Ala Leu Lys Leu Ala Thr Lys Tyr | |
| 835 840 845 | |
| aaa tat gta gta cac agt act gat gct tca gat gct gtt acc gta gcc | 2592 |
| Lys Tyr Val Val His Ser Thr Asp Ala Ser Asp Ala Val Thr Val Ala | |
| 850 855 860 | |
| aaa aat cta atg agt gaa aac aaa ttt act ttc tta gaa aaa tta aat | 2640 |
| Lys Asn Leu Met Ser Glu Asn Lys Phe Thr Phe Leu Glu Lys Leu Asn | |
| 865 870 875 880 | |
| gaa gag tat tct aaa ata aga gag acc ttc tct act aat aag att gaa | 2688 |
| Glu Glu Tyr Ser Lys Ile Arg Glu Thr Phe Ser Thr Asn Lys Ile Glu | |
| 885 890 895 | |
| ctt atc tcc att caa aac gca aga aaa aac aga ttt act att gac tgg | 2736 |
| Leu Ile Ser Ile Gln Asn Ala Arg Lys Asn Arg Phe Thr Ile Asp Trp | |
| 900 905 910 | |
| aat aaa act aaa ata act gaa cct aaa ttt gtc ggt ata aaa aaa tta | 2784 |
| Asn Lys Thr Lys Ile Thr Glu Pro Lys Phe Val Gly Ile Lys Lys Leu | |
| 915 920 925 | |
| caa gct gta cct ata aat gaa tta aga aag tat ata gat tgg act ttc | 2832 |
| Gln Ala Val Pro Ile Asn Glu Leu Arg Lys Tyr Ile Asp Trp Thr Phe | |
| 930 935 940 | |
| ttc ttt acg tct tgg gat atg gga atg aat tac ccc aaa ata atg aaa | 2880 |
| Phe Phe Thr Ser Trp Asp Met Gly Met Asn Tyr Pro Lys Ile Met Lys | |
| 945 950 955 960 | |
| gat cct aaa tac gga gct gaa gct caa aaa ctc ttt aag gat gcc aat | 2928 |
| Asp Pro Lys Tyr Gly Ala Glu Ala Gln Lys Leu Phe Lys Asp Ala Asn | |
| 965 970 975 | |
| gaa atg ctt gat tta ttg caa aaa gaa aat tta atc act tgt aat gga | 2976 |
| Glu Met Leu Asp Leu Leu Gln Lys Glu Asn Leu Ile Thr Cys Asn Gly | |
| 980 985 990 | |
| gtt ttt gga ata ttc cca gct aat tct gtt aat gat gat ata gaa atc | 3024 |
| Val Phe Gly Ile Phe Pro Ala Asn Ser Val Asn Asp Asp Ile Glu Ile | |
| 995 1000 1005 | |
| tac act gat aaa gga act gta acc ata aat act ctt cgt cag cag cag | 3072 |
| Tyr Thr Asp Lys Gly Thr Val Thr Ile Asn Thr Leu Arg Gln Gln Gln | |
| 1010 1015 1020 | |
| ata ctt aaa gac agc gat tat aaa gct cta tct gat tat atc gct cca | 3120 |
| Ile Leu Lys Asp Ser Asp Tyr Lys Ala Leu Ser Asp Tyr Ile Ala Pro | |
| 1025 1030 1035 1040 | |
| aag ggt att ggc atc aaa gat tat ata ggt ggt ttt att gta act gct | 3168 |
| Lys Gly Ile Gly Ile Lys Asp Tyr Ile Gly Gly Phe Ile Val Thr Ala | |
| 1045 1050 1055 | |

166

gga ata ggt gca aag gaa tat tcc gat aaa tta aag aaa aaa tgc gac 3216
 Gly Ile Gly Ala Lys Glu Tyr Ser Asp Lys Leu Lys Lys Lys Cys Asp
 1060 1065 1070

gat tat gga gct act atg ctt aaa ctt ata tgc gat aga ctt gca gag 3264
 Asp Tyr Gly Ala Thr Met Leu Lys Leu Ile Cys Asp Arg Leu Ala Glu
 1075 1080 1085

gcc ttt tca gaa ctt ctt cac cta agg gta aga aaa gaa tac tgg gga 3312
 Ala Phe Ser Glu Leu Leu His Leu Arg Val Arg Lys Glu Tyr Trp Gly
 1090 1095 1100

tac tct caa gat gaa aac tta tcc tta gaa aaa ctt ctt aaa gga agt 3360
 Tyr Ser Gln Asp Glu Asn Leu Ser Leu Glu Lys Leu Leu Lys Gly Ser
 1105 1110 1115 1120

tac aga ggg ata aaa cca gct att gga tat cct tct att ccc gat cac 3408
 Tyr Arg Gly Ile Lys Pro Ala Ile Gly Tyr Pro Ser Ile Pro Asp His
 1125 1130 1135

tct gaa aaa gca aag tta ttt gat tta ctt tta ggt aaa act tca ata 3456
 Ser Glu Lys Ala Lys Leu Phe Asp Leu Leu Leu Gly Lys Thr Ser Ile
 1140 1145 1150

gga gtg gaa ttg acg gaa agt tat atg atg aat cca act tca agt gta 3504
 Gly Val Glu Leu Thr Glu Ser Tyr Met Met Asn Pro Thr Ser Ser Val
 1155 1160 1165

tgc ggt ttg tat ttt gca aat gaa cga gca aaa tac ttt aat ata aat 3552
 Cys Gly Leu Tyr Phe Ala Asn Glu Arg Ala Lys Tyr Phe Asn Ile Asn
 1170 1175 1180

aaa ata gga aaa gat caa ctt gag gac tat gct gtt cga agt aat aaa 3600
 Lys Ile Gly Lys Asp Gln Leu Glu Asp Tyr Ala Val Arg Ser Asn Lys
 1185 1190 1195 1200

gac att aat gaa ata aaa aaa tta tta gat act ctg tta taa 3642
 Asp Ile Asn Glu Ile Lys Lys Leu Leu Asp Thr Leu Leu
 1205 1210

<210> 38
 <211> 1213
 <212> PRT
 <213> Clostridium acetobutylicum

<400> 38
 Leu Met Asn Ser Ser Leu Lys Asn Leu Leu Asn Asn Lys Ile Leu Val
 1 5 10 15
 Leu Asp Gly Ala Met Gly Thr Cys Ile Gln Ser Phe Asn Leu Asp Glu
 20 25 30
 Gly Asp Phe Lys Gly Ser Leu Ser Cys Thr Cys His Ser Asn Gln Lys
 35 40 45
 Gly Asn Asn Asp Val Leu Asn Leu Thr Lys Pro Glu Ile Ile Lys Glu
 50 55 60
 Ile His Lys Arg Tyr Leu Glu Ala Gly Ala Asp Ile Ile Glu Thr Asn
 65 70 75 80

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| Thr | Phe | Asn | Ala | Thr | Glu | Ile | Ser | Gln | Lys | Asp | Tyr | Asn | Met | Gln | Asp | |
| | | | | | | | | | | | | | | | | 85 |
| | | | | | | | | | | | | | | | | 90 |
| | | | | | | | | | | | | | | | | 95 |
| Lys | Ile | Tyr | Asp | Ile | Asn | Phe | Lys | Gly | Ala | Lys | Leu | Ala | Lys | Glu | Ala | |
| | | | 100 | | | | | 105 | | | | | | 110 | | |
| Cys | Thr | Tyr | Tyr | Thr | Lys | Leu | Asn | Pro | Asn | Lys | Pro | Arg | Phe | Ala | Ala | |
| | | | 115 | | | | 120 | | | | | 125 | | | | |
| Gly | Ser | Ile | Gly | Pro | Thr | Asn | Arg | Thr | Ala | Ser | Leu | Ser | Pro | Asp | Val | |
| | | 130 | | | | 135 | | | | | | 140 | | | | |
| Glu | Asn | Pro | Gly | Phe | Arg | Asn | Val | Thr | Phe | Asp | Glu | Leu | Cys | Asn | Ala | |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 | |
| Tyr | Lys | His | Gln | Ile | Glu | Ala | Leu | Ile | Asp | Gly | Gly | Val | Asp | Leu | Leu | |
| | | | | 165 | | | | | 170 | | | | | 175 | | |
| Leu | Ile | Glu | Thr | Ile | Phe | Asp | Thr | Leu | Asn | Ala | Arg | Ala | Ala | Ile | Phe | |
| | | | 180 | | | | | 185 | | | | | | 190 | | |
| Ala | Ala | Glu | Thr | Val | Phe | Glu | Asn | Lys | Lys | Ile | Lys | Leu | Pro | Ile | Ile | |
| | | 195 | | | | | 200 | | | | | 205 | | | | |
| Ile | Ser | Gly | Thr | Ile | Ala | Asp | Lys | Ser | Gly | Arg | Ile | Leu | Ser | Gly | Gln | |
| | 210 | | | | | 215 | | | | | 220 | | | | | |
| Thr | Leu | Asp | Ala | Phe | Ala | Glu | Ser | Leu | Lys | Asn | Glu | Asn | Ile | Ile | Ala | |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 | |
| Ile | Gly | Leu | Asn | Cys | Ser | Phe | Gly | Ala | Glu | Glu | Leu | Ile | Pro | Phe | Ile | |
| | | | | 245 | | | | | 250 | | | | | 255 | | |
| Lys | Arg | Leu | Ser | Glu | Thr | Gln | Asn | Arg | Tyr | Ile | Ser | Phe | His | Pro | Asn | |
| | | | 260 | | | | | 265 | | | | | 270 | | | |
| Ala | Gly | Leu | Pro | Asn | Ser | Leu | Gly | Glu | Tyr | Glu | Glu | Leu | Pro | Glu | Glu | |
| | | 275 | | | | | 280 | | | | | 285 | | | | |
| Thr | Ala | Ser | Ile | Val | Lys | Lys | Leu | Ala | Leu | Glu | Gly | His | Leu | Asn | Ile | |
| | | | | | | 295 | | | | | 300 | | | | | |
| Val | Gly | Gly | Cys | Cys | Gly | Thr | Thr | Pro | Glu | His | Ile | Arg | Ala | Ile | Ser | |
| 305 | | | | | 310 | | | | | 315 | | | | | 320 | |
| Ser | Val | Val | Lys | Gly | Ile | Ser | Pro | Arg | Lys | Val | Pro | Asn | Leu | Glu | Pro | |
| | | | | 325 | | | | | 330 | | | | 335 | | | |
| Lys | Thr | Ile | Tyr | Ser | Gly | Leu | Glu | Asn | Ile | Lys | Ile | Asp | Lys | Asn | Ser | |
| | | | 340 | | | | | 345 | | | | | 350 | | | |
| Asn | Phe | Ile | Asn | Ile | Gly | Glu | Arg | Thr | Asn | Val | Ala | Gly | Ser | Arg | Lys | |
| | | 355 | | | | | 360 | | | | | 365 | | | | |
| Phe | Ala | Arg | Leu | Ile | Arg | Glu | Lys | Asn | Tyr | Glu | Glu | Ala | Leu | Thr | Ile | |
| | | 370 | | | | 375 | | | | | 380 | | | | | |
| Ala | Arg | His | Gln | Val | Glu | Asn | Gly | Ala | Gln | Ile | Ile | Asp | Ile | Asn | Phe | |
| 385 | | | | | | | | | | | | | | | | |

168

405 410 415
 Leu Ile Ala Ser Glu Pro Glu Ile Ser Lys Val Pro Val Met Ile Asp
 420 425 430
 Ser Ser Asn Phe Glu Val Leu Lys Val Gly Leu Lys Ser Ile Gln Gly
 435 440 445
 Lys Ala Ile Val Asn Ser Ile Ser Leu Lys Val Gly Glu Glu Lys Phe
 450 455 460
 Ile Glu Glu Ala Lys Phe Ile Lys Asn Phe Gly Ala Gly Val Val Val
 465 470 475 480
 Met Ala Phe Asp Glu Glu Gly Gln Ala Ala Thr Tyr Glu Arg Lys Ile
 485 490 495
 Glu Ile Cys Lys Arg Ala Tyr Thr Ile Leu Thr Glu Lys Val Glu Phe
 500 505 510
 Pro Pro Glu Asn Ile Ile Phe Asp Pro Asn Ile Leu Ser Ile Ala Thr
 515 520 525
 Gly Ile Glu Glu His Asp Asn Tyr Ala Val Asn Tyr Ile Lys Ala Val
 530 535 540
 Lys Trp Ile Lys Glu Asn Leu Pro Tyr Ala Lys Val Ser Gly Gly Val
 545 550 555 560
 Ser Asn Leu Ser Phe Ser Phe Arg Gly Asn Asp Ala Ile Arg Arg Ala
 565 570 575
 Met His Ser Val Phe Leu Tyr His Ala Ile Asn Ala Gly Met Asp Met
 580 585 590
 Gly Ile Val Asn Pro Ala Met Ile Asp Leu Tyr Asp Asp Ile Asp Lys
 595 600 605
 Asp Leu Leu Glu Lys Val Glu Asn Val Val Leu Asn Lys Ser Ser Asn
 610 615 620
 Ala Ser Glu Ser Leu Leu Glu Phe Ala Gln Thr Tyr Lys Lys Thr Thr
 625 630 635 640
 Glu Thr Leu Glu Lys His Glu Asp Glu Trp Arg Gln Lys Ser Pro Ser
 645 650 655
 Glu Arg Leu Ser Tyr Ala Leu Val Lys Gly Asn Val Glu Phe Ile Glu
 660 665 670
 Glu Asp Ile Glu Glu Ala Arg Lys Glu Tyr Thr Asn Ala Leu Glu Ile
 675 680 685
 Ile Glu Val Pro Leu Met Asn Gly Met Lys Lys Val Gly Lys Leu Phe
 690 695 700
 Gly Glu Gly Lys Met Phe Leu Pro Gln Val Val Lys Ser Ala Arg Val
 705 710 715 720
 Met Lys Lys Ala Val Glu Cys Leu Leu Pro Tyr Ile Asn Glu Glu Lys
 725 730 735

169

Ser Lys Asn His Asn Lys Ser Ala Gly Lys Val Val Phe Ala Thr Val
 740 745 750
 Lys Gly Asp Val His Asp Ile Gly Lys Asn Ile Val Ser Val Val Leu
 755 760 765
 Ser Cys Asn Asn Phe Glu Val Ile Asp Leu Gly Val Met Val Pro Pro
 770 775 780
 Glu Thr Ile Leu Glu Thr Ala Lys Arg Glu Asn Ala Asp Ile Ile Ala
 785 790 795 800
 Leu Ser Gly Leu Ile Thr Pro Ser Leu Asn Glu Met Ala Tyr Val Ala
 805 810 815
 Glu Glu Met Lys Arg Leu Asn Phe Asp Ile Pro Leu Met Val Gly Gly
 820 825 830
 Ala Ala Thr Ser Lys Thr His Thr Ala Leu Lys Leu Ala Thr Lys Tyr
 835 840 845
 Lys Tyr Val Val His Ser Thr Asp Ala Ser Asp Ala Val Thr Val Ala
 850 855 860
 Lys Asn Leu Met Ser Glu Asn Lys Phe Thr Phe Leu Glu Lys Leu Asn
 865 870 875 880
 Glu Glu Tyr Ser Lys Ile Arg Glu Thr Phe Ser Thr Asn Lys Ile Glu
 885 890 895
 Leu Ile Ser Ile Gln Asn Ala Arg Lys Asn Arg Phe Thr Ile Asp Trp
 900 905 910
 Asn Lys Thr Lys Ile Thr Glu Pro Lys Phe Val Gly Ile Lys Lys Leu
 915 920 925
 Gln Ala Val Pro Ile Asn Glu Leu Arg Lys Tyr Ile Asp Trp Thr Phe
 930 935 940
 Phe Phe Thr Ser Trp Asp Met Gly Met Asn Tyr Pro Lys Ile Met Lys
 945 950 955 960
 Asp Pro Lys Tyr Gly Ala Glu Ala Gln Lys Leu Phe Lys Asp Ala Asn
 965 970 975
 Glu Met Leu Asp Leu Leu Gln Lys Glu Asn Leu Ile Thr Cys Asn Gly
 980 985 990
 Val Phe Gly Ile Phe Pro Ala Asn Ser Val Asn Asp Asp Ile Glu Ile
 995 1000 1005
 Tyr Thr Asp Lys Gly Thr Val Thr Ile Asn Thr Leu Arg Gln Gln Gln
 1010 1015 1020
 Ile Leu Lys Asp Ser Asp Tyr Lys Ala Leu Ser Asp Tyr Ile Ala Pro
 1025 1030 1035 1040
 Lys Gly Ile Gly Ile Lys Asp Tyr Ile Gly Gly Phe Ile Val Thr Ala
 1045 1050 1055
 Gly Ile Gly Ala Lys Glu Tyr Ser Asp Lys Leu Lys Lys Lys Cys Asp
 1060 1065 1070

170

Asp Tyr Gly Ala Thr Met Leu Lys Leu Ile Cys Asp Arg Leu Ala Glu
 1075 1080 1085

Ala Phe Ser Glu Leu Leu His Leu Arg Val Arg Lys Glu Tyr Trp Gly
 1090 1095 1100

Tyr Ser Gln Asp Glu Asn Leu Ser Leu Glu Lys Leu Leu Lys Gly Ser
 1105 1110 1115 1120

Tyr Arg Gly Ile Lys Pro Ala Ile Gly Tyr Pro Ser Ile Pro Asp His
 1125 1130 1135

Ser Glu Lys Ala Lys Leu Phe Asp Leu Leu Leu Gly Lys Thr Ser Ile
 1140 1145 1150

Gly Val Glu Leu Thr Glu Ser Tyr Met Met Asn Pro Thr Ser Ser Val
 1155 1160 1165

Cys Gly Leu Tyr Phe Ala Asn Glu Arg Ala Lys Tyr Phe Asn Ile Asn
 1170 1175 1180

Lys Ile Gly Lys Asp Gln Leu Glu Asp Tyr Ala Val Arg Ser Asn Lys
 1185 1190 1195 1200

Asp Ile Asn Glu Ile Lys Lys Leu Leu Asp Thr Leu Leu
 1205 1210

<210> 39

<211> 3954

<212> DNA

<213> *Caulobacter_crescentus*

<220>

<221> CDS

<222> (1)..(3951)

<223> RCO02271

<400> 39

atg acc gat ctc tcc atc cgc gcc aac cgc gtc gcc gcc ctg aag gcc 48
 Met Thr Asp Leu Ser Ile Arg Ala Asn Arg Val Ala Ala Leu Lys Ala
 1 5 10 15

gcc gcc aag gag cgt att ctc att ctc gac ggc tcc tgg ggc gtg atg 96
 Ala Ala Lys Glu Arg Ile Leu Ile Leu Asp Gly Ser Trp Gly Val Met
 20 25 30

ttc cag aag aag ggg ctg acc gag gcc gac tac cgc gcc gag cgc ttc 144
 Phe Gln Lys Lys Gly Leu Thr Glu Ala Asp Tyr Arg Ala Glu Arg Phe
 35 40 45

gcc gcc tac aac ggc cag atg aag ggc aat aac gac atc ctg tgc ctg 192
 Ala Ala Tyr Asn Gly Gln Met Lys Gly Asn Asn Asp Ile Leu Cys Leu
 50 55 60

acg cgg ccc gat ctc gtg gcc gag ctg cac gac gcc tat ttc agc gcc 240
 Thr Arg Pro Asp Leu Val Ala Glu Leu His Asp Ala Tyr Phe Ser Ala
 65 70 75 80

ggc gcc gac atc tcc gag acc aac acc ttc tcg ggc acc acc atc gcc 288
 Gly Ala Asp Ile Ser Glu Thr Asn Thr Phe Ser Gly Thr Thr Ile Ala

| | | | 171 | | | |
|---|--|--|-----|-----|--|--|
| | | | 90 | | | |
| 85 | | | | 95 | | |
| cag gcc gac tat cat ctg ggt gaa cag gat gtc tgg gac atc aac ctg | | | | | | |
| Gln Ala Asp Tyr His Leu Gly Glu Gln Asp Val Trp Asp Ile Asn Leu | | | | | | |
| 100 | | | | 105 | | |
| 110 | | | | | | |
| 336 | | | | | | |
| gaa ggc gcc aag atc ggc cgc tgc gtg gcc gac cgc tgg aac gcg cag | | | | | | |
| Glu Gly Ala Lys Ile Gly Arg Ser Val Ala Asp Arg Trp Asn Ala Gln | | | | | | |
| 115 | | | | 120 | | |
| 125 | | | | | | |
| 384 | | | | | | |
| aat ccc gac cgc ccg aag ttc atc gcc ggc tgc atg ggg ccg ctg aac | | | | | | |
| Asn Pro Asp Arg Pro Lys Phe Ile Ala Gly Ser Met Gly Pro Leu Asn | | | | | | |
| 130 | | | | 135 | | |
| 140 | | | | | | |
| 432 | | | | | | |
| gtc atg ctg tgc atg tgc tgc gac gtg aac gat ccg ggc gcg cgc aag | | | | | | |
| Val Met Leu Ser Met Ser Ser Asp Val Asn Asp Pro Gly Ala Arg Lys | | | | | | |
| 145 | | | | 150 | | |
| 155 | | | | 160 | | |
| 480 | | | | | | |
| gtg acc ttc gac cag gtc tac gag gcc tat cgc cag cag gtg gat gcg | | | | | | |
| Val Thr Phe Asp Gln Val Tyr Glu Ala Tyr Arg Gln Gln Val Asp Ala | | | | | | |
| 165 | | | | 170 | | |
| 175 | | | | | | |
| 528 | | | | | | |
| ctt tac cag ggc ggg gtc gat ctc ttc ctg atc gag acc atc acc gac | | | | | | |
| Leu Tyr Gln Gly Gly Val Asp Leu Phe Leu Ile Glu Thr Ile Thr Asp | | | | | | |
| 180 | | | | 185 | | |
| 190 | | | | | | |
| 576 | | | | | | |
| acc ctg aac tgc aag gcc gcg atc aag gcg atc ctg gac tgg cgc gac | | | | | | |
| Thr Leu Asn Cys Lys Ala Ala Ile Lys Ala Ile Leu Asp Trp Arg Asp | | | | | | |
| 195 | | | | 200 | | |
| 205 | | | | | | |
| 624 | | | | | | |
| gag ggc cac gag gag ctg ccg atc tgg atc agc ggc acc atc acc gat | | | | | | |
| Glu Gly His Glu Glu Leu Pro Ile Trp Ile Ser Gly Thr Ile Thr Asp | | | | | | |
| 210 | | | | 215 | | |
| 220 | | | | | | |
| 672 | | | | | | |
| cgc tgc ggc cgc acc ctg tgc ggc cag acg gcc gag gcg ttc tgg aac | | | | | | |
| Arg Ser Gly Arg Thr Leu Ser Gly Gln Thr Ala Glu Ala Phe Trp Asn | | | | | | |
| 225 | | | | 230 | | |
| 235 | | | | 240 | | |
| 720 | | | | | | |
| agc gtc aag cac gcc aag ccg ttc gca gtg ggc ttc aac tgc gcc ctg | | | | | | |
| Ser Val Lys His Ala Lys Pro Phe Ala Val Gly Phe Asn Cys Ala Leu | | | | | | |
| 245 | | | | 250 | | |
| 255 | | | | | | |
| 768 | | | | | | |
| ggc gcg gat ttg atg cgt ccg cac atc gcc gag atg gcc cgt atc gcc | | | | | | |
| Gly Ala Asp Leu Met Arg Pro His Ile Ala Glu Met Ala Arg Ile Ala | | | | | | |
| 260 | | | | 265 | | |
| 270 | | | | | | |
| 816 | | | | | | |
| gac acc ctg gtc gca gcc tat ccc aac gcc ggc ctg ccc aac gcc atg | | | | | | |
| Asp Thr Leu Val Ala Ala Tyr Pro Asn Ala Gly Leu Pro Asn Ala Met | | | | | | |
| 275 | | | | 280 | | |
| 285 | | | | | | |
| 864 | | | | | | |
| ggc cag tac gac gag gag ccg cac gag acc ggc cac gcc ctg cac gag | | | | | | |
| Gly Gln Tyr Asp Glu Glu Pro His Glu Thr Gly His Ala Leu His Glu | | | | | | |
| 290 | | | | 295 | | |
| 300 | | | | | | |
| 912 | | | | | | |
| tgg gcc aag gac ggc ctc gtc aac atc ctg ggc ggc tgc tgc ggc acg | | | | | | |
| Trp Ala Lys Asp Gly Leu Val Asn Ile Leu Gly Gly Cys Cys Gly Thr | | | | | | |
| 305 | | | | 310 | | |
| 315 | | | | 320 | | |
| 960 | | | | | | |
| aca ccg gac cac atc cgt cac gtc gcc gac gag gtg cgc ggc gtg acg | | | | | | |
| Thr Pro Asp His Ile Arg His Val Ala Asp Glu Val Arg Gly Val Thr | | | | | | |
| 325 | | | | 330 | | |
| 335 | | | | | | |
| 1008 | | | | | | |

172

| | |
|---|------|
| ccg cgc cag atc ccc gag cgc ccc aag gcc atg cgc ctg gcg ggc ctc | 1056 |
| Pro Arg Gln Ile Pro Glu Arg Pro Lys Ala Met Arg Leu Ala Gly Leu | |
| 340 345 350 | |
| gaa ccg ttc gag ttg gct tag tgg cta cgg ccg caa att ccc ttc tcc | 1104 |
| Glu Pro Phe Glu Leu Ala Xaa Trp Leu Arg Pro Gln Ile Pro Phe Ser | |
| 355 360 365 | |
| cct tgc ggg aga agg tgt cgc cga agg cga cgg atg agg ggt ctc gcc | 1152 |
| Pro Cys Gly Arg Arg Cys Arg Arg Arg Arg Met Arg Gly Leu Ala | |
| 370 375 380 | |
| ggc cct tca acc gct gtc tcg cgg cgg cga cgt tct tca acc cct cat | 1200 |
| Gly Pro Ser Thr Ala Val Ser Arg Arg Arg Arg Ser Ser Thr Pro His | |
| 385 390 395 400 | |
| ccg acc cgc tgc gcg ggc cac ctt ctc ccg caa ggg gag aag gga tga | 1248 |
| Pro Thr Arg Cys Ala Gly His Leu Leu Pro Gln Gly Glu Lys Gly Xaa | |
| 405 410 415 | |
| ctg cta ttg gat cct gaa atg cgc ccc gtc ttc gtc aac atc ggt gag | 1296 |
| Leu Leu Leu Asp Pro Glu Met Arg Pro Val Phe Val Asn Ile Gly Glu | |
| 420 425 430 | |
| cgc acc aac gtc acc ggc tcg gcc aag ttc aag aag ctg atc gtc gaa | 1344 |
| Arg Thr Asn Val Thr Gly Ser Ala Lys Phe Lys Lys Leu Ile Val Glu | |
| 435 440 445 | |
| ggg aac tat ccc gag gcg ctg tcg gtc gcg cgc cag cag gtc gag gcc | 1392 |
| Gly Asn Tyr Pro Glu Ala Leu Ser Val Ala Arg Gln Gln Val Glu Ala | |
| 450 455 460 | |
| ggg gcc cag gtc atc gac gtg aac atg gac gag ggt ctg ctg gac agc | 1440 |
| Gly Ala Gln Val Ile Asp Val Asn Met Asp Glu Gly Leu Leu Asp Ser | |
| 465 470 475 480 | |
| cag cag gcc atg gtc acc ttc ctg aat ctg atg gcg gcc gag ccc gac | 1488 |
| Gln Gln Ala Met Val Thr Phe Leu Asn Leu Met Ala Ala Glu Pro Asp | |
| 485 490 495 | |
| atc gcg cgc gtg ccg gtg atg atc gac agc tcc aag tgg gag gtg atc | 1536 |
| Ile Ala Arg Val Pro Val Met Ile Asp Ser Ser Lys Trp Glu Val Ile | |
| 500 505 510 | |
| gag gcg ggc ctg aag tgc gta caa ggc aag gcg atc gtc aac tcg atc | 1584 |
| Glu Ala Gly Leu Lys Cys Val Gln Gly Lys Ala Ile Val Asn Ser Ile | |
| 515 520 525 | |
| agc ctg aag gaa ggc gag gaa aag ttc ctc gaa cag gcc acg ctc tgc | 1632 |
| Ser Leu Lys Glu Gly Glu Lys Phe Leu Glu Gln Ala Thr Leu Cys | |
| 530 535 540 | |
| ctg cgc tat ggc gca gcc gtg gtg gtc atg gcc ttc gac gag gtt ggc | 1680 |
| Leu Arg Tyr Gly Ala Ala Val Val Val Met Ala Phe Asp Glu Val Gly | |
| 545 550 555 560 | |
| cag gcc gac acc gaa aag cgc aag gtc gag atc tgt acg cgg gcc tac | 1728 |
| Gln Ala Asp Thr Glu Lys Arg Lys Val Glu Ile Cys Thr Arg Ala Tyr | |
| 565 570 575 | |
| aac acg ctc gtg gac aag gtc ggc ttc ccg ccc gag gac atc atc ttc | 1776 |
| Asn Thr Leu Val Asp Lys Val Gly Phe Pro Pro Glu Asp Ile Ile Phe | |

173

| 580 | 585 | 590 | |
|---|-----|-----|------|
| gac ccc aac atc ttc gcc gtg gcg acg ggg atc gag gag cac gac aac Asp Pro Asn Ile Phe Ala Val Ala Thr Gly Ile Glu Glu His Asp Asn 595 600 605 | | | 1824 |
| tac gcc gtc gac ttc atc gag gcc acg cgg cgc atc aag cag atg ttg Tyr Ala Val Asp Phe Ile Glu Ala Thr Arg Arg Ile Lys Gln Met Leu 610 615 620 | | | 1872 |
| ccc tat gcg cgg gtg tcg ggc ggg gtg tcg aac gtc tcg ttc agc ttc Pro Tyr Ala Arg Val Ser Gly Gly Val Ser Asn Val Ser Phe Ser Phe 625 630 635 640 | | | 1920 |
| cgg ggc aat gag ccg gtg cgc cgg gcg atc cac tcg gtg ttc ctg tac Arg Gly Asn Glu Pro Val Arg Arg Ala Ile His Ser Val Phe Leu Tyr 645 650 655 | | | 1968 |
| cac gcc atc aac gcc ggc atg gac atg ggc atc gtc aac gcc ggc gac His Ala Ile Asn Ala Gly Met Asp Met Gly Ile Val Asn Ala Gly Asp 660 665 670 | | | 2016 |
| ctg ccg gtc tat gac gac atc gat ccg gcc ctg cgc gag gcc gtc gag Leu Pro Val Tyr Asp Asp Ile Asp Pro Ala Leu Arg Glu Ala Val Glu 675 680 685 | | | 2064 |
| gac gtg atc ctc aac cgg ccg cag cgc gat ccg gtg atg acc aac acc Asp Val Ile Leu Asn Arg Pro Gln Arg Asp Pro Val Met Thr Asn Thr 690 695 700 | | | 2112 |
| gag cgc ctg gtc gag atg gcc ccg cgc tat aag ggc gag aag ggg cag Glu Arg Leu Val Glu Met Ala Pro Arg Tyr Lys Gly Glu Lys Gly Gln 705 710 715 720 | | | 2160 |
| cag cag gtc gcc aac ctg gag tgg cga aag ggc acg gtg aac gag cgc Gln Gln Val Ala Asn Leu Glu Trp Arg Lys Gly Thr Val Asn Glu Arg 725 730 735 | | | 2208 |
| ctg acc cat gct ctc gtt cac ggc atc acc gag ttc atc gag cag gac Leu Thr His Ala Leu Val His Gly Ile Thr Glu Phe Ile Glu Gln Asp 740 745 750 | | | 2256 |
| acc gag gag gcg cgc ctg gcc gcc gag cgc ccc ttg cac gtg att gaa Thr Glu Glu Ala Arg Leu Ala Ala Glu Arg Pro Leu His Val Ile Glu 755 760 765 | | | 2304 |
| ggc ccg ctg atg gac ggc atg aac gtc gtc ggc gac ctg ttc ggc gcg Gly Pro Leu Met Asp Gly Met Asn Val Val Gly Asp Leu Phe Gly Ala 770 775 780 | | | 2352 |
| ggc aag atg ttc ctg ccc cag gtg gtg aag tcg gcc cgc gtg atg aag Gly Lys Met Phe Leu Pro Gln Val Val Lys Ser Ala Arg Val Met Lys 785 790 795 800 | | | 2400 |
| cag gcc gtc gcc tgg ctg atg ccg ttc atg gag gcc gag aag gaa ggc Gln Ala Val Ala Trp Leu Met Pro Phe Met Glu Ala Glu Lys Glu Gly 805 810 815 | | | 2448 |
| cag gag cgc aag gcc gcc ggc aag gtg ctg atg gcc acc gtc aag ggc Gln Glu Arg Lys Ala Ala Gly Lys Val Leu Met Ala Thr Val Lys Gly 820 825 830 | | | 2496 |

174

| | |
|---|------|
| gac gtc cac gac atc ggt aag aac atc gtc ggc gtc gtg ctg cag tgt | 2544 |
| Asp Val His Asp Ile Gly Lys Asn Ile Val Gly Val Val Leu Gln Cys | |
| 835 840 845 | |
| aac aac tac gag gtc gtg gac ctg ggt gtc atg gtg ccc gcc gac cgc | 2592 |
| Asn Asn Tyr Glu Val Val Asp Leu Gly Val Met Val Pro Ala Asp Arg | |
| 850 855 860 | |
| atc ctg gac gaa gcc aag aag cac aag gtc gac atg atc ggc ctg tcg | 2640 |
| Ile Leu Asp Glu Ala Lys Lys His Lys Val Asp Met Ile Gly Leu Ser | |
| 865 870 875 880 | |
| ggc ctg atc acc ccc tcg ctg gac gag atg gtg ttc gtg gcc gcc gag | 2688 |
| Gly Leu Ile Thr Pro Ser Leu Asp Glu Met Val Phe Val Ala Ala Glu | |
| 885 890 895 | |
| atg gag cgc cag ggc ttt gat atc ccg ctg ctg atc ggc ggc gcc acc | 2736 |
| Met Glu Arg Gln Gly Phe Asp Ile Pro Leu Leu Ile Gly Gly Ala Thr | |
| 900 905 910 | |
| acc agc cgc acc cac acc gcg gtg aag atc gag ccg gcc tat cgc cgg | 2784 |
| Thr Ser Arg Thr His Thr Ala Val Lys Ile Glu Pro Ala Tyr Arg Arg | |
| 915 920 925 | |
| ggt ccg acg acc tat gtc gtc gac gcc agc cgc gcc gtg ggc gtg gtc | 2832 |
| Gly Pro Thr Thr Tyr Val Val Asp Ala Ser Arg Ala Val Gly Val Val | |
| 930 935 940 | |
| tcg ggc ctg ctg tcg gaa ggc gag cgt gac cgg atc atc gcc gag acc | 2880 |
| Ser Gly Leu Leu Ser Glu Gly Glu Arg Asp Arg Ile Ile Ala Glu Thr | |
| 945 950 955 960 | |
| cgc gcc gag tat gtg aag gtc cgc gag caa tac gcg cgc ggc cag acc | 2928 |
| Arg Ala Glu Tyr Val Lys Val Arg Glu Gln Tyr Ala Arg Gly Gln Thr | |
| 965 970 975 | |
| acc aag gcc cgc gcc tcg atc cag gag gcc cgc aag cgc gcc ttc gcc | 2976 |
| Thr Lys Ala Arg Ala Ser Ile Gln Glu Ala Arg Lys Arg Ala Phe Ala | |
| 980 985 990 | |
| att gac tgg aag ggc tat gcg ccg ccc aag ccc gcc ttc atc ggc acg | 3024 |
| Ile Asp Trp Lys Gly Tyr Ala Pro Pro Lys Pro Ala Phe Ile Gly Thr | |
| 995 1000 1005 | |
| cgg gtg ttc gag ccg tcg ctg gcc gag ctg gtc ccg ttc atc gac tgg | 3072 |
| Arg Val Phe Glu Pro Ser Leu Ala Glu Leu Val Pro Phe Ile Asp Trp | |
| 1010 1015 1020 | |
| tcg ccg ttc ttc gcc agc tgg gag ctg atc ggc cgc ttc ccg cag atc | 3120 |
| Ser Pro Phe Phe Ala Ser Trp Glu Leu Ile Gly Arg Phe Pro Gln Ile | |
| 1025 1030 1035 1040 | |
| ctg gag gac gac gtg gtc ggc cag gcc gcc acc gac ctc tac cgc gac | 3168 |
| Leu Glu Asp Asp Val Val Gly Gln Ala Ala Thr Asp Leu Tyr Arg Asp | |
| 1045 1050 1055 | |
| gcc cgc gcc atg ctg gac aag gtg gtc gag gaa aag tgg ttc ggc gcc | 3216 |
| Ala Arg Ala Met Leu Asp Lys Val Val Glu Glu Lys Trp Phe Gly Ala | |
| 1060 1065 1070 | |
| aag ggc gtg atc ggc ttc tgg ccg gcc cag gcc cag ggc gac gac atc | 3264 |
| Lys Gly Val Ile Gly Phe Trp Pro Ala Gln Ala Gln Gly Asp Asp Ile | |

175

| 1075 | 1080 | 1085 | |
|---|------|------|------|
| gtg ctc tat acc gac gag acc cgc gtg gcc gag ttc tcg cgc ctg cac Val Leu Tyr Thr Asp Glu Thr Arg Val Ala Glu Phe Ser Arg Leu His 1090 1095 1100 | | | 3312 |
| acc ctt cgc cag cag atg gac aag ggc gcc gac aag agc ggc gag gcc Thr Leu Arg Gln Gln Met Asp Lys Gly Ala Asp Lys Ser Gly Glu Ala 1105 1110 1115 1120 | | | 3360 |
| aag gcc aat gtc gcc ctg tcg gac ttc gtc gcg ccg atc ggg cag ggg Lys Ala Asn Val Ala Leu Ser Asp Phe Val Ala Pro Ile Gly Gln Gly 1125 1130 1135 | | | 3408 |
| gct gac tat gtc ggc ggc ttc gcc gtc acc gca ggc cat ggc gag gac Ala Asp Tyr Val Gly Gly Phe Ala Val Thr Ala Gly His Gly Glu Asp 1140 1145 1150 | | | 3456 |
| gag atc gtc gcc aag ttc aag gcg gcc ggc gac gac tac aac gcc atc Glu Ile Val Ala Lys Phe Lys Ala Ala Gly Asp Asp Tyr Asn Ala Ile 1155 1160 1165 | | | 3504 |
| atg gcc tcg gcc ctg gcc gac cgc ctg gcc gaa gcc ttc gcc gag tgg Met Ala Ser Ala Leu Ala Asp Arg Leu Ala Glu Ala Phe Ala Glu Trp 1170 1175 1180 | | | 3552 |
| ctg cac tac aaa gcc cgt gtc gag ctg tgg ggc tac gcc gcc gac gag Leu His Tyr Lys Ala Arg Val Glu Leu Trp Gly Tyr Ala Ala Asp Glu 1185 1190 1195 1200 | | | 3600 |
| gac gcc gac gtc gag cgc ctg atc gcc gaa aag tac cag ggc atc cgc Asp Ala Asp Val Glu Arg Leu Ile Ala Glu Lys Tyr Gln Gly Ile Arg 1205 1210 1215 | | | 3648 |
| ccc gcg ccc ggc tat ccg gcc cag ccc gac cac acc gag aaa ggt acg Pro Ala Pro Gly Tyr Pro Ala Gln Pro Asp His Thr Glu Lys Gly Thr 1220 1225 1230 | | | 3696 |
| ctg ttc aag ctg ctc gac gcc gag gcg gcc acc ggt ctg cag ctg acc Leu Phe Lys Leu Leu Asp Ala Glu Ala Ala Thr Gly Leu Gln Leu Thr 1235 1240 1245 | | | 3744 |
| gag agc tac gcc atg acc cct ggc gcg gcg gtc tcc ggc ctg ttc ttc Glu Ser Tyr Ala Met Thr Pro Gly Ala Ala Val Ser Gly Leu Phe Phe 1250 1255 1260 | | | 3792 |
| agc cac cgc cag gcg cac tat ttc ggg gtc ggc aag atc gac gcc gac Ser His Arg Gln Ala His Tyr Phe Gly Val Gly Lys Ile Asp Ala Asp 1265 1270 1275 1280 | | | 3840 |
| cag gtc gag gac tac gcc cgc cgc aag ggc tgg gat atg gag acg gcc Gln Val Glu Asp Tyr Ala Arg Arg Lys Gly Trp Asp Met Glu Thr Ala 1285 1290 1295 | | | 3888 |
| gag cgc tgg ctg tcg ccg atc ctg aac tac gat ccg cta gcg cgg gcg Glu Arg Trp Leu Ser Pro Ile Leu Asn Tyr Asp Pro Leu Ala Arg Ala 1300 1305 1310 | | | 3936 |
| cgc ggg gcg gcg gct tag Arg Gly Ala Ala Ala 1315 | | | 3954 |

176

<210> 40
 <211> 1317
 <212> PRT
 <213> *Caulobacter_crescentus*

<220>
 <221> unsure
 <222> 359 .. 359
 <223> All occurrences of Xaa indicate any amino acid

<220>
 <221> unsure
 <222> 416 .. 416
 <223> All occurrences of Xaa indicate any amino acid

<400> 40
 Met Thr Asp Leu Ser Ile Arg Ala Asn Arg Val Ala Ala Leu Lys Ala
 1 5 10 15
 Ala Ala Lys Glu Arg Ile Leu Ile Leu Asp Gly Ser Trp Gly Val Met
 20 25 30
 Phe Gln Lys Lys Gly Leu Thr Glu Ala Asp Tyr Arg Ala Glu Arg Phe
 35 40 45
 Ala Ala Tyr Asn Gly Gln Met Lys Gly Asn Asn Asp Ile Leu Cys Leu
 50 55 60
 Thr Arg Pro Asp Leu Val Ala Glu Leu His Asp Ala Tyr Phe Ser Ala
 65 70 75 80
 Gly Ala Asp Ile Ser Glu Thr Asn Thr Phe Ser Gly Thr Thr Ile Ala
 85 90 95
 Gln Ala Asp Tyr His Leu Gly Glu Gln Asp Val Trp Asp Ile Asn Leu
 100 105 110
 Glu Gly Ala Lys Ile Gly Arg Ser Val Ala Asp Arg Trp Asn Ala Gln
 115 120 125
 Asn Pro Asp Arg Pro Lys Phe Ile Ala Gly Ser Met Gly Pro Leu Asn
 130 135 140
 Val Met Leu Ser Met Ser Ser Asp Val Asn Asp Pro Gly Ala Arg Lys
 145 150 155 160
 Val Thr Phe Asp Gln Val Tyr Glu Ala Tyr Arg Gln Gln Val Asp Ala
 165 170 175
 Leu Tyr Gln Gly Gly Val Asp Leu Phe Leu Ile Glu Thr Ile Thr Asp
 180 185 190
 Thr Leu Asn Cys Lys Ala Ala Ile Lys Ala Ile Leu Asp Trp Arg Asp
 195 200 205
 Glu Gly His Glu Glu Leu Pro Ile Trp Ile Ser Gly Thr Ile Thr Asp
 210 215 220
 Arg Ser Gly Arg Thr Leu Ser Gly Gln Thr Ala Glu Ala Phe Trp Asn
 225 230 235 240

177

Ser Val Lys His Ala Lys Pro Phe Ala Val Gly Phe Asn Cys Ala Leu
 245 250 255
 Gly Ala Asp Leu Met Arg Pro His Ile Ala Glu Met Ala Arg Ile Ala
 260 265 270
 Asp Thr Leu Val Ala Ala Tyr Pro Asn Ala Gly Leu Pro Asn Ala Met
 275 280 285
 Gly Gln Tyr Asp Glu Glu Pro His Glu Thr Gly His Ala Leu His Glu
 290 295 300
 Trp Ala Lys Asp Gly Leu Val Asn Ile Leu Gly Gly Cys Cys Gly Thr
 305 310 315 320
 Thr Pro Asp His Ile Arg His Val Ala Asp Glu Val Arg Gly Val Thr
 325 330 335
 Pro Arg Gln Ile Pro Glu Arg Pro Lys Ala Met Arg Leu Ala Gly Leu
 340 345 350
 Glu Pro Phe Glu Leu Ala Xaa Trp Leu Arg Pro Gln Ile Pro Phe Ser
 355 360 365
 Pro Cys Gly Arg Arg Cys Arg Arg Arg Arg Met Arg Gly Leu Ala
 370 375 380
 Gly Pro Ser Thr Ala Val Ser Arg Arg Arg Arg Ser Ser Thr Pro His
 385 390 395 400
 Pro Thr Arg Cys Ala Gly His Leu Leu Pro Gln Gly Glu Lys Gly Xaa
 405 410 415
 Leu Leu Leu Asp Pro Glu Met Arg Pro Val Phe Val Asn Ile Gly Glu
 420 425 430
 Arg Thr Asn Val Thr Gly Ser Ala Lys Phe Lys Lys Leu Ile Val Glu
 435 440 445
 Gly Asn Tyr Pro Glu Ala Leu Ser Val Ala Arg Gln Gln Val Glu Ala
 450 455 460
 Gly Ala Gln Val Ile Asp Val Asn Met Asp Glu Gly Leu Leu Asp Ser
 465 470 475 480
 Gln Gln Ala Met Val Thr Phe Leu Asn Leu Met Ala Ala Glu Pro Asp
 485 490 495
 Ile Ala Arg Val Pro Val Met Ile Asp Ser Ser Lys Trp Glu Val Ile
 500 505 510
 Glu Ala Gly Leu Lys Cys Val Gln Gly Lys Ala Ile Val Asn Ser Ile
 515 520 525
 Ser Leu Lys Glu Gly Glu Glu Lys Phe Leu Glu Gln Ala Thr Leu Cys
 530 535 540
 Leu Arg Tyr Gly Ala Ala Val Val Val Met Ala Phe Asp Glu Val Gly
 545 550 555 560
 Gln Ala Asp Thr Glu Lys Arg Lys Val Glu Ile Cys Thr Arg Ala Tyr
 565 570 575

178

Asn Thr Leu Val Asp Lys Val Gly Phe Pro Pro Glu Asp Ile Ile Phe
 580 585 590
 Asp Pro Asn Ile Phe Ala Val Ala Thr Gly Ile Glu Glu His Asp Asn
 595 600 605
 Tyr Ala Val Asp Phe Ile Glu Ala Thr Arg Arg Ile Lys Gln Met Leu
 610 615 620
 Pro Tyr Ala Arg Val Ser Gly Gly Val Ser Asn Val Ser Phe Ser Phe
 625 630 635 640
 Arg Gly Asn Glu Pro Val Arg Arg Ala Ile His Ser Val Phe Leu Tyr
 645 650 655
 His Ala Ile Asn Ala Gly Met Asp Met Gly Ile Val Asn Ala Gly Asp
 660 665 670
 Leu Pro Val Tyr Asp Asp Ile Asp Pro Ala Leu Arg Glu Ala Val Glu
 675 680 685
 Asp Val Ile Leu Asn Arg Pro Gln Arg Asp Pro Val Met Thr Asn Thr
 690 695 700
 Glu Arg Leu Val Glu Met Ala Pro Arg Tyr Lys Gly Glu Lys Gly Gln
 705 710 715 720
 Gln Gln Val Ala Asn Leu Glu Trp Arg Lys Gly Thr Val Asn Glu Arg
 725 730 735
 Leu Thr His Ala Leu Val His Gly Ile Thr Glu Phe Ile Glu Gln Asp
 740 745 750
 Thr Glu Glu Ala Arg Leu Ala Ala Glu Arg Pro Leu His Val Ile Glu
 755 760 765
 Gly Pro Leu Met Asp Gly Met Asn Val Val Gly Asp Leu Phe Gly Ala
 770 775 780
 Gly Lys Met Phe Leu Pro Gln Val Val Lys Ser Ala Arg Val Met Lys
 785 790 795 800
 Gln Ala Val Ala Trp Leu Met Pro Phe Met Glu Ala Glu Lys Glu Gly
 805 810 815
 Gln Glu Arg Lys Ala Ala Gly Lys Val Leu Met Ala Thr Val Lys Gly
 820 825 830
 Asp Val His Asp Ile Gly Lys Asn Ile Val Gly Val Val Leu Gln Cys
 835 840 845
 Asn Asn Tyr Glu Val Val Asp Leu Gly Val Met Val Pro Ala Asp Arg
 850 855 860
 Ile Leu Asp Glu Ala Lys Lys His Lys Val Asp Met Ile Gly Leu Ser
 865 870 875 880
 Gly Leu Ile Thr Pro Ser Leu Asp Glu Met Val Phe Val Ala Ala Glu
 885 890 895
 Met Glu Arg Gln Gly Phe Asp Ile Pro Leu Leu Ile Gly Gly Ala Thr

179

| | | |
|---|------|------|
| 900 | 905 | 910 |
| Thr Ser Arg Thr His Thr Ala Val Lys Ile Glu Pro Ala Tyr Arg Arg | | |
| 915 | 920 | 925 |
| Gly Pro Thr Thr Tyr Val Val Asp Ala Ser Arg Ala Val Gly Val Val | | |
| 930 | 935 | 940 |
| Ser Gly Leu Leu Ser Glu Gly Glu Arg Asp Arg Ile Ile Ala Glu Thr | | |
| 945 | 950 | 955 |
| Arg Ala Glu Tyr Val Lys Val Arg Glu Gln Tyr Ala Arg Gly Gln Thr | | |
| 965 | 970 | 975 |
| Thr Lys Ala Arg Ala Ser Ile Gln Glu Ala Arg Lys Arg Ala Phe Ala | | |
| 980 | 985 | 990 |
| Ile Asp Trp Lys Gly Tyr Ala Pro Pro Lys Pro Ala Phe Ile Gly Thr | | |
| 995 | 1000 | 1005 |
| Arg Val Phe Glu Pro Ser Leu Ala Glu Leu Val Pro Phe Ile Asp Trp | | |
| 1010 | 1015 | 1020 |
| Ser Pro Phe Phe Ala Ser Trp Glu Leu Ile Gly Arg Phe Pro Gln Ile | | |
| 1025 | 1030 | 1035 |
| Leu Glu Asp Asp Val Val Gly Gln Ala Ala Thr Asp Leu Tyr Arg Asp | | |
| 1045 | 1050 | 1055 |
| Ala Arg Ala Met Leu Asp Lys Val Val Glu Glu Lys Trp Phe Gly Ala | | |
| 1060 | 1065 | 1070 |
| Lys Gly Val Ile Gly Phe Trp Pro Ala Gln Ala Gln Gly Asp Asp Ile | | |
| 1075 | 1080 | 1085 |
| Val Leu Tyr Thr Asp Glu Thr Arg Val Ala Glu Phe Ser Arg Leu His | | |
| 1090 | 1095 | 1100 |
| Thr Leu Arg Gln Gln Met Asp Lys Gly Ala Asp Lys Ser Gly Glu Ala | | |
| 1105 | 1110 | 1115 |
| Lys Ala Asn Val Ala Leu Ser Asp Phe Val Ala Pro Ile Gly Gln Gly | | |
| 1125 | 1130 | 1135 |
| Ala Asp Tyr Val Gly Gly Phe Ala Val Thr Ala Gly His Gly Glu Asp | | |
| 1140 | 1145 | 1150 |
| Glu Ile Val Ala Lys Phe Lys Ala Ala Gly Asp Asp Tyr Asn Ala Ile | | |
| 1155 | 1160 | 1165 |
| Met Ala Ser Ala Leu Ala Asp Arg Leu Ala Glu Ala Phe Ala Glu Trp | | |
| 1170 | 1175 | 1180 |
| Leu His Tyr Lys Ala Arg Val Glu Leu Trp Gly Tyr Ala Ala Asp Glu | | |
| 1185 | 1190 | 1195 |
| Asp Ala Asp Val Glu Arg Leu Ile Ala Glu Lys Tyr Gln Gly Ile Arg | | |
| 1205 | 1210 | 1215 |
| Pro Ala Pro Gly Tyr Pro Ala Gln Pro Asp His Thr Glu Lys Gly Thr | | |
| 1220 | 1225 | 1230 |

180

Leu Phe Lys Leu Leu Asp Ala Glu Ala Ala Thr Gly Leu Gln Leu Thr
 1235 1240 1245

Glu Ser Tyr Ala Met Thr Pro Gly Ala Ala Val Ser Gly Leu Phe Phe
 1250 1255 1260

Ser His Arg Gln Ala His Tyr Phe Gly Val Gly Lys Ile Asp Ala Asp
 1265 1270 1275 1280

Gln Val Glu Asp Tyr Ala Arg Arg Lys Gly Trp Asp Met Glu Thr Ala
 1285 1290 1295

Glu Arg Trp Leu Ser Pro Ile Leu Asn Tyr Asp Pro Leu Ala Arg Ala
 1300 1305 1310

Arg Gly Ala Ala Ala
 1315

<210> 41

<211> 3759

<212> DNA

<213> Rhodobacter capsulatus

<220>

<221> CDS

<222> (1) .. (3756)

<223> RRC01731

<400> 41

atg ctg acc cag acc ctg ccc cga tct gcg gcc ttt gcc gca att gag 48
 Met Leu Thr Gln Thr Leu Pro Arg Ser Ala Ala Phe Ala Ala Ile Glu
 1 5 10 15

gcg ctt tcg cgc cag cgg atc ttg atc ctt gac ggg gcg atg ggc acg 96
 Ala Leu Ser Arg Gln Arg Ile Leu Ile Leu Asp Gly Ala Met Gly Thr
 20 25 30

cag atc cag cag ctt ggc ctg agc gag gac gat ttt ctg ggc cac ggc 144
 Gln Ile Gln Gln Leu Gly Leu Ser Glu Asp Asp Phe Leu Gly His Gly
 35 40 45

tcg ggc tgc gcc tgc cgc cat gcc acc gat cat ccg caa aag ggc aac 192
 Ser Gly Cys Ala Cys Arg His Ala Thr Asp His Pro Gln Lys Gly Asn
 50 55 60

aac gac ctg ctg gtg ctg acc cag ccg caa gcg atc gag gag atc cat 240
 Asn Asp Leu Leu Val Leu Thr Gln Pro Gln Ala Ile Glu Glu Ile His
 65 70 75 80

ttc cgc tat gcg atg gcg ggg gcg gat atc gtc gag acg aac acc ttt 288
 Phe Arg Tyr Ala Met Ala Gly Ala Asp Ile Val Glu Thr Asn Thr Phe
 85 90 95

tcg gcc acc acc atc gcg cag gcc gat tac ggg ctg gaa agc gcg gtg 336
 Ser Ala Thr Thr Ile Ala Gln Ala Asp Tyr Gly Leu Glu Ser Ala Val
 100 105 110

ttc gac ctg aac gcc gcg ggg gcg cgg gtg gcg cgg gcg gcg atg gac 384
 Phe Asp Leu Asn Ala Ala Gly Ala Arg Val Ala Arg Ala Ala Met Asp
 115 120 125

181

| | |
|---|------|
| cgc gcc gag gcc acc gac gga cgg cgc cgc ttc gtt gcg ggg gcg gtg | 432 |
| Arg Ala Glu Ala Thr Asp Gly Arg Arg Arg Phe Val Ala Gly Ala Val | |
| 130 135 140 | |
| ggg ccg acg aac cgc acc gcc tcg ctc tcg ccc gat gtg aac gac ccg | 480 |
| Gly Pro Thr Asn Arg Thr Ala Ser Leu Ser Pro Asp Val Asn Asp Pro | |
| 145 150 155 160 | |
| ggc ttt cgc gcc gtc acc ttc gac gat ctg cgc acg gcc tat ggc cag | 528 |
| Gly Phe Arg Ala Val Thr Phe Asp Asp Leu Arg Thr Ala Tyr Gly Gln | |
| 165 170 175 | |
| cag gtg cgc ggt ctg atc gcg ggg ggc gcc gat atc ctg ctg atc gag | 576 |
| Gln Val Arg Gly Leu Ile Ala Gly Gly Ala Asp Ile Leu Leu Ile Glu | |
| 180 185 190 | |
| acg atc ttt gac acg ctg aac gcc aag gcg gcg att ttc gcc tgt ttc | 624 |
| Thr Ile Phe Asp Thr Leu Asn Ala Lys Ala Ala Ile Phe Ala Cys Phe | |
| 195 200 205 | |
| gaa gcc ttt gcc gaa cgg ggc gag cgg ctg ccg gtg atg att tcc ggc | 672 |
| Glu Ala Phe Ala Glu Arg Gly Glu Arg Leu Pro Val Met Ile Ser Gly | |
| 210 215 220 | |
| acg atc acc gat gcc tcg ggg cgc aca ttg tcg ggg cag acg ccg acc | 720 |
| Thr Ile Thr Asp Ala Ser Gly Arg Thr Leu Ser Gly Gln Thr Pro Thr | |
| 225 230 235 240 | |
| gcg ttc tgg cat tcg gtg gct cat gcc cgg ccc ttt acc gtg ggg ctg | 768 |
| Ala Phe Trp His Ser Val Ala His Ala Arg Pro Phe Thr Val Gly Leu | |
| 245 250 255 | |
| aac tgc gcg ctg ggc gcc agt gcg atg cgt ccg cat ctg gcg gaa ctg | 816 |
| Asn Cys Ala Leu Gly Ala Ser Ala Met Arg Pro His Leu Ala Glu Leu | |
| 260 265 270 | |
| gcg ggc gtc gcc ccc tgc gcg atc tgc gcc tat ccc aat gcc ggg ctg | 864 |
| Ala Gly Val Ala Pro Cys Ala Ile Cys Ala Tyr Pro Asn Ala Gly Leu | |
| 275 280 285 | |
| ccc aat gcc ttt ggc caa tat gac gaa acc ccc gac cgg acc gcc gcg | 912 |
| Pro Asn Ala Phe Gly Gln Tyr Asp Glu Thr Pro Asp Arg Thr Ala Ala | |
| 290 295 300 | |
| cag gtg gcc gaa ttt gcc cgc gaa ggg ctg gtc aat gtc gtg ggc ggt | 960 |
| Gln Val Ala Glu Phe Ala Arg Glu Gly Leu Val Asn Val Val Gly Gly | |
| 305 310 315 320 | |
| tgc tgc ggc acc acc ccc gat cac atc cgc gcc atc gcg gaa gcc gtg | 1008 |
| Cys Cys Gly Thr Thr Pro Asp His Ile Arg Ala Ile Ala Glu Ala Val | |
| 325 330 335 | |
| aaa cct ttc ccg ccg agg gcc ctg cca agc cgt tat ctg cgc ctt tcg | 1056 |
| Lys Pro Phe Pro Pro Arg Ala Leu Pro Ser Arg Tyr Leu Arg Leu Ser | |
| 340 345 350 | |
| ggg ctt gag ccc ttt acc ctg acg ccc gac att ccc ttc gtg aac atc | 1104 |
| Gly Leu Glu Pro Phe Thr Leu Thr Pro Asp Ile Pro Phe Val Asn Ile | |
| 355 360 365 | |
| ggc gag cgc acg aat gtc acc ggc tcg gcc cgg ttc cgc aag atg atc | 1152 |
| Gly Glu Arg Thr Asn Val Thr Gly Ser Ala Arg Phe Arg Lys Met Ile | |

182

| 370 | 375 | 380 | |
|---|-----|-----|------|
| gtc gcc cgc gac tat gcc gcc gcg ctg gat gtc gcc cgc gat cag gtg Val Ala Arg Asp Tyr Ala Ala Ala Leu Asp Val Ala Arg Asp Gln Val 385 390 395 400 | | | 1200 |
| gaa aac ggc gcg cag atc ctt gac atc aac atg gac gag ggg ctg atc Glu Asn Gly Ala Gln Ile Leu Asp Ile Asn Met Asp Glu Gly Leu Ile 405 410 415 | | | 1248 |
| gac agt cag gcg gcg atg gtc gcc ttc ctc aac ctc ttg gcc gcc gag Asp Ser Gln Ala Ala Met Val Ala Phe Leu Asn Leu Leu Ala Ala Glu 420 425 430 | | | 1296 |
| ccc gac att gcc cgg gtg ccg gtg atg atc gac agc tcg aaa tgg gag Pro Asp Ile Ala Arg Val Pro Val Met Ile Asp Ser Ser Lys Trp Glu 435 440 445 | | | 1344 |
| gtg atc gag gcc ggg ctg aaa tgc gtg cag ggc aag ccc gtc gtc aat Val Ile Glu Ala Gly Leu Lys Cys Val Gln Gly Lys Pro Val Val Asn 450 455 460 | | | 1392 |
| tcg atc agc ctg aag gag ggc gag gag atc ttc cgc cat cac gcg gcg Ser Ile Ser Leu Lys Glu Gly Glu Glu Ile Phe Arg His His Ala Ala 465 470 475 480 | | | 1440 |
| ctg tgt ctg gcc tat ggc gcg gcg gtc gtc gtg atg gcc ttt gac gaa Leu Cys Leu Ala Tyr Gly Ala Ala Val Val Val Met Ala Phe Asp Glu 485 490 495 | | | 1488 |
| gag ggg cag gcc gac agt ttc gcc cga aag acc agc atc tgc gcc cgc Glu Gly Gln Ala Asp Ser Phe Ala Arg Lys Thr Ser Ile Cys Ala Arg 500 505 510 | | | 1536 |
| gcc tat cgc att ctg gtc gag gag atc ggc ttt ccg ccc gaa gac atc Ala Tyr Arg Ile Leu Val Glu Glu Ile Gly Phe Pro Pro Glu Asp Ile 515 520 525 | | | 1584 |
| atc ttt gac ccg aac gtc ttt gcc gtc gcc acg ggc atc gaa gaa cac Ile Phe Asp Pro Asn Val Phe Ala Val Ala Thr Gly Ile Glu Glu His 530 535 540 | | | 1632 |
| gac aat tac ggc gtt gat ttc atc gag gcc gct cgc tgg atc cgg gcc Asp Asn Tyr Gly Val Asp Phe Ile Glu Ala Ala Arg Trp Ile Arg Ala 545 550 555 560 | | | 1680 |
| aac ctg ccg cat gcc cat gtc tcg ggc ggg gtg tcg aac ctg tcc ttc Asn Leu Pro His Ala His Val Ser Gly Gly Val Ser Asn Leu Ser Phe 565 570 575 | | | 1728 |
| agc ttt cgc ggc aac gaa ccc gtg cgc gcg gcg atg cat gcg gtg ttt Ser Phe Arg Gly Asn Glu Pro Val Arg Ala Ala Met His Ala Val Phe 580 585 590 | | | 1776 |
| ctt tac cac gcc atc cgc gcc ggg atg gat atg ggg atc gtc aat gcc Leu Tyr His Ala Ile Arg Ala Gly Met Asp Met Gly Ile Val Asn Ala 595 600 605 | | | 1824 |
| ggg cag ctg gtg gtc tat gac cag atc gac ccc gag ctg cgc cag gcc Gly Gln Leu Val Val Tyr Asp Gln Ile Asp Pro Glu Leu Arg Gln Ala 610 615 620 | | | 1872 |

183

| | |
|---|------|
| tgc gag gat gtg gtg ctc aac cgc cag ccc aaa tcg ggc ggc acc gcg | 1920 |
| Cys Glu Asp Val Val Leu Asn Arg Gln Pro Lys Ser Gly Gly Thr Ala | |
| 625 630 635 640 | |
| acc gag cgg atg ctg gag gtg gcc gag cgc ttc cgc ggc ggc gcg cgc | 1968 |
| Thr Glu Arg Met Leu Glu Val Ala Glu Arg Phe Arg Gly Gly Ala Arg | |
| 645 650 655 | |
| gag gaa aag acc cgc gat ctg gcc tgg cgc gac tgg ccg gtg gaa aag | 2016 |
| Glu Glu Lys Thr Arg Asp Leu Ala Trp Arg Asp Trp Pro Val Glu Lys | |
| 660 665 670 | |
| cgg ctc gaa cat gcg ctg gtc aat ggc atc acc gaa ttc atc gag gcc | 2064 |
| Arg Leu Glu His Ala Leu Val Asn Gly Ile Thr Glu Phe Ile Glu Ala | |
| 675 680 685 | |
| gat acc gaa gcc gca agg ctt ctg gcc gaa cgc ccg ctg cat gtg atc | 2112 |
| Asp Thr Glu Ala Ala Arg Leu Leu Ala Glu Arg Pro Leu His Val Ile | |
| 690 695 700 | |
| gaa ggg ccg ctg atg gcg ggg atg aat gtc gtc ggt gat ctg ttc ggc | 2160 |
| Glu Gly Pro Leu Met Ala Gly Met Asn Val Val Gly Asp Leu Phe Gly | |
| 705 710 715 720 | |
| gcg ggc aag atg ttc ctg cca cag gtg gtg aaa tcg gcg cgc gtg atg | 2208 |
| Ala Gly Lys Met Phe Leu Pro Gln Val Val Lys Ser Ala Arg Val Met | |
| 725 730 735 | |
| aaa cag gcc gtc gcc gtt ctg ctg ccc tac atg gat gcc gaa aag gcc | 2256 |
| Lys Gln Ala Val Ala Val Leu Leu Pro Tyr Met Asp Ala Glu Lys Ala | |
| 740 745 750 | |
| gcg cgc ggc ggc gag ggg cgc gaa acc gcg ggc aag atc ctg atg gcc | 2304 |
| Ala Arg Gly Gly Glu Gly Arg Glu Thr Ala Gly Lys Ile Leu Met Ala | |
| 755 760 765 | |
| acg gtc aag ggc gat gtg cat gac atc ggc aag aac atc gtc ggc gtc | 2352 |
| Thr Val Lys Gly Asp Val His Asp Ile Gly Lys Asn Ile Val Gly Val | |
| 770 775 780 | |
| gtg ctg gcc tgc aac aat tac gac atc gtc gac ctg ggc gtg atg gtg | 2400 |
| Val Leu Ala Cys Asn Asn Tyr Asp Ile Val Asp Leu Gly Val Met Val | |
| 785 790 795 800 | |
| ccg ccg caa aag atc ctg gaa gtg gcg cgg gcc gaa aag gtc gat gcg | 2448 |
| Pro Pro Gln Lys Ile Leu Glu Val Ala Arg Ala Glu Lys Val Asp Ala | |
| 805 810 815 | |
| atc ggg ctt tcc ggg ctg atc acg cca agc ctg gac gag atg gtg cat | 2496 |
| Ile Gly Leu Ser Gly Leu Ile Thr Pro Ser Leu Asp Glu Met Val His | |
| 820 825 830 | |
| ctg gcc gcg gaa atg gag cgc gag ggc ttt gac att ccg ctg ctg atc | 2544 |
| Leu Ala Ala Glu Met Glu Arg Glu Gly Phe Asp Ile Pro Leu Leu Ile | |
| 835 840 845 | |
| ggc ggg gcg acc acg tcg aaa gtg cat acg gcg gtg aag atc gcc ccc | 2592 |
| Gly Gly Ala Thr Thr Ser Lys Val His Thr Ala Val Lys Ile Ala Pro | |
| 850 855 860 | |
| gcc tac agc cgc ggg cag gcg gtt tat gtg ctc gat gcc agc cgg gcc | 2640 |
| Ala Tyr Ser Arg Gly Gln Ala Val Tyr Val Leu Asp Ala Ser Arg Ala | |

| 184 | | | | | | | | | | | | | | | |
|---|------|--|--|-----|------|--|--|-----|------|--|--|-----|------|--|--|
| 865 | | | | 870 | | | | 875 | | | | 880 | | | |
| gtg ggg gtg gtg ggg gcg ctt ttg agc ccg aac cag aag gtc gat tac | 2688 | | | | | | | | | | | | | | |
| Val Gly Val Val Gly Ala Leu Leu Ser Pro Asn Gln Lys Val Asp Tyr | 885 | | | | 890 | | | | 895 | | | | | | |
| gcg gcg cag atc cgc gcg gac tat gcg cag atc gcc gcc cgt cat gcc | 2736 | | | | | | | | | | | | | | |
| Ala Ala Gln Ile Arg Ala Asp Tyr Ala Gln Ile Ala Ala Arg His Ala | 900 | | | | 905 | | | | 910 | | | | | | |
| cgc gac gag gcc gcc aag gtg cgg ctg cct ttg gcc gcg gcc cgg gcc | 2784 | | | | | | | | | | | | | | |
| Arg Asp Glu Ala Ala Lys Val Arg Leu Pro Leu Ala Ala Arg Ala | 915 | | | | 920 | | | | 925 | | | | | | |
| aat gcg ctg cgg ctc gac tgg tgc gcc tat gcc gtg ccc gcg ccg caa | 2832 | | | | | | | | | | | | | | |
| Asn Ala Leu Arg Leu Asp Trp Ser Gly Tyr Ala Val Pro Ala Pro Gln | 930 | | | | 935 | | | | 940 | | | | | | |
| ttc ctt ggc ccg cgc gtg atc gac gac tgg gat ctg gcc gaa gtg gcg | 2880 | | | | | | | | | | | | | | |
| Phe Leu Gly Pro Arg Val Ile Asp Asp Trp Asp Leu Ala Glu Val Ala | 945 | | | | 950 | | | | 955 | | | | 960 | | |
| cgg tat atc gac tgg acg ccc ttc ttc cat gcc tgg gaa ttg aag ggg | 2928 | | | | | | | | | | | | | | |
| Arg Tyr Ile Asp Trp Thr Pro Phe Phe His Ala Trp Glu Leu Lys Gly | 965 | | | | 970 | | | | 975 | | | | | | |
| gtc tat ccg cgg att ctc gat gac gcc gaa aag gcc gaa gcg gcg cgg | 2976 | | | | | | | | | | | | | | |
| Val Tyr Pro Arg Ile Leu Asp Asp Ala Glu Lys Gly Glu Ala Ala Arg | 980 | | | | 985 | | | | 990 | | | | | | |
| gca ctt ttc gcc gat gcc cag gcg atg ctg gcg cag atc att gcc gaa | 3024 | | | | | | | | | | | | | | |
| Ala Leu Phe Ala Asp Ala Gln Ala Met Leu Ala Gln Ile Ile Ala Glu | 995 | | | | 1000 | | | | 1005 | | | | | | |
| cgc tgg ttc acc ccg cgc gcc gtg gtg ggg ttc tgg ccc gcg cag gcg | 3072 | | | | | | | | | | | | | | |
| Arg Trp Phe Thr Pro Arg Ala Val Val Gly Phe Trp Pro Ala Gln Ala | 1010 | | | | 1015 | | | | 1020 | | | | | | |
| gtg ggc gac gat atc cgg ctt tac acc gac gag agc ccg acc gaa gac | 3120 | | | | | | | | | | | | | | |
| Val Gly Asp Asp Ile Arg Leu Tyr Thr Asp Glu Ser Arg Thr Glu Asp | 1025 | | | | 1030 | | | | 1035 | | | | 1040 | | |
| ctc gcc act ttc ttc acc ctg cgc cag cag acc gcc aag cgc gaa gcc | 3168 | | | | | | | | | | | | | | |
| Leu Ala Thr Phe Phe Thr Leu Arg Gln Gln Thr Gly Lys Arg Glu Gly | 1045 | | | | 1050 | | | | 1055 | | | | | | |
| cgc ccg aat gtg gct ttg gcc gat ttc gtc gcg cct gcg gcc acg gtg | 3216 | | | | | | | | | | | | | | |
| Arg Pro Asn Val Ala Leu Ala Asp Phe Val Ala Pro Ala Gly Thr Val | 1060 | | | | 1065 | | | | 1070 | | | | | | |
| ccc gat tat ctg gcc gcc ttc gtg gtc acc gcg gcc ccc gag gaa gcc | 3264 | | | | | | | | | | | | | | |
| Pro Asp Tyr Leu Gly Gly Phe Val Val Thr Ala Gly Pro Glu Glu Ala | 1075 | | | | 1080 | | | | 1085 | | | | | | |
| gag atc gcc gcg cgg ttc gaa gct gcc aat gac cat tat tcc gcg atc | 3312 | | | | | | | | | | | | | | |
| Glu Ile Ala Ala Arg Phe Glu Ala Ala Asn Asp His Tyr Ser Ala Ile | 1090 | | | | 1095 | | | | 1100 | | | | | | |
| ctg gtc aag gcg ctg gcc gac cgc ttt gcc gaa gcc ctg gcc gag gcc | 3360 | | | | | | | | | | | | | | |
| Leu Val Lys Ala Leu Ala Asp Arg Phe Ala Glu Ala Leu Ala Glu Ala | 1105 | | | | 1110 | | | | 1115 | | | | 1120 | | |

185

ctg cat cag cgg gtg cgg cgc gac tat tgg ggc tat gcg ccc gaa gaa 3408
 Leu His Gln Arg Val Arg Arg Asp Tyr Trp Gly Tyr Ala Pro Glu Glu
 1125 1130 1135

 agc ttc gcc ccc gat cag ctg gtg ggc gag ccc tat cgc ggc atc cgc 3456
 Ser Phe Ala Pro Asp Gln Leu Val Gly Glu Pro Tyr Arg Gly Ile Arg
 1140 1145 1150

 ccg gcg ccc ggc tat ccg gcc cag ccc gac cac acg gaa aag ctg acg 3504
 Pro Ala Pro Gly Tyr Pro Ala Gln Pro Asp His Thr Glu Lys Leu Thr
 1155 1160 1165

 ctg ttc cgg ctg ctt ggg gcc gag gcc gcg acc ggc gtg cat ctg acc 3552
 Leu Phe Arg Leu Leu Gly Ala Glu Ala Ala Thr Gly Val His Leu Thr
 1170 1175 1180

 gac agc atg gcg atg tgg ccc ggc tct tcg gtc tcg ggg ctc tat atc 3600
 Asp Ser Met Ala Met Trp Pro Gly Ser Ser Val Ser Gly Leu Tyr Ile
 1185 1190 1195 1200

 ggc cat ccg gag gcc tat tat ttc ggt ctg gcc cgg atc gag cag gat 3648
 Gly His Pro Glu Ala Tyr Tyr Phe Gly Leu Ala Arg Ile Glu Gln Asp
 1205 1210 1215

 cag gcc gcc gat tac gcc gcc cgc aag ggc atg gcc ttg gcc gag gtg 3696
 Gln Ala Ala Asp Tyr Ala Ala Arg Lys Gly Met Ala Leu Ala Glu Val
 1220 1225 1230

 cag cgc tgg ctg gcc ccg gtg ctg ggg tcg gcc gcg ccc gcc gcc gct 3744
 Gln Arg Trp Leu Ala Pro Val Leu Gly Ser Ala Ala Pro Ala Ala Ala
 1235 1240 1245

 gcg gtg gcc gcg tga 3759
 Ala Val Ala Ala
 1250

<210> 42
 <211> 1252
 <212> PRT
 <213> Rhodobacter capsulatus

<400> 42
 Met Leu Thr Gln Thr Leu Pro Arg Ser Ala Ala Phe Ala Ala Ile Glu
 1 5 10 15

 Ala Leu Ser Arg Gln Arg Ile Leu Ile Leu Asp Gly Ala Met Gly Thr
 20 25 30

 Gln Ile Gln Gln Leu Gly Leu Ser Glu Asp Asp Phe Leu Gly His Gly
 35 40 45

 Ser Gly Cys Ala Cys Arg His Ala Thr Asp His Pro Gln Lys Gly Asn
 50 55 60

 Asn Asp Leu Leu Val Leu Thr Gln Pro Gln Ala Ile Glu Glu Ile His
 65 70 75 80

 Phe Arg Tyr Ala Met Ala Gly Ala Asp Ile Val Glu Thr Asn Thr Phe
 85 90 95

 Ser Ala Thr Thr Ile Ala Gln Ala Asp Tyr Gly Leu Glu Ser Ala Val

186

| | | |
|--|-----|-----|
| 100 | 105 | 110 |
| Phe Asp Leu Asn Ala Ala Gly Ala Arg Val Ala Arg Ala Ala Met Asp 115 120 125 | | |
| Arg Ala Glu Ala Thr Asp Gly Arg Arg Arg Phe Val Ala Gly Ala Val 130 135 140 | | |
| Gly Pro Thr Asn Arg Thr Ala Ser Leu Ser Pro Asp Val Asn Asp Pro 145 150 155 160 | | |
| Gly Phe Arg Ala Val Thr Phe Asp Asp Leu Arg Thr Ala Tyr Gly Gln 165 170 175 | | |
| Gln Val Arg Gly Leu Ile Ala Gly Gly Ala Asp Ile Leu Leu Ile Glu 180 185 190 | | |
| Thr Ile Phe Asp Thr Leu Asn Ala Lys Ala Ala Ile Phe Ala Cys Phe 195 200 205 | | |
| Glu Ala Phe Ala Glu Arg Gly Glu Arg Leu Pro Val Met Ile Ser Gly 210 215 220 | | |
| Thr Ile Thr Asp Ala Ser Gly Arg Thr Leu Ser Gly Gln Thr Pro Thr 225 230 235 240 | | |
| Ala Phe Trp His Ser Val Ala His Ala Arg Pro Phe Thr Val Gly Leu 245 250 255 | | |
| Asn Cys Ala Leu Gly Ala Ser Ala Met Arg Pro His Leu Ala Glu Leu 260 265 270 | | |
| Ala Gly Val Ala Pro Cys Ala Ile Cys Ala Tyr Pro Asn Ala Gly Leu 275 280 285 | | |
| Pro Asn Ala Phe Gly Gln Tyr Asp Glu Thr Pro Asp Arg Thr Ala Ala 290 295 300 | | |
| Gln Val Ala Glu Phe Ala Arg Glu Gly Leu Val Asn Val Val Gly Gly 305 310 315 320 | | |
| Cys Cys Gly Thr Thr Pro Asp His Ile Arg Ala Ile Ala Glu Ala Val 325 330 335 | | |
| Lys Pro Phe Pro Pro Arg Ala Leu Pro Ser Arg Tyr Leu Arg Leu Ser 340 345 350 | | |
| Gly Leu Glu Pro Phe Thr Leu Thr Pro Asp Ile Pro Phe Val Asn Ile 355 360 365 | | |
| Gly Glu Arg Thr Asn Val Thr Gly Ser Ala Arg Phe Arg Lys Met Ile 370 375 380 | | |
| Val Ala Arg Asp Tyr Ala Ala Ala Leu Asp Val Ala Arg Asp Gln Val 385 390 395 400 | | |
| Glu Asn Gly Ala Gln Ile Leu Asp Ile Asn Met Asp Glu Gly Leu Ile 405 410 415 | | |
| Asp Ser Gln Ala Ala Met Val Ala Phe Leu Asn Leu Leu Ala Ala Glu 420 425 430 | | |

187

Pro Asp Ile Ala Arg Val Pro Val Met Ile Asp Ser Ser Lys Trp Glu
 435 440 445
 Val Ile Glu Ala Gly Leu Lys Cys Val Gln Gly Lys Pro Val Val Asn
 450 455 460
 Ser Ile Ser Leu Lys Glu Gly Glu Glu Ile Phe Arg His His Ala Ala
 465 470 475 480
 Leu Cys Leu Ala Tyr Gly Ala Ala Val Val Val Met Ala Phe Asp Glu
 485 490 495
 Glu Gly Gln Ala Asp Ser Phe Ala Arg Lys Thr Ser Ile Cys Ala Arg
 500 505 510
 Ala Tyr Arg Ile Leu Val Glu Glu Ile Gly Phe Pro Pro Glu Asp Ile
 515 520 525
 Ile Phe Asp Pro Asn Val Phe Ala Val Ala Thr Gly Ile Glu Glu His
 530 535 540
 Asp Asn Tyr Gly Val Asp Phe Ile Glu Ala Ala Arg Trp Ile Arg Ala
 545 550 555 560
 Asn Leu Pro His Ala His Val Ser Gly Gly Val Ser Asn Leu Ser Phe
 565 570 575
 Ser Phe Arg Gly Asn Glu Pro Val Arg Ala Ala Met His Ala Val Phe
 580 585 590
 Leu Tyr His Ala Ile Arg Ala Gly Met Asp Met Gly Ile Val Asn Ala
 595 600 605
 Gly Gln Leu Val Val Tyr Asp Gln Ile Asp Pro Glu Leu Arg Gln Ala
 610 615 620
 Cys Glu Asp Val Val Leu Asn Arg Gln Pro Lys Ser Gly Gly Thr Ala
 625 630 635 640
 Thr Glu Arg Met Leu Glu Val Ala Glu Arg Phe Arg Gly Gly Ala Arg
 645 650 655
 Glu Glu Lys Thr Arg Asp Leu Ala Trp Arg Asp Trp Pro Val Glu Lys
 660 665 670
 Arg Leu Glu His Ala Leu Val Asn Gly Ile Thr Glu Phe Ile Glu Ala
 675 680 685
 Asp Thr Glu Ala Ala Arg Leu Leu Ala Glu Arg Pro Leu His Val Ile
 690 695 700
 Glu Gly Pro Leu Met Ala Gly Met Asn Val Val Gly Asp Leu Phe Gly
 705 710 715 720
 Ala Gly Lys Met Phe Leu Pro Gln Val Val Lys Ser Ala Arg Val Met
 725 730 735
 Lys Gln Ala Val Ala Val Leu Leu Pro Tyr Met Asp Ala Glu Lys Ala
 740 745 750
 Ala Arg Gly Gly Glu Gly Arg Glu Thr Ala Gly Lys Ile Leu Met Ala
 755 760 765

188

Thr Val Lys Gly Asp Val His Asp Ile Gly Lys Asn Ile Val Gly Val
 770 775 780
 Val Leu Ala Cys Asn Asn Tyr Asp Ile Val Asp Leu Gly Val Met Val
 785 790 795 800
 Pro Pro Gln Lys Ile Leu Glu Val Ala Arg Ala Glu Lys Val Asp Ala
 805 810 815
 Ile Gly Leu Ser Gly Leu Ile Thr Pro Ser Leu Asp Glu Met Val His
 820 825 830
 Leu Ala Ala Glu Met Glu Arg Glu Gly Phe Asp Ile Pro Leu Leu Ile
 835 840 845
 Gly Gly Ala Thr Thr Ser Lys Val His Thr Ala Val Lys Ile Ala Pro
 850 855 860
 Ala Tyr Ser Arg Gly Gln Ala Val Tyr Val Leu Asp Ala Ser Arg Ala
 865 870 875 880
 Val Gly Val Val Gly Ala Leu Leu Ser Pro Asn Gln Lys Val Asp Tyr
 885 890 895
 Ala Ala Gln Ile Arg Ala Asp Tyr Ala Gln Ile Ala Ala Arg His Ala
 900 905 910
 Arg Asp Glu Ala Ala Lys Val Arg Leu Pro Leu Ala Ala Ala Arg Ala
 915 920 925
 Asn Ala Leu Arg Leu Asp Trp Ser Gly Tyr Ala Val Pro Ala Pro Gln
 930 935 940
 Phe Leu Gly Pro Arg Val Ile Asp Asp Trp Asp Leu Ala Glu Val Ala
 945 950 955 960
 Arg Tyr Ile Asp Trp Thr Pro Phe Phe His Ala Trp Glu Leu Lys Gly
 965 970 975
 Val Tyr Pro Arg Ile Leu Asp Asp Ala Glu Lys Gly Glu Ala Ala Arg
 980 985 990
 Ala Leu Phe Ala Asp Ala Gln Ala Met Leu Ala Gln Ile Ile Ala Glu
 995 1000 1005
 Arg Trp Phe Thr Pro Arg Ala Val Val Gly Phe Trp Pro Ala Gln Ala
 1010 1015 1020
 Val Gly Asp Asp Ile Arg Leu Tyr Thr Asp Glu Ser Arg Thr Glu Asp
 1025 1030 1035 1040
 Leu Ala Thr Phe Phe Thr Leu Arg Gln Gln Thr Gly Lys Arg Glu Gly
 1045 1050 1055
 Arg Pro Asn Val Ala Leu Ala Asp Phe Val Ala Pro Ala Gly Thr Val
 1060 1065 1070
 Pro Asp Tyr Leu Gly Gly Phe Val Val Thr Ala Gly Pro Glu Glu Ala
 1075 1080 1085
 Glu Ile Ala Ala Arg Phe Glu Ala Ala Asn Asp His Tyr Ser Ala Ile

189

| | | | |
|---|------|------|------|
| 1090 | 1095 | 1100 | |
| Leu Val Lys Ala Leu Ala Asp Arg Phe Ala Glu Ala Leu Ala Glu Ala | | | |
| 1105 | 1110 | 1115 | 1120 |
| Leu His Gln Arg Val Arg Arg Asp Tyr Trp Gly Tyr Ala Pro Glu Glu | | | |
| | 1125 | 1130 | 1135 |
| Ser Phe Ala Pro Asp Gln Leu Val Gly Glu Pro Tyr Arg Gly Ile Arg | | | |
| | 1140 | 1145 | 1150 |
| Pro Ala Pro Gly Tyr Pro Ala Gln Pro Asp His Thr Glu Lys Leu Thr | | | |
| | 1155 | 1160 | 1165 |
| Leu Phe Arg Leu Leu Gly Ala Glu Ala Ala Thr Gly Val His Leu Thr | | | |
| | 1170 | 1175 | 1180 |
| Asp Ser Met Ala Met Trp Pro Gly Ser Ser Val Ser Gly Leu Tyr Ile | | | |
| 1185 | 1190 | 1195 | 1200 |
| Gly His Pro Glu Ala Tyr Tyr Phe Gly Leu Ala Arg Ile Glu Gln Asp | | | |
| | 1205 | 1210 | 1215 |
| Gln Ala Ala Asp Tyr Ala Ala Arg Lys Gly Met Ala Leu Ala Glu Val | | | |
| | 1220 | 1225 | 1230 |
| Gln Arg Trp Leu Ala Pro Val Leu Gly Ser Ala Ala Pro Ala Ala Ala | | | |
| | 1235 | 1240 | 1245 |
| Ala Val Ala Ala | | | |
| 1250 | | | |

<210> 43
 <211> 3798
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1) .. (3795)
 <223> RHS24705

<400> 43

| | |
|---|-----|
| atg tca ccc gcg ctc caa gac ctg tcg caa ccc gaa ggt ctg aag aaa | 48 |
| Met Ser Pro Ala Leu Gln Asp Leu Ser Gln Pro Glu Gly Leu Lys Lys | |
| 1 5 10 15 | |
| acc ctg cgg gat gag atc aat gcc att ctg cag aag agg att atg gtg | 96 |
| Thr Leu Arg Asp Glu Ile Asn Ala Ile Leu Gln Lys Arg Ile Met Val | |
| 20 25 30 | |
| ctg gat gga ggg atg ggg acc atg atc cag cgg gag aag cta aac gaa | 144 |
| Leu Asp Gly Gly Met Gly Thr Met Ile Gln Arg Glu Lys Leu Asn Glu | |
| 35 40 45 | |
| gaa cac ttc cga ggt cag gaa ttt aaa gat cat gcc agg ccg ctg aaa | 192 |
| Glu His Phe Arg Gly Gln Glu Phe Lys Asp His Ala Arg Pro Leu Lys | |
| 50 55 60 | |
| ggc aac aat gac att tta agt ata act cag cct gat gtc att tac caa | 240 |
| Gly Asn Asn Asp Ile Leu Ser Ile Thr Gln Pro Asp Val Ile Tyr Gln | |

| 65 | 70 | 190 | 75 | 80 | |
|---|-----|-----|-----|-----|-----|
| atc cat aag gaa tac ttg ctg gct ggg gca gat atc att gaa aca aat | | | | | 288 |
| Ile His Lys Glu Tyr Leu Leu Ala Gly Ala Asp Ile Ile Glu Thr Asn | 85 | | 90 | 95 | |
| act ttt agc agc act agt att gcc caa gct gac tat ggc ctt gaa cac | | | | | 336 |
| Thr Phe Ser Ser Thr Ser Ile Ala Gln Ala Asp Tyr Gly Leu Glu His | 100 | | 105 | 110 | |
| ttg gcc tac cgg atg aac atg tgc tct gca gga gtg gcc aga aaa gct | | | | | 384 |
| Leu Ala Tyr Arg Met Asn Met Cys Ser Ala Gly Val Ala Arg Lys Ala | 115 | | 120 | 125 | |
| gcc gag gag gta act ctc cag aca gga att aag agg ttt gtg gca ggg | | | | | 432 |
| Ala Glu Glu Val Thr Leu Gln Thr Gly Ile Lys Arg Phe Val Ala Gly | 130 | | 135 | 140 | |
| gct ctg ggt ccg act aat aag aca ctc tct gtg tcc cca tct gtg gaa | | | | | 480 |
| Ala Leu Gly Pro Thr Asn Lys Thr Leu Ser Val Ser Pro Ser Val Glu | 145 | | 150 | 155 | 160 |
| agg ccg gat tat agg aac atc aca ttt gat gag ctt gtt gaa gca tac | | | | | 528 |
| Arg Pro Asp Tyr Arg Asn Ile Thr Phe Asp Glu Leu Val Glu Ala Tyr | 165 | | 170 | 175 | |
| caa gag cag gcc aaa gga ctt ctg gat ggc ggg gtt gat atc tta ctc | | | | | 576 |
| Gln Glu Gln Ala Lys Gly Leu Leu Asp Gly Gly Val Asp Ile Leu Leu | 180 | | 185 | 190 | |
| att gaa act att ttt gat act gcc aat gcc aag gca gcc ttg ttt gca | | | | | 624 |
| Ile Glu Thr Ile Phe Asp Thr Ala Asn Ala Lys Ala Ala Leu Phe Ala | 195 | | 200 | 205 | |
| ctc caa aat ctt ttt gag gag aaa tat gct ccc cgg cct atc ttt att | | | | | 672 |
| Leu Gln Asn Leu Phe Glu Glu Lys Tyr Ala Pro Arg Pro Ile Phe Ile | 210 | | 215 | 220 | |
| tca ggg acg atc gtt gat aaa agt ggg cgg act ctt tcc gga cag aca | | | | | 720 |
| Ser Gly Thr Ile Val Asp Lys Ser Gly Arg Thr Leu Ser Gly Gln Thr | 225 | | 230 | 235 | 240 |
| gga gag gga ttt gtc atc agc gtg tct cat gga gaa cca ctc tgc att | | | | | 768 |
| Gly Glu Gly Phe Val Ile Ser Val Ser His Gly Glu Pro Leu Cys Ile | 245 | | 250 | 255 | |
| gga tta aat tgt gct ttg ggt gca gct gaa atg aga cct ttt att gaa | | | | | 816 |
| Gly Leu Asn Cys Ala Leu Gly Ala Ala Glu Met Arg Pro Phe Ile Glu | 260 | | 265 | 270 | |
| ata att gga aaa tgt aca aca gcc tat gtc ctc tgt tat ccc aat gca | | | | | 864 |
| Ile Ile Gly Lys Cys Thr Thr Ala Tyr Val Leu Cys Tyr Pro Asn Ala | 275 | | 280 | 285 | |
| ggt ctt ccc aac acc ttt ggt gac tat gat gaa acg cct tct atg atg | | | | | 912 |
| Gly Leu Pro Asn Thr Phe Gly Asp Tyr Asp Glu Thr Pro Ser Met Met | 290 | | 295 | 300 | |
| gcc aag cac cta aag gat ttt gct atg gat ggc ttg gtc aat ata gtt | | | | | 960 |
| Ala Lys His Leu Lys Asp Phe Ala Met Asp Gly Leu Val Asn Ile Val | 305 | | 310 | 315 | 320 |

191

| | |
|---|------|
| gga gga tgc tgt ggg tca aca cca gat cat atc agg gaa att gct gaa | 1008 |
| Gly Gly Cys Cys Gly Ser Thr Pro Asp His Ile Arg Glu Ile Ala Glu | |
| 325 330 335 | |
| gct gtg aaa aat tgt aag cct aga gtt cca cct gcc act gct ttt gaa | 1056 |
| Ala Val Lys Asn Cys Lys Pro Arg Val Pro Pro Ala Thr Ala Phe Glu | |
| 340 345 350 | |
| gga cat atg tta ctg tct ggt cta gag ccc ttc agg att gga ccg tac | 1104 |
| Gly His Met Leu Leu Ser Gly Leu Glu Pro Phe Arg Ile Gly Pro Tyr | |
| 355 360 365 | |
| acc aac ttt gtt aac att gga gag cgc tgt aat gtt gca gga tca agg | 1152 |
| Thr Asn Phe Val Asn Ile Gly Glu Arg Cys Asn Val Ala Gly Ser Arg | |
| 370 375 380 | |
| aag ttt gct aaa ctc atc atg gca gga aac tat gaa gaa gcc ttg tgt | 1200 |
| Lys Phe Ala Lys Leu Ile Met Ala Gly Asn Tyr Glu Glu Ala Leu Cys | |
| 385 390 395 400 | |
| gtt gcc aaa gtg cag gtg gaa atg gga gcc cag gtg ttg gat gtc aac | 1248 |
| Val Ala Lys Val Gln Val Glu Met Gly Ala Gln Val Leu Asp Val Asn | |
| 405 410 415 | |
| atg gat gat ggc atg cta gat ggt cca agt gca atg acc aga ttt tgc | 1296 |
| Met Asp Asp Gly Met Leu Asp Gly Pro Ser Ala Met Thr Arg Phe Cys | |
| 420 425 430 | |
| aac tta att gct tcc gag cca gac atc gca aag gta cct ttg tgc atc | 1344 |
| Asn Leu Ile Ala Ser Glu Pro Asp Ile Ala Lys Val Pro Leu Cys Ile | |
| 435 440 445 | |
| gac tcc tcc aat ttt gct gtg att gaa gct ggg tta aag tgc tgc caa | 1392 |
| Asp Ser Ser Asn Phe Ala Val Ile Glu Ala Gly Leu Lys Cys Cys Gln | |
| 450 455 460 | |
| ggg aag tgc att gtc aat agc att agt ctg aag gaa gga gag gac gac | 1440 |
| Gly Lys Cys Ile Val Asn Ser Ile Ser Leu Lys Glu Gly Glu Asp Asp | |
| 465 470 475 480 | |
| ttc ttg gag aag gcc agg aag att aaa aag tat gga gct gct atg gtg | 1488 |
| Phe Leu Glu Lys Ala Arg Lys Ile Lys Lys Tyr Gly Ala Ala Met Val | |
| 485 490 495 | |
| gtc atg gct ttt gat gaa gaa gga cag gca aca gaa aca gac aca aaa | 1536 |
| Val Met Ala Phe Asp Glu Glu Gly Gln Ala Thr Glu Thr Asp Thr Lys | |
| 500 505 510 | |
| atc aga gtg tgc acc cgg gcc tac cat ctg ctt gtg aaa aaa ctg ggc | 1584 |
| Ile Arg Val Cys Thr Arg Ala Tyr His Leu Leu Val Lys Lys Leu Gly | |
| 515 520 525 | |
| ttt aat cca aat gac att att ttt gac cct aat atc cta acc att ggg | 1632 |
| Phe Asn Pro Asn Asp Ile Ile Phe Asp Pro Asn Ile Leu Thr Ile Gly | |
| 530 535 540 | |
| act gga atg gag gaa cac aac ttg tat gcc att aat ttt atc cat gca | 1680 |
| Thr Gly Met Glu Glu His Asn Leu Tyr Ala Ile Asn Phe Ile His Ala | |
| 545 550 555 560 | |
| aca aaa gtc att aaa gaa aca tta cct gga gcc aga ata agt gga ggt | 1728 |
| Thr Lys Val Ile Lys Glu Thr Leu Pro Gly Ala Arg Ile Ser Gly Gly | |

| 192 | | | | | | | | | | | | | | | |
|---|------|--|--|--|-----|-----|--|--|--|-----|-----|--|--|--|--|
| 565 | | | | | 570 | | | | | 575 | | | | | |
| ctt tcc aac ttg tcc ttc tcc ttc cga gga atg gaa gcc att cga gaa | 1776 | | | | | | | | | | | | | | |
| Leu Ser Asn Leu Ser Phe Ser Phe Arg Gly Met Glu Ala Ile Arg Glu | | | | | | | | | | | | | | | |
| 580 | 585 | | | | | 590 | | | | | | | | | |
| gca atg cat ggg gtt ttc ctt tac cat gca atc aag tct ggc atg gac | 1824 | | | | | | | | | | | | | | |
| Ala Met His Gly Val Phe Leu Tyr His Ala Ile Lys Ser Gly Met Asp | | | | | | | | | | | | | | | |
| 595 | 600 | | | | | 605 | | | | | | | | | |
| atg ggg ata gtg aat gct gga aac ctc cct gtg tat gat gat atc cat | 1872 | | | | | | | | | | | | | | |
| Met Gly Ile Val Asn Ala Gly Asn Leu Pro Val Tyr Asp Asp Ile His | | | | | | | | | | | | | | | |
| 610 | 615 | | | | | 620 | | | | | | | | | |
| aag gaa ctt ctg cag ctc tgt gaa gat ctc atc tgg aat aaa gac cct | 1920 | | | | | | | | | | | | | | |
| Lys Glu Leu Leu Gln Leu Cys Glu Asp Leu Ile Trp Asn Lys Asp Pro | | | | | | | | | | | | | | | |
| 625 | 630 | | | | | 635 | | | | | 640 | | | | |
| gag gcc act gag aag ctc tta cgt tat gcc cag act caa ggc aca gga | 1968 | | | | | | | | | | | | | | |
| Glu Ala Thr Glu Lys Leu Leu Arg Tyr Ala Gln Thr Gln Gly Thr Gly | | | | | | | | | | | | | | | |
| 645 | 650 | | | | | 655 | | | | | | | | | |
| ggg aag aaa gtc att cag act gat gag tgg aga aat ggc cct gtc gaa | 2016 | | | | | | | | | | | | | | |
| Gly Lys Lys Val Ile Gln Thr Asp Glu Trp Arg Asn Gly Pro Val Glu | | | | | | | | | | | | | | | |
| 660 | 665 | | | | | 670 | | | | | | | | | |
| gaa cgc ctt gag tat gcc ctt gtg aag ggc att gaa aaa cat att att | 2064 | | | | | | | | | | | | | | |
| Glu Arg Leu Glu Tyr Ala Leu Val Lys Gly Ile Glu Lys His Ile Ile | | | | | | | | | | | | | | | |
| 675 | 680 | | | | | 685 | | | | | | | | | |
| gag gat act gag gaa gcc agg tta aac caa aaa aaa tat ccc cga cct | 2112 | | | | | | | | | | | | | | |
| Glu Asp Thr Glu Glu Ala Arg Leu Asn Gln Lys Lys Tyr Pro Arg Pro | | | | | | | | | | | | | | | |
| 690 | 695 | | | | | 700 | | | | | | | | | |
| ctc aat ata att gaa gga ccc ctg atg aat gga atg aaa att gtt ggt | 2160 | | | | | | | | | | | | | | |
| Leu Asn Ile Ile Glu Gly Pro Leu Met Asn Gly Met Lys Ile Val Gly | | | | | | | | | | | | | | | |
| 705 | 710 | | | | | 715 | | | | | 720 | | | | |
| gat ctt ttt gga gct gga aaa atg ttt cta cct cag gtt ata aag tca | 2208 | | | | | | | | | | | | | | |
| Asp Leu Phe Gly Ala Gly Lys Met Phe Leu Pro Gln Val Ile Lys Ser | | | | | | | | | | | | | | | |
| 725 | 730 | | | | | 735 | | | | | | | | | |
| gcc cgg gtt atg aag aag gct gtt ggc cac ctt atc cct ttc atg gaa | 2256 | | | | | | | | | | | | | | |
| Ala Arg Val Met Lys Lys Ala Val Gly His Leu Ile Pro Phe Met Glu | | | | | | | | | | | | | | | |
| 740 | 745 | | | | | 750 | | | | | | | | | |
| aaa gaa aga gaa gaa acc aga gtg ctt aac ggc aca gta gaa gaa gag | 2304 | | | | | | | | | | | | | | |
| Lys Glu Arg Glu Glu Thr Arg Val Leu Asn Gly Thr Val Glu Glu Glu | | | | | | | | | | | | | | | |
| 755 | 760 | | | | | 765 | | | | | | | | | |
| gac cct tac cag ggc acc atc gtg ctg gcc act gtt aaa ggc gac gtg | 2352 | | | | | | | | | | | | | | |
| Asp Pro Tyr Gln Gly Thr Ile Val Leu Ala Thr Val Lys Gly Asp Val | | | | | | | | | | | | | | | |
| 770 | 775 | | | | | 780 | | | | | | | | | |
| cac gac ata ggc aag aac ata gtt gga gta gtc ctt ggc tgc aat aat | 2400 | | | | | | | | | | | | | | |
| His Asp Ile Gly Lys Asn Ile Val Gly Val Leu Gly Cys Asn Asn | | | | | | | | | | | | | | | |
| 785 | 790 | | | | | 795 | | | | | 800 | | | | |
| ttc cga gtt att gat tta gga gtc atg act cca tgt gat aag ata ctg | 2448 | | | | | | | | | | | | | | |
| Phe Arg Val Ile Asp Leu Gly Val Met Thr Pro Cys Asp Lys Ile Leu | | | | | | | | | | | | | | | |
| 805 | 810 | | | | | 815 | | | | | | | | | |

193

| | |
|---|------|
| aaa gct gct ctt gac cac aaa gca gat ata att ggc ctg tca gga ctc | 2496 |
| Lys Ala Ala Leu Asp His Lys Ala Asp Ile Ile Gly Leu Ser Gly Leu | |
| 820 825 830 | |
| atc act cct tcc ctg gat gaa atg att ttt gtt gcc aag gaa atg gag | 2544 |
| Ile Thr Pro Ser Leu Asp Glu Met Ile Phe Val Ala Lys Glu Met Glu | |
| 835 840 845 | |
| aga tta gct ata agg att cca ttg ttg att gga gga gca acc act tca | 2592 |
| Arg Leu Ala Ile Arg Ile Pro Leu Leu Ile Gly Gly Ala Thr Thr Ser | |
| 850 855 860 | |
| aaa acc cac aca gca gtt aaa ata gct ccg aga tac agt gca cct gta | 2640 |
| Lys Thr His Thr Ala Val Lys Ile Ala Pro Arg Tyr Ser Ala Pro Val | |
| 865 870 875 880 | |
| atc cat gtc ctg gac gcg tcc aag agt gtg gtg gtg tgt tcc cag ctg | 2688 |
| Ile His Val Leu Asp Ala Ser Lys Ser Val Val Val Cys Ser Gln Leu | |
| 885 890 895 | |
| tta gat gaa aat cta aag gat gaa tac ttt gag gaa atc atg gaa gaa | 2736 |
| Leu Asp Glu Asn Leu Lys Asp Glu Tyr Phe Glu Glu Ile Met Glu Glu | |
| 900 905 910 | |
| tat gaa gat att aga cag gac cat tat gag tct ctc aag gag agg aga | 2784 |
| Tyr Glu Asp Ile Arg Gln Asp His Tyr Glu Ser Leu Lys Glu Arg Arg | |
| 915 920 925 | |
| tac tta ccc tta agt caa gcc aga aaa agt ggt ttc caa atg gat tgg | 2832 |
| Tyr Leu Pro Leu Ser Gln Ala Arg Lys Ser Gly Phe Gln Met Asp Trp | |
| 930 935 940 | |
| ctg tct gaa cct cac cca gtg aag ccc acg ttt att ggg acc cag gtc | 2880 |
| Leu Ser Glu Pro His Pro Val Lys Pro Thr Phe Ile Gly Thr Gln Val | |
| 945 950 955 960 | |
| ttt gaa gac tat gac ctg cag aag ctg gtg gac tac att gac tgg aag | 2928 |
| Phe Glu Asp Tyr Asp Leu Gln Lys Leu Val Asp Tyr Ile Asp Trp Lys | |
| 965 970 975 | |
| cct ttc ttt gat gtc tgg cag ctc cgg ggc aag tac ccg aat cga ggc | 2976 |
| Pro Phe Phe Asp Val Trp Gln Leu Arg Gly Lys Tyr Pro Asn Arg Gly | |
| 980 985 990 | |
| ttt ccc aag ata ttt aac gac aaa aca gta ggt gga gag gcc agg aag | 3024 |
| Phe Pro Lys Ile Phe Asn Asp Lys Thr Val Gly Gly Glu Ala Arg Lys | |
| 995 1000 1005 | |
| gtc tac gat gat gcc cac aat atg ctg aac aca ctg att agt caa aag | 3072 |
| Val Tyr Asp Asp Ala His Asn Met Leu Asn Thr Leu Ile Ser Gln Lys | |
| 1010 1015 1020 | |
| aaa ctc cgg gcc cgg ggt gtg gtt ggg ttc tgg cca gca cag agt atc | 3120 |
| Lys Leu Arg Ala Arg Gly Val Val Gly Phe Trp Pro Ala Gln Ser Ile | |
| 1025 1030 1035 1040 | |
| caa gac gac att cac ctg tac gcg gag gct gct gtg ccc cag gct gca | 3168 |
| Gln Asp Asp Ile His Leu Tyr Ala Glu Ala Ala Val Pro Gln Ala Ala | |
| 1045 1050 1055 | |
| gag ccc ata gcc acc ttc tat ggg tta agg caa cag gct gag aag gac | 3216 |
| Glu Pro Ile Ala Thr Phe Tyr Gly Leu Arg Gln Gln Ala Glu Lys Asp | |

194

| 1060 | 1065 | 1070 | |
|---|------|------|------|
| tct gcc agc acg gag cca tac tac tgc ctc tca gac ttc atc gct ccc | | | 3264 |
| Ser Ala Ser Thr Glu Pro Tyr Tyr Cys Leu Ser Asp Phe Ile Ala Pro | | | |
| 1075 | 1080 | 1085 | |
| ttg cat tct ggc atc cgt gac tac ctg ggc ctg ttt gcc gtt gcc tgc | | | 3312 |
| Leu His Ser Gly Ile Arg Asp Tyr Leu Gly Leu Phe Ala Val Ala Cys | | | |
| 1090 | 1095 | 1100 | |
| ttt ggg gta gaa gag ctg agc aag gcc tat gag gat gat ggt gac gac | | | 3360 |
| Phe Gly Val Glu Glu Leu Ser Lys Ala Tyr Glu Asp Asp Gly Asp Asp | | | |
| 1105 | 1110 | 1115 | 1120 |
| tac agc agc atc atg gtc aag gcg ctg ggg gac cgg ctg gca gag gcc | | | 3408 |
| Tyr Ser Ser Ile Met Val Lys Ala Leu Gly Asp Arg Leu Ala Glu Ala | | | |
| 1125 | 1130 | 1135 | |
| ttt gca gaa gag ctc cat gaa aga gtt cgc cga gaa ctg tgg gcc tac | | | 3456 |
| Phe Ala Glu Glu Leu His Glu Arg Val Arg Arg Glu Leu Trp Ala Tyr | | | |
| 1140 | 1145 | 1150 | |
| tgt ggc agt gag cag ctg gac gtc gca gac ctg cgc agg ctg cgg tac | | | 3504 |
| Cys Gly Ser Glu Gln Leu Asp Val Ala Asp Leu Arg Arg Leu Arg Tyr | | | |
| 1155 | 1160 | 1165 | |
| aag ggc atc cgc ccg gct cct ggc tac ccc agc cag ccc gac tac acc | | | 3552 |
| Lys Gly Ile Arg Pro Ala Pro Gly Tyr Pro Ser Gln Pro Asp His Thr | | | |
| 1170 | 1175 | 1180 | |
| gag aag ctc acc atg tgg aga ctt gca gac atc gag cag tct aca ggc | | | 3600 |
| Glu Lys Leu Thr Met Trp Arg Leu Ala Asp Ile Glu Gln Ser Thr Gly | | | |
| 1185 | 1190 | 1195 | 1200 |
| att agg tta aca gaa tca tta gca atg gca cct gct tca gca gtc tca | | | 3648 |
| Ile Arg Leu Thr Glu Ser Leu Ala Met Ala Pro Ala Ser Ala Val Ser | | | |
| 1205 | 1210 | 1215 | |
| ggc ctc tac ttc tcc aat ttg aag tcc aaa tat ttt gct gtg ggg aag | | | 3696 |
| Gly Leu Tyr Phe Ser Asn Leu Lys Ser Lys Tyr Phe Ala Val Gly Lys | | | |
| 1220 | 1225 | 1230 | |
| att tcc aag gat cag gtt gag gat tat gca ttg agg aag aac ata tct | | | 3744 |
| Ile Ser Lys Asp Gln Val Glu Asp Tyr Ala Leu Arg Lys Asn Ile Ser | | | |
| 1235 | 1240 | 1245 | |
| gtg gct gag gtt gag aaa tgg ctt gga ccc att ttg gga tat gat aca | | | 3792 |
| Val Ala Glu Val Glu Lys Trp Leu Gly Pro Ile Leu Gly Tyr Asp Thr | | | |
| 1250 | 1255 | 1260 | |
| gac taa | | | 3798 |
| Asp | | | |
| 1265 | | | |

<210> 44

<211> 1265

<212> PRT

<213> Homo sapiens

<400> 44

Met Ser Pro Ala Leu Gln Asp Leu Ser Gln Pro Glu Gly Leu Lys Lys

195

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 1 | 5 | 10 | 15 | | | | | | | | | | | | |
| Thr | Leu | Arg | Asp | Glu | Ile | Asn | Ala | Ile | Leu | Gln | Lys | Arg | Ile | Met | Val |
| | | | 20 | | | | | 25 | | | | | | 30 | |
| Leu | Asp | Gly | Gly | Met | Gly | Thr | Met | Ile | Gln | Arg | Glu | Lys | Leu | Asn | Glu |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Glu | His | Phe | Arg | Gly | Gln | Glu | Phe | Lys | Asp | His | Ala | Arg | Pro | Leu | Lys |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Gly | Asn | Asn | Asp | Ile | Leu | Ser | Ile | Thr | Gln | Pro | Asp | Val | Ile | Tyr | Gln |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 |
| Ile | His | Lys | Glu | Tyr | Leu | Leu | Ala | Gly | Ala | Asp | Ile | Ile | Glu | Thr | Asn |
| | | | | 85 | | | | | 90 | | | | | 95 | |
| Thr | Phe | Ser | Ser | Thr | Ser | Ile | Ala | Gln | Ala | Asp | Tyr | Gly | Leu | Glu | His |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Leu | Ala | Tyr | Arg | Met | Asn | Met | Cys | Ser | Ala | Gly | Val | Ala | Arg | Lys | Ala |
| | | 115 | | | | | 120 | | | | | 125 | | | |
| Ala | Glu | Glu | Val | Thr | Leu | Gln | Thr | Gly | Ile | Lys | Arg | Phe | Val | Ala | Gly |
| 130 | | | | | | 135 | | | | | 140 | | | | |
| Ala | Leu | Gly | Pro | Thr | Asn | Lys | Thr | Leu | Ser | Val | Ser | Pro | Ser | Val | Glu |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 |
| Arg | Pro | Asp | Tyr | Arg | Asn | Ile | Thr | Phe | Asp | Glu | Leu | Val | Glu | Ala | Tyr |
| | | | 165 | | | | | 170 | | | | | | 175 | |
| Gln | Glu | Gln | Ala | Lys | Gly | Leu | Leu | Asp | Gly | Gly | Val | Asp | Ile | Leu | Leu |
| | | | 180 | | | | | 185 | | | | | 190 | | |
| Ile | Glu | Thr | Ile | Phe | Asp | Thr | Ala | Asn | Ala | Lys | Ala | Ala | Leu | Phe | Ala |
| | 195 | | | | | | 200 | | | | | 205 | | | |
| Leu | Gln | Asn | Leu | Phe | Glu | Glu | Lys | Tyr | Ala | Pro | Arg | Pro | Ile | Phe | Ile |
| 210 | | | | | | 215 | | | | | 220 | | | | |
| Ser | Gly | Thr | Ile | Val | Asp | Lys | Ser | Gly | Arg | Thr | Leu | Ser | Gly | Gln | Thr |
| 225 | | | | 230 | | | | | 235 | | | | | 240 | |
| Gly | Glu | Gly | Phe | Val | Ile | Ser | Val | Ser | His | Gly | Glu | Pro | Leu | Cys | Ile |
| | | | 245 | | | | | 250 | | | | | | 255 | |
| Gly | Leu | Asn | Cys | Ala | Leu | Gly | Ala | Ala | Glu | Met | Arg | Pro | Phe | Ile | Glu |
| | | 260 | | | | | 265 | | | | | | 270 | | |
| Ile | Ile | Gly | Lys | Cys | Thr | Thr | Ala | Tyr | Val | Leu | Cys | Tyr | Pro | Asn | Ala |
| | 275 | | | | | | 280 | | | | | 285 | | | |
| Gly | Leu | Pro | Asn | Thr | Phe | Gly | Asp | Tyr | Asp | Glu | Thr | Pro | Ser | Met | Met |
| 290 | | | | | | 295 | | | | | 300 | | | | |
| Ala | Lys | His | Leu | Lys | Asp | Phe | Ala | Met | Asp | Gly | Leu | Val | Asn | Ile | Val |
| 305 | | | | 310 | | | | | | 315 | | | | 320 | |
| Gly | Gly | Cys | Cys | Gly | Ser | Thr | Pro | Asp | His | Ile | Arg | Glu | Ile | Ala | Glu |
| | | | 325 | | | | | | 330 | | | | | 335 | |

196

Ala Val Lys Asn Cys Lys Pro Arg Val Pro Pro Ala Thr Ala Phe Glu
 340 345 350
 Gly His Met Leu Leu Ser Gly Leu Glu Pro Phe Arg Ile Gly Pro Tyr
 355 360 365
 Thr Asn Phe Val Asn Ile Gly Glu Arg Cys Asn Val Ala Gly Ser Arg
 370 375 380
 Lys Phe Ala Lys Leu Ile Met Ala Gly Asn Tyr Glu Glu Ala Leu Cys
 385 390 395 400
 Val Ala Lys Val Gln Val Glu Met Gly Ala Gln Val Leu Asp Val Asn
 405 410 415
 Met Asp Asp Gly Met Leu Asp Gly Pro Ser Ala Met Thr Arg Phe Cys
 420 425 430
 Asn Leu Ile Ala Ser Glu Pro Asp Ile Ala Lys Val Pro Leu Cys Ile
 435 440 445
 Asp Ser Ser Asn Phe Ala Val Ile Glu Ala Gly Leu Lys Cys Cys Gln
 450 455 460
 Gly Lys Cys Ile Val Asn Ser Ile Ser Leu Lys Glu Gly Glu Asp Asp
 465 470 475 480
 Phe Leu Glu Lys Ala Arg Lys Ile Lys Lys Tyr Gly Ala Ala Met Val
 485 490 495
 Val Met Ala Phe Asp Glu Glu Gly Gln Ala Thr Glu Thr Asp Thr Lys
 500 505 510
 Ile Arg Val Cys Thr Arg Ala Tyr His Leu Leu Val Lys Lys Leu Gly
 515 520 525
 Phe Asn Pro Asn Asp Ile Ile Phe Asp Pro Asn Ile Leu Thr Ile Gly
 530 535 540
 Thr Gly Met Glu Glu His Asn Leu Tyr Ala Ile Asn Phe Ile His Ala
 545 550 555 560
 Thr Lys Val Ile Lys Glu Thr Leu Pro Gly Ala Arg Ile Ser Gly Gly
 565 570 575
 Leu Ser Asn Leu Ser Phe Ser Phe Arg Gly Met Glu Ala Ile Arg Glu
 580 585 590
 Ala Met His Gly Val Phe Leu Tyr His Ala Ile Lys Ser Gly Met Asp
 595 600 605
 Met Gly Ile Val Asn Ala Gly Asn Leu Pro Val Tyr Asp Asp Ile His
 610 615 620
 Lys Glu Leu Leu Gln Leu Cys Glu Asp Leu Ile Trp Asn Lys Asp Pro
 625 630 635 640
 Glu Ala Thr Glu Lys Leu Leu Arg Tyr Ala Gln Thr Gln Gly Thr Gly
 645 650 655
 Gly Lys Lys Val Ile Gln Thr Asp Glu Trp Arg Asn Gly Pro Val Glu
 660 665 670

Glu Arg Leu Glu Tyr Ala Leu Val Lys Gly Ile Glu Lys His Ile Ile
 675 680 685
 Glu Asp Thr Glu Glu Ala Arg Leu Asn Gln Lys Lys Tyr Pro Arg Pro
 690 695 700
 Leu Asn Ile Ile Glu Gly Pro Leu Met Asn Gly Met Lys Ile Val Gly
 705 710 715 720
 Asp Leu Phe Gly Ala Gly Lys Met Phe Leu Pro Gln Val Ile Lys Ser
 725 730 735
 Ala Arg Val Met Lys Lys Ala Val Gly His Leu Ile Pro Phe Met Glu
 740 745 750
 Lys Glu Arg Glu Glu Thr Arg Val Leu Asn Gly Thr Val Glu Glu Glu
 755 760 765
 Asp Pro Tyr Gln Gly Thr Ile Val Leu Ala Thr Val Lys Gly Asp Val
 770 775 780
 His Asp Ile Gly Lys Asn Ile Val Gly Val Val Leu Gly Cys Asn Asn
 785 790 795 800
 Phe Arg Val Ile Asp Leu Gly Val Met Thr Pro Cys Asp Lys Ile Leu
 805 810 815
 Lys Ala Ala Leu Asp His Lys Ala Asp Ile Ile Gly Leu Ser Gly Leu
 820 825 830
 Ile Thr Pro Ser Leu Asp Glu Met Ile Phe Val Ala Lys Glu Met Glu
 835 840 845
 Arg Leu Ala Ile Arg Ile Pro Leu Leu Ile Gly Gly Ala Thr Thr Ser
 850 855 860
 Lys Thr His Thr Ala Val Lys Ile Ala Pro Arg Tyr Ser Ala Pro Val
 865 870 875 880
 Ile His Val Leu Asp Ala Ser Lys Ser Val Val Val Cys Ser Gln Leu
 885 890 895
 Leu Asp Glu Asn Leu Lys Asp Glu Tyr Phe Glu Glu Ile Met Glu Glu
 900 905 910
 Tyr Glu Asp Ile Arg Gln Asp His Tyr Glu Ser Leu Lys Glu Arg Arg
 915 920 925
 Tyr Leu Pro Leu Ser Gln Ala Arg Lys Ser Gly Phe Gln Met Asp Trp
 930 935 940
 Leu Ser Glu Pro His Pro Val Lys Pro Thr Phe Ile Gly Thr Gln Val
 945 950 955 960
 Phe Glu Asp Tyr Asp Leu Gln Lys Leu Val Asp Tyr Ile Asp Trp Lys
 965 970 975
 Pro Phe Phe Asp Val Trp Gln Leu Arg Gly Lys Tyr Pro Asn Arg Gly
 980 985 990
 Phe Pro Lys Ile Phe Asn Asp Lys Thr Val Gly Gly Glu Ala Arg Lys

198

995 1000 1005
 Val Tyr Asp Asp Ala His Asn Met Leu Asn Thr Leu Ile Ser Gln Lys
 1010 1015 1020
 Lys Leu Arg Ala Arg Gly Val Val Gly Phe Trp Pro Ala Gln Ser Ile
 1025 1030 1035 1040
 Gln Asp Asp Ile His Leu Tyr Ala Glu Ala Ala Val Pro Gln Ala Ala
 1045 1050 1055
 Glu Pro Ile Ala Thr Phe Tyr Gly Leu Arg Gln Gln Ala Glu Lys Asp
 1060 1065 1070
 Ser Ala Ser Thr Glu Pro Tyr Tyr Cys Leu Ser Asp Phe Ile Ala Pro
 1075 1080 1085
 Leu His Ser Gly Ile Arg Asp Tyr Leu Gly Leu Phe Ala Val Ala Cys
 1090 1095 1100
 Phe Gly Val Glu Glu Leu Ser Lys Ala Tyr Glu Asp Asp Gly Asp Asp
 1105 1110 1115 1120
 Tyr Ser Ser Ile Met Val Lys Ala Leu Gly Asp Arg Leu Ala Glu Ala
 1125 1130 1135
 Phe Ala Glu Glu Leu His Glu Arg Val Arg Arg Glu Leu Trp Ala Tyr
 1140 1145 1150
 Cys Gly Ser Glu Gln Leu Asp Val Ala Asp Leu Arg Arg Leu Arg Tyr
 1155 1160 1165
 Lys Gly Ile Arg Pro Ala Pro Gly Tyr Pro Ser Gln Pro Asp His Thr
 1170 1175 1180
 Glu Lys Leu Thr Met Trp Arg Leu Ala Asp Ile Glu Gln Ser Thr Gly
 1185 1190 1195 1200
 Ile Arg Leu Thr Glu Ser Leu Ala Met Ala Pro Ala Ser Ala Val Ser
 1205 1210 1215
 Gly Leu Tyr Phe Ser Asn Leu Lys Ser Lys Tyr Phe Ala Val Gly Lys
 1220 1225 1230
 Ile Ser Lys Asp Gln Val Glu Asp Tyr Ala Leu Arg Lys Asn Ile Ser
 1235 1240 1245
 Val Ala Glu Val Glu Lys Trp Leu Gly Pro Ile Leu Gly Tyr Asp Thr
 1250 1255 1260

Asp
 1265

<210> 45
 <211> 3681
 <212> DNA
 <213> Vibrio fischeri

<220>
 <221> CDS
 <222> (1)..(3678)

199

<223> AB039955

<400> 45

| | |
|---|-----|
| gtg gca gga agc aat ata aaa gta caa ata gaa aag caa ctt tca gag | 48 |
| Val Ala Gly Ser Asn Ile Lys Val Gln Ile Glu Lys Gln Leu Ser Glu | |
| 1 5 10 15 | |
| cga att tta ttg att gat ggt ggt atg ggc acc atg att caa ggt tat | 96 |
| Arg Ile Leu Leu Ile Asp Gly Gly Met Gly Thr Met Ile Gln Gly Tyr | |
| 20 25 30 | |
| aag ttt gaa gag aaa gat tat aga ggg gga cgc ttt aat caa tgg cat | 144 |
| Lys Phe Glu Glu Lys Asp Tyr Arg Gly Gly Arg Phe Asn Gln Trp His | |
| 35 40 45 | |
| tgt gat ctt aaa ggt aac aat gat tta tta gtt ctt tca caa cca caa | 192 |
| Cys Asp Leu Lys Gly Asn Asn Asp Leu Leu Val Leu Ser Gln Pro Gln | |
| 50 55 60 | |
| att ata aga gat ata cac gaa gcc tat tta gaa gct ggt gct gat atc | 240 |
| Ile Ile Arg Asp Ile His Glu Ala Tyr Leu Glu Ala Gly Ala Asp Ile | |
| 65 70 75 80 | |
| ctt gaa act aat acc ttt aat gca aca act att gct atg gct gat tat | 288 |
| Leu Glu Thr Asn Thr Phe Asn Ala Thr Thr Ile Ala Met Ala Asp Tyr | |
| 85 90 95 | |
| gat atg gaa agc ctt agt gaa gag att aac ttt gaa gca gca aag ctt | 336 |
| Asp Met Glu Ser Leu Ser Glu Glu Ile Asn Phe Glu Ala Ala Lys Leu | |
| 100 105 110 | |
| gct cgt gaa gtt gca gat aaa tgg aca gaa aaa aca cca aac aaa cct | 384 |
| Ala Arg Glu Val Ala Asp Lys Trp Thr Glu Lys Thr Pro Asn Lys Pro | |
| 115 120 125 | |
| cgc tat gta gca gga gtg ctt gga cca aca aat cga act tgt tct att | 432 |
| Arg Tyr Val Ala Gly Val Leu Gly Pro Thr Asn Arg Thr Cys Ser Ile | |
| 130 135 140 | |
| tct cca gac gta aat gac cct ggc ttt cgt aat gta tcg ttt gat gaa | 480 |
| Ser Pro Asp Val Asn Asp Pro Gly Phe Arg Asn Val Ser Phe Asp Glu | |
| 145 150 155 160 | |
| tta gtc gaa gct tat tca gag tca act cga gca ctt att aga ggt ggt | 528 |
| Leu Val Glu Ala Tyr Ser Glu Ser Thr Arg Ala Leu Ile Arg Gly Gly | |
| 165 170 175 | |
| tca gat ctt atc ctc atc gaa act ata ttt gat aca tta aat gct aaa | 576 |
| Ser Asp Leu Ile Leu Ile Glu Thr Ile Phe Asp Thr Leu Asn Ala Lys | |
| 180 185 190 | |
| gcg tgt tct ttt gct gtt gaa tct gtt ttt gaa gag ctt ggt att act | 624 |
| Ala Cys Ser Phe Ala Val Glu Ser Val Phe Glu Glu Leu Gly Ile Thr | |
| 195 200 205 | |
| ttg cct gtt atg att tca ggg acc att acc gat gca tca gga aga aca | 672 |
| Leu Pro Val Met Ile Ser Gly Thr Ile Thr Asp Ala Ser Gly Arg Thr | |
| 210 215 220 | |
| tta tcg ggg caa aca aca gaa gct ttt tat aat gca tta aga cat gta | 720 |
| Leu Ser Gly Gln Thr Thr Glu Ala Phe Tyr Asn Ala Leu Arg His Val | |
| 225 230 235 240 | |

200

| | |
|---|------|
| aaa cct att tct ttt ggt ctt aac tgt gca ctt ggt cct gat gaa tta | 768 |
| Lys Pro Ile Ser Phe Gly Leu Asn Cys Ala Leu Gly Pro Asp Glu Leu | |
| 245 250 255 | |
| cgt gaa tat gta agc gag ctt tca cgt att tct gaa tgt tat gtt tct | 816 |
| Arg Glu Tyr Val Ser Glu Leu Ser Arg Ile Ser Glu Cys Tyr Val Ser | |
| 260 265 270 | |
| gcg cac cca aac gct ggt ttg cct aat gca ttt ggt gag tat gat tta | 864 |
| Ala His Pro Asn Ala Gly Leu Pro Asn Ala Phe Gly Glu Tyr Asp Leu | |
| 275 280 285 | |
| tct ccc gaa gat atg gct gag cat gtt gcg gaa tgg gca agc agc gga | 912 |
| Ser Pro Glu Asp Met Ala Glu His Val Ala Glu Trp Ala Ser Ser Gly | |
| 290 295 300 | |
| ttt tta aat ctt att ggt ggg tgt tgt ggc acc act cct gaa cat att | 960 |
| Phe Leu Asn Leu Ile Gly Gly Cys Cys Gly Thr Thr Pro Glu His Ile | |
| 305 310 315 320 | |
| cgt caa atg gct tta gtt gtt gaa ggt gtg aaa cct cga caa tta cct | 1008 |
| Arg Gln Met Ala Leu Val Val Glu Gly Val Lys Pro Arg Gln Leu Pro | |
| 325 330 335 | |
| gaa tta ccc gta gct tgt cgt ctt tcc gga tta gag cct tta aca ata | 1056 |
| Glu Leu Pro Val Ala Cys Arg Leu Ser Gly Leu Glu Pro Leu Thr Ile | |
| 340 345 350 | |
| gaa aaa gat tct ttg ttt att aat gtt ggt gaa cgt aca aat gtt act | 1104 |
| Glu Lys Asp Ser Leu Phe Ile Asn Val Gly Glu Arg Thr Asn Val Thr | |
| 355 360 365 | |
| gga tct gca cgt ttt aaa cgc tta att aaa gaa gag ctt tat gac gaa | 1152 |
| Gly Ser Ala Arg Phe Lys Arg Leu Ile Lys Glu Glu Leu Tyr Asp Glu | |
| 370 375 380 | |
| gca cta agt gtt gct caa gag caa gtt gaa aac ggt gct caa att atc | 1200 |
| Ala Leu Ser Val Ala Gln Glu Gln Val Glu Asn Gly Ala Gln Ile Ile | |
| 385 390 395 400 | |
| gat atc aac atg gat gaa ggc atg ctt gat gct gaa gca tgt atg gtt | 1248 |
| Asp Ile Asn Met Asp Glu Gly Met Leu Asp Ala Glu Ala Cys Met Val | |
| 405 410 415 | |
| cgt ttt tta aat ctt tgt gca tca gaa cct gaa ata tct aaa gta cca | 1296 |
| Arg Phe Leu Asn Leu Cys Ala Ser Glu Pro Glu Ile Ser Lys Val Pro | |
| 420 425 430 | |
| gtg atg gtt gat tct tct aaa tgg gaa gta att gaa gct gga tta aag | 1344 |
| Val Met Val Asp Ser Ser Lys Trp Glu Val Ile Glu Ala Gly Leu Lys | |
| 435 440 445 | |
| tgt att caa ggt aag ggg ata gtt aat tca atc tct tta aag gaa ggc | 1392 |
| Cys Ile Gln Gly Lys Gly Ile Val Asn Ser Ile Ser Leu Lys Glu Gly | |
| 450 455 460 | |
| aaa gaa aag ttt gta cat caa gcc aag tta ata cgt cgt tat ggt gct | 1440 |
| Lys Glu Lys Phe Val His Gln Ala Lys Leu Ile Arg Arg Tyr Gly Ala | |
| 465 470 475 480 | |
| gca gtg atc gtt atg gct ttt gat gaa gtt ggc caa gcg gac act cgg | 1488 |

201

| | |
|---|------|
| Ala Val Ile Val Met Ala Phe Asp Glu Val Gly Gln Ala Asp Thr Arg | |
| 485 490 495 | |
| gag cgt aaa att gaa att tgt acc aat gcc tac aat att tta gtt gat | 1536 |
| Glu Arg Lys Ile Glu Ile Cys Thr Asn Ala Tyr Asn Ile Leu Val Asp | |
| 500 505 510 | |
| gaa gtt ggc ttc cca cct gaa gat att att ttt gac cct aat att ttt | 1584 |
| Glu Val Gly Phe Pro Pro Glu Asp Ile Ile Phe Asp Pro Asn Ile Phe | |
| 515 520 525 | |
| gcg gtt gct aca ggt atc gat gaa cat aat aac tat gca gta gac ttt | 1632 |
| Ala Val Ala Thr Gly Ile Asp Glu His Asn Asn Tyr Ala Val Asp Phe | |
| 530 535 540 | |
| att gaa gcc gtt ggt gat ata aag cga acg ctt cct cat gca atg att | 1680 |
| Ile Glu Ala Val Gly Asp Ile Lys Arg Thr Leu Pro His Ala Met Ile | |
| 545 550 555 560 | |
| tca ggt ggt gtt tct aac gtc tct ttt tct ttc cgt gga aat aac tac | 1728 |
| Ser Gly Gly Val Ser Asn Val Ser Phe Ser Phe Arg Gly Asn Asn Tyr | |
| 565 570 575 | |
| gtt cgt gaa gct atc cat gcc gta ttt tta tat cac tgt ttt aaa aat | 1776 |
| Val Arg Glu Ala Ile His Ala Val Phe Leu Tyr His Cys Phe Lys Asn | |
| 580 585 590 | |
| ggt atg gat atg ggc atc gta aat gcg ggg cag ctg gaa ata tat gat | 1824 |
| Gly Met Asp Met Gly Ile Val Asn Ala Gly Gln Leu Glu Ile Tyr Asp | |
| 595 600 605 | |
| aac gta cca gaa gat ctg cgt gaa gcg gtt gaa gat gtg gta ttg aat | 1872 |
| Asn Val Pro Glu Asp Leu Arg Glu Ala Val Glu Asp Val Val Leu Asn | |
| 610 615 620 | |
| cgt cga gat gat tct acg gag cgt tta ctt gat att gca act gag tat | 1920 |
| Arg Arg Asp Asp Ser Thr Glu Arg Leu Leu Asp Ile Ala Thr Glu Tyr | |
| 625 630 635 640 | |
| tta gaa cga gct gtt ggt aaa gtt gaa gat aaa tct gct tta gag tgg | 1968 |
| Leu Glu Arg Ala Val Gly Lys Val Glu Asp Lys Ser Ala Leu Glu Trp | |
| 645 650 655 | |
| cgt gac tgg cct gtt gaa aaa cgt ctt gag cat tct cta gtg aag ggg | 2016 |
| Arg Asp Trp Pro Val Glu Lys Arg Leu Glu His Ser Leu Val Lys Gly | |
| 660 665 670 | |
| ata aca gag ttt att gtc gaa gat aca gaa gaa gca cga atc aat gca | 2064 |
| Ile Thr Glu Phe Ile Val Glu Asp Thr Glu Glu Ala Arg Ile Asn Ala | |
| 675 680 685 | |
| gaa aga cca ata gag gta att gaa ggg cca ttg atg gac gga atg aac | 2112 |
| Glu Arg Pro Ile Glu Val Ile Glu Gly Pro Leu Met Asp Gly Met Asn | |
| 690 695 700 | |
| gtc gtt ggt gat ctt ttt ggg gaa gga aaa atg ttc ctt ccc caa gta | 2160 |
| Val Val Gly Asp Leu Phe Gly Glu Gly Lys Met Phe Leu Pro Gln Val | |
| 705 710 715 720 | |
| gta aag tct gct cgt gta atg aaa caa gct gtt gct cat tta gaa ccg | 2208 |
| Val Lys Ser Ala Arg Val Met Lys Gln Ala Val Ala His Leu Glu Pro | |
| 725 730 735 | |

202

| | |
|---|------|
| ttt att aat gcg tct aaa gaa gtt gga gca aca aac ggt aaa ata ctt Phe Ile Asn Ala Ser Lys Glu Val Gly Ala Thr Asn Gly Lys Ile Leu 740 745 750 | 2256 |
| tta gca aca gta aaa ggt gat gtt cat gat att ggt aag aat atc gtt Leu Ala Thr Val Lys Gly Asp Val His Asp Ile Gly Lys Asn Ile Val 755 760 765 | 2304 |
| ggc gtg gtt tta cag tgt aat aac tat gaa ata att gat ctt ggt gtc Gly Val Val Leu Gln Cys Asn Asn Tyr Glu Ile Ile Asp Leu Gly Val 770 775 780 | 2352 |
| atg gtc tct tgt gaa act atc tta aaa gta gcc aaa gaa gaa aat gta Met Val Ser Cys Glu Thr Ile Leu Lys Val Ala Lys Glu Glu Asn Val 785 790 795 800 | 2400 |
| gac atc att ggt tta tct gga tta ata aca cca tca tta gat gaa atg Asp Ile Ile Gly Leu Ser Gly Leu Ile Thr Pro Ser Leu Asp Glu Met 805 810 815 | 2448 |
| gtc cat gtt gct aaa gag atg gaa cga caa ggg ttt gat tta cca ttg Val His Val Ala Lys Glu Met Glu Arg Gln Gly Phe Asp Leu Pro Leu 820 825 830 | 2496 |
| ttg att ggt gga gca aca act tca aaa gca cat aca gcg gta aaa att Leu Ile Gly Gly Ala Thr Thr Ser Lys Ala His Thr Ala Val Lys Ile 835 840 845 | 2544 |
| gaa caa aac tat tct caa cct gtt gtg tac gtt aat aat gct tct cga Glu Gln Asn Tyr Ser Gln Pro Val Val Tyr Val Asn Asn Ala Ser Arg 850 855 860 | 2592 |
| gct gta ggt gta tgt act tca tta ctt tca aat gaa cta aaa cct tct Ala Val Gly Val Cys Thr Ser Leu Leu Ser Asn Glu Leu Lys Pro Ser 865 870 875 880 | 2640 |
| ttt gtt gag aag cta gat att gat tac gaa cgt gtt aga gag cag cat Phe Val Glu Lys Leu Asp Ile Asp Tyr Glu Arg Val Arg Glu Gln His 885 890 895 | 2688 |
| agt cgt aaa caa ccg cga act aag cct gtg act tta gag gtt gct cga Ser Arg Lys Gln Pro Arg Thr Lys Pro Val Thr Leu Glu Val Ala Arg 900 905 910 | 2736 |
| gcg aat aaa gtc gct att gac tgg gct tct tat aca cct cct gtc cca Ala Asn Lys Val Ala Ile Asp Trp Ala Ser Tyr Thr Pro Pro Val Pro 915 920 925 | 2784 |
| cta aag cct ggt gta cat ata ttt gat aac ttt gat gtt tca aca ttg Leu Lys Pro Gly Val His Ile Phe Asp Asn Phe Asp Val Ser Thr Leu 930 935 940 | 2832 |
| cgt aat tat att gat tgg acc cca ttt ttt atg acg tgg tct ctt gtt Arg Asn Tyr Ile Asp Trp Thr Pro Phe Phe Met Thr Trp Ser Leu Val 945 950 955 960 | 2880 |
| gga aaa tac ccg aag atc tta gag cat gaa gaa gtt ggt gaa gaa gcc Gly Lys Tyr Pro Lys Ile Leu Glu His Glu Glu Val Gly Glu Glu Ala 965 970 975 | 2928 |
| aaa cga tta ttt aaa gat gca aat gat cta tta gat cga gtt gaa aaa | 2976 |

203

Lys Arg Leu Phe Lys Asp Ala Asn Asp Leu Leu Asp Arg Val Glu Lys
 980 985 990

gaa ggg tta ctt aaa gcc cgt gga atg tgt gcg cta ttt cca gct tcc 3024
 Glu Gly Leu Leu Lys Ala Arg Gly Met Cys Ala Leu Phe Pro Ala Ser
 995 1000 1005

agt gtt ggt gat gat att gaa gta tat act gat gaa tca cgc act aca 3072
 Ser Val Gly Asp Asp Ile Glu Val Tyr Thr Asp Glu Ser Arg Thr Thr
 1010 1015 1020

gtt gca aaa gta ctt cat aat ttg cga caa caa acg gag aag ccg aaa 3120
 Val Ala Lys Val Leu His Asn Leu Arg Gln Gln Thr Glu Lys Pro Lys
 1025 1030 1035 1040

ggt ttt aat tat tgt tta tct gat tat ata gca ccc aaa gag tcg ggt 3168
 Gly Phe Asn Tyr Cys Leu Ser Asp Tyr Ile Ala Pro Lys Glu Ser Gly
 1045 1050 1055

aaa aat gat tgg atc ggt ggt ttt gct gta act ggt ggt att ggt gag 3216
 Lys Asn Asp Trp Ile Gly Gly Phe Ala Val Thr Gly Gly Ile Gly Glu
 1060 1065 1070

cgt gaa cta gct gat gaa tat aaa gca aat ggt gat gat tat aac gct 3264
 Arg Glu Leu Ala Asp Glu Tyr Lys Ala Asn Gly Asp Asp Tyr Asn Ala
 1075 1080 1085

atc atg att caa gcg gtg gct gat cgt cta gct gaa gct ttt gct gaa 3312
 Ile Met Ile Gln Ala Val Ala Asp Arg Leu Ala Glu Ala Phe Ala Glu
 1090 1095 1100

tat tta cat gaa aaa gta cgt aag gaa att tgg ggt tac tct cct aat 3360
 Tyr Leu His Glu Lys Val Arg Lys Glu Ile Trp Gly Tyr Ser Pro Asn
 1105 1110 1115 1120

gag acg ctt tca aat gat gat tta atc cgt gaa aaa tac caa ggc att 3408
 Glu Thr Leu Ser Asn Asp Asp Leu Ile Arg Glu Lys Tyr Gln Gly Ile
 1125 1130 1135

cgt cct gct cct ggt tac cca gct tgt cct gaa cat aca gaa aaa ggg 3456
 Arg Pro Ala Pro Gly Tyr Pro Ala Cys Pro Glu His Thr Glu Lys Gly
 1140 1145 1150

gct tta tgg gag tta atg aat gtt gaa gaa tct att gga atg tct tta 3504
 Ala Leu Trp Glu Leu Met Asn Val Glu Glu Ser Ile Gly Met Ser Leu
 1155 1160 1165

aca tca agc tat gca atg tgg ccc ggt gca tct gtg tca gga atg tat 3552
 Thr Ser Ser Tyr Ala Met Trp Pro Gly Ala Ser Val Ser Gly Met Tyr
 1170 1175 1180

ttt tca cac cca gat tct cgt tat ttt gcg att gct cag att cag caa 3600
 Phe Ser His Pro Asp Ser Arg Tyr Phe Ala Ile Ala Gln Ile Gln Gln
 1185 1190 1195 1200

gat caa gcc gaa agc tat gcc gat cgt aaa ggt tgg aat atg ctt gaa 3648
 Asp Gln Ala Glu Ser Tyr Ala Asp Arg Lys Gly Trp Asn Met Leu Glu
 1205 1210 1215

gct gag aag tgg tta ggt cca aat ttg aat taa 3681
 Ala Glu Lys Trp Leu Gly Pro Asn Leu Asn
 1220 1225

<210> 46
 <211> 1226
 <212> PRT
 <213> *Vibrio fisheri*

<400> 46
 Val Ala Gly Ser Asn Ile Lys Val Gln Ile Glu Lys Gln Leu Ser Glu
 1 5 10 15
 Arg Ile Leu Leu Ile Asp Gly Gly Met Gly Thr Met Ile Gln Gly Tyr
 20 25 30
 Lys Phe Glu Glu Lys Asp Tyr Arg Gly Gly Arg Phe Asn Gln Trp His
 35 40 45
 Cys Asp Leu Lys Gly Asn Asn Asp Leu Leu Val Leu Ser Gln Pro Gln
 50 55 60
 Ile Ile Arg Asp Ile His Glu Ala Tyr Leu Glu Ala Gly Ala Asp Ile
 65 70 75 80
 Leu Glu Thr Asn Thr Phe Asn Ala Thr Thr Ile Ala Met Ala Asp Tyr
 85 90 95
 Asp Met Glu Ser Leu Ser Glu Glu Ile Asn Phe Glu Ala Ala Lys Leu
 100 105 110
 Ala Arg Glu Val Ala Asp Lys Trp Thr Glu Lys Thr Pro Asn Lys Pro
 115 120 125
 Arg Tyr Val Ala Gly Val Leu Gly Pro Thr Asn Arg Thr Cys Ser Ile
 130 135 140
 Ser Pro Asp Val Asn Asp Pro Gly Phe Arg Asn Val Ser Phe Asp Glu
 145 150 155 160
 Leu Val Glu Ala Tyr Ser Glu Ser Thr Arg Ala Leu Ile Arg Gly Gly
 165 170 175
 Ser Asp Leu Ile Leu Ile Glu Thr Ile Phe Asp Thr Leu Asn Ala Lys
 180 185 190
 Ala Cys Ser Phe Ala Val Glu Ser Val Phe Glu Glu Leu Gly Ile Thr
 195 200 205
 Leu Pro Val Met Ile Ser Gly Thr Ile Thr Asp Ala Ser Gly Arg Thr
 210 215 220
 Leu Ser Gly Gln Thr Thr Glu Ala Phe Tyr Asn Ala Leu Arg His Val
 225 230 235 240
 Lys Pro Ile Ser Phe Gly Leu Asn Cys Ala Leu Gly Pro Asp Glu Leu
 245 250 255
 Arg Glu Tyr Val Ser Glu Leu Ser Arg Ile Ser Glu Cys Tyr Val Ser
 260 265 270
 Ala His Pro Asn Ala Gly Leu Pro Asn Ala Phe Gly Glu Tyr Asp Leu
 275 280 285

205

Ser Pro Glu Asp Met Ala Glu His Val Ala Glu Trp Ala Ser Ser Gly
 290 295 300
 Phe Leu Asn Leu Ile Gly Gly Cys Cys Gly Thr Thr Pro Glu His Ile
 305 310 315 320
 Arg Gln Met Ala Leu Val Val Glu Gly Val Lys Pro Arg Gln Leu Pro
 325 330 335
 Glu Leu Pro Val Ala Cys Arg Leu Ser Gly Leu Glu Pro Leu Thr Ile
 340 345 350
 Glu Lys Asp Ser Leu Phe Ile Asn Val Gly Glu Arg Thr Asn Val Thr
 355 360 365
 Gly Ser Ala Arg Phe Lys Arg Leu Ile Lys Glu Glu Leu Tyr Asp Glu
 370 375 380
 Ala Leu Ser Val Ala Gln Glu Gln Val Glu Asn Gly Ala Gln Ile Ile
 385 390 395 400
 Asp Ile Asn Met Asp Glu Gly Met Leu Asp Ala Glu Ala Cys Met Val
 405 410 415
 Arg Phe Leu Asn Leu Cys Ala Ser Glu Pro Glu Ile Ser Lys Val Pro
 420 425 430
 Val Met Val Asp Ser Ser Lys Trp Glu Val Ile Glu Ala Gly Leu Lys
 435 440 445
 Cys Ile Gln Gly Lys Gly Ile Val Asn Ser Ile Ser Leu Lys Glu Gly
 450 455 460
 Lys Glu Lys Phe Val His Gln Ala Lys Leu Ile Arg Arg Tyr Gly Ala
 465 470 475 480
 Ala Val Ile Val Met Ala Phe Asp Glu Val Gly Gln Ala Asp Thr Arg
 485 490 495
 Glu Arg Lys Ile Glu Ile Cys Thr Asn Ala Tyr Asn Ile Leu Val Asp
 500 505 510
 Glu Val Gly Phe Pro Pro Glu Asp Ile Ile Phe Asp Pro Asn Ile Phe
 515 520 525
 Ala Val Ala Thr Gly Ile Asp Glu His Asn Asn Tyr Ala Val Asp Phe
 530 535 540
 Ile Glu Ala Val Gly Asp Ile Lys Arg Thr Leu Pro His Ala Met Ile
 545 550 555 560
 Ser Gly Gly Val Ser Asn Val Ser Phe Ser Phe Arg Gly Asn Asn Tyr
 565 570 575
 Val Arg Glu Ala Ile His Ala Val Phe Leu Tyr His Cys Phe Lys Asn
 580 585 590
 Gly Met Asp Met Gly Ile Val Asn Ala Gly Gln Leu Glu Ile Tyr Asp
 595 600 605
 Asn Val Pro Glu Asp Leu Arg Glu Ala Val Glu Asp Val Val Leu Asn
 610 615 620

206

Arg Arg Asp Asp Ser Thr Glu Arg Leu Leu Asp Ile Ala Thr Glu Tyr
 625 630 635 640
 Leu Glu Arg Ala Val Gly Lys Val Glu Asp Lys Ser Ala Leu Glu Trp
 645 650 655
 Arg Asp Trp Pro Val Glu Lys Arg Leu Glu His Ser Leu Val Lys Gly
 660 665 670
 Ile Thr Glu Phe Ile Val Glu Asp Thr Glu Glu Ala Arg Ile Asn Ala
 675 680 685
 Glu Arg Pro Ile Glu Val Ile Glu Gly Pro Leu Met Asp Gly Met Asn
 690 695 700
 Val Val Gly Asp Leu Phe Gly Glu Gly Lys Met Phe Leu Pro Gln Val
 705 710 715 720
 Val Lys Ser Ala Arg Val Met Lys Gln Ala Val Ala His Leu Glu Pro
 725 730 735
 Phe Ile Asn Ala Ser Lys Glu Val Gly Ala Thr Asn Gly Lys Ile Leu
 740 745 750
 Leu Ala Thr Val Lys Gly Asp Val His Asp Ile Gly Lys Asn Ile Val
 755 760 765
 Gly Val Val Leu Gln Cys Asn Asn Tyr Glu Ile Ile Asp Leu Gly Val
 770 775 780
 Met Val Ser Cys Glu Thr Ile Leu Lys Val Ala Lys Glu Glu Asn Val
 785 790 795 800
 Asp Ile Ile Gly Leu Ser Gly Leu Ile Thr Pro Ser Leu Asp Glu Met
 805 810 815
 Val His Val Ala Lys Glu Met Glu Arg Gln Gly Phe Asp Leu Pro Leu
 820 825 830
 Leu Ile Gly Gly Ala Thr Thr Ser Lys Ala His Thr Ala Val Lys Ile
 835 840 845
 Glu Gln Asn Tyr Ser Gln Pro Val Val Tyr Val Asn Asn Ala Ser Arg
 850 855 860
 Ala Val Gly Val Cys Thr Ser Leu Leu Ser Asn Glu Leu Lys Pro Ser
 865 870 875 880
 Phe Val Glu Lys Leu Asp Ile Asp Tyr Glu Arg Val Arg Glu Gln His
 885 890 895
 Ser Arg Lys Gln Pro Arg Thr Lys Pro Val Thr Leu Glu Val Ala Arg
 900 905 910
 Ala Asn Lys Val Ala Ile Asp Trp Ala Ser Tyr Thr Pro Pro Val Pro
 915 920 925
 Leu Lys Pro Gly Val His Ile Phe Asp Asn Phe Asp Val Ser Thr Leu
 930 935 940
 Arg Asn Tyr Ile Asp Trp Thr Pro Phe Phe Met Thr Trp Ser Leu Val

207

| | | | |
|---|------|------|------|
| 945 | 950 | 955 | 960 |
| Gly Lys Tyr Pro Lys Ile Leu Glu His Glu Glu Val Gly Glu Glu Ala | 965 | 970 | 975 |
| Lys Arg Leu Phe Lys Asp Ala Asn Asp Leu Leu Asp Arg Val Glu Lys | 980 | 985 | 990 |
| Glu Gly Leu Leu Lys Ala Arg Gly Met Cys Ala Leu Phe Pro Ala Ser | 995 | 1000 | 1005 |
| Ser Val Gly Asp Asp Ile Glu Val Tyr Thr Asp Glu Ser Arg Thr Thr | 1010 | 1015 | 1020 |
| Val Ala Lys Val Leu His Asn Leu Arg Gln Gln Thr Glu Lys Pro Lys | 1025 | 1030 | 1035 |
| Gly Phe Asn Tyr Cys Leu Ser Asp Tyr Ile Ala Pro Lys Glu Ser Gly | 1045 | 1050 | 1055 |
| Lys Asn Asp Trp Ile Gly Gly Phe Ala Val Thr Gly Gly Ile Gly Glu | 1060 | 1065 | 1070 |
| Arg Glu Leu Ala Asp Glu Tyr Lys Ala Asn Gly Asp Asp Tyr Asn Ala | 1075 | 1080 | 1085 |
| Ile Met Ile Gln Ala Val Ala Asp Arg Leu Ala Glu Ala Phe Ala Glu | 1090 | 1095 | 1100 |
| Tyr Leu His Glu Lys Val Arg Lys Glu Ile Trp Gly Tyr Ser Pro Asn | 1105 | 1110 | 1115 |
| Glu Thr Leu Ser Asn Asp Asp Leu Ile Arg Glu Lys Tyr Gln Gly Ile | 1125 | 1130 | 1135 |
| Arg Pro Ala Pro Gly Tyr Pro Ala Cys Pro Glu His Thr Glu Lys Gly | 1140 | 1145 | 1150 |
| Ala Leu Trp Glu Leu Met Asn Val Glu Glu Ser Ile Gly Met Ser Leu | 1155 | 1160 | 1165 |
| Thr Ser Ser Tyr Ala Met Trp Pro Gly Ala Ser Val Ser Gly Met Tyr | 1170 | 1175 | 1180 |
| Phe Ser His Pro Asp Ser Arg Tyr Phe Ala Ile Ala Gln Ile Gln Gln | 1185 | 1190 | 1195 |
| Asp Gln Ala Glu Ser Tyr Ala Asp Arg Lys Gly Trp Asn Met Leu Glu | 1205 | 1210 | 1215 |
| Ala Glu Lys Trp Leu Gly Pro Asn Leu Asn | 1220 | 1225 | |

<210> 47
 <211> 3780
 <212> DNA
 <213> Agrobacterium tumefaciens

<220>
 <221> CDS
 <222> (1) .. (3777)

208

<223> 15887359

<400> 47

| | |
|---|-----|
| gtg ccc gtg ttt gac gac ctg ttt ggc cct gaa ggg gca aag cgc gac | 48 |
| Val Pro Val Phe Asp Asp Leu Phe Gly Pro Glu Gly Ala Lys Arg Asp | |
| 1 5 10 15 | |
| ggc gcg gaa att ttc aag gcg ttg cgc gat gcc gcc agc gaa cgc atc | 96 |
| Gly Ala Glu Ile Phe Lys Ala Leu Arg Asp Ala Ala Ser Glu Arg Ile | |
| 20 25 30 | |
| ctc att ctc gat ggt gcc atg ggc acg cag atc cag ggt ctc ggt ttt | 144 |
| Leu Ile Leu Asp Gly Ala Met Gly Thr Gln Ile Gln Gly Leu Gly Phe | |
| 35 40 45 | |
| gac gag gat cat ttt cgt ggc gac cgt ttt atc ggc tgc gcc tgt cac | 192 |
| Asp Glu Asp His Phe Arg Gly Asp Arg Phe Ile Gly Cys Ala Cys His | |
| 50 55 60 | |
| cag aag ggc aat aac gac ctt ctg atc ctg aca cag ccc gat gcc atc | 240 |
| Gln Lys Gly Asn Asn Asp Leu Leu Ile Leu Thr Gln Pro Asp Ala Ile | |
| 65 70 75 80 | |
| gag gaa atc cac tat cgc tac gcc atg gcg ggc gcg gat att ctc gaa | 288 |
| Glu Glu Ile His Tyr Arg Tyr Ala Met Ala Gly Ala Asp Ile Leu Glu | |
| 85 90 95 | |
| acc aac acg ttt tcc tcc acc cgc atc gcg cag gcc gat tac gag atg | 336 |
| Thr Asn Thr Phe Ser Ser Thr Arg Ile Ala Gln Ala Asp Tyr Glu Met | |
| 100 105 110 | |
| gag aat gcc gtc tac gat ctc aac cgc gag ggc gcg gcg atc gtg cgc | 384 |
| Glu Asn Ala Val Tyr Asp Leu Asn Arg Glu Gly Ala Ala Ile Val Arg | |
| 115 120 125 | |
| cgg gcg gct cag cgc gcc gag cgc gag gat ggc cgc cgc cgt ttc gtg | 432 |
| Arg Ala Ala Gln Arg Ala Glu Arg Glu Asp Gly Arg Arg Arg Phe Val | |
| 130 135 140 | |
| gcc ggt gcc atc ggt ccg acc aac cgc acg gcc tcg atc tcg cct gac | 480 |
| Ala Gly Ala Ile Gly Pro Thr Asn Arg Thr Ala Ser Ile Ser Pro Asp | |
| 145 150 155 160 | |
| gtc aac aat ccc ggt tac cgc gcc gtc agt ttc gac gat ctg cgc att | 528 |
| Val Asn Asn Pro Gly Tyr Arg Ala Val Ser Phe Asp Asp Leu Arg Ile | |
| 165 170 175 | |
| gcc tat ggc gag cag atc gat ggc ctg atc gac ggt ggt gcc gat atc | 576 |
| Ala Tyr Gly Glu Gln Ile Asp Gly Leu Ile Asp Gly Gly Ala Asp Ile | |
| 180 185 190 | |
| atc ctc atc gag acg atc ttc gat acg ctg aac gcc aag gcg gcg atc | 624 |
| Ile Leu Ile Glu Thr Ile Phe Asp Thr Leu Asn Ala Lys Ala Ala Ile | |
| 195 200 205 | |
| ttc gcc tgc gag gaa cgt ttc gag gct aag ggc atc cgc ctg ccg gtc | 672 |
| Phe Ala Cys Glu Glu Arg Phe Glu Ala Lys Gly Ile Arg Leu Pro Val | |
| 210 215 220 | |
| atg atc tca ggc acg atc acc gac ctt tcc ggt cgc acg ttg tcc ggc | 720 |
| Met Ile Ser Gly Thr Ile Thr Asp Leu Ser Gly Arg Thr Leu Ser Gly | |
| 225 230 235 240 | |

209

| | |
|---|------|
| cag acg cct tcg gcg ttc tgg aac tcg gtg cgc cac gcc aac ccc ttc Gln Thr Pro Ser Ala Phe Trp Asn Ser Val Arg His Ala Asn Pro Phe 245 250 255 | 768 |
| acc atc ggc ctc aac tgc gcg ctc ggt gcg gat gcc atg cgc ccg cat Thr Ile Gly Leu Asn Cys Ala Leu Gly Ala Asp Ala Met Arg Pro His 260 265 270 | 816 |
| ctg cag gaa ctg tcc gat gtg gcc gac acc ttt gtc tgc gcc tat ccg Leu Gln Glu Leu Ser Asp Val Ala Asp Thr Phe Val Cys Ala Tyr Pro 275 280 285 | 864 |
| aat gcc ggc ctg ccg aac gag ttc ggc caa tat gac gaa acg ccc gag Asn Ala Gly Leu Pro Asn Glu Phe Gly Gln Tyr Asp Glu Thr Pro Glu 290 295 300 | 912 |
| atg atg gcg cgc cag gtt gag ggc ttc gtt cgt gac ggt ctc gtc aac Met Met Ala Arg Gln Val Glu Gly Phe Val Arg Asp Gly Leu Val Asn 305 310 315 320 | 960 |
| atc gtc ggc ggt tgc tgc ggt tcg acg ccg gaa cat atc cgg gcg att Ile Val Gly Gly Cys Cys Gly Ser Thr Pro Glu His Ile Arg Ala Ile 325 330 335 | 1008 |
| gcc gaa gcc gtc aag gat tac aag ccc cgc gaa att cct gaa cac aag Ala Glu Ala Val Lys Asp Tyr Lys Pro Arg Glu Ile Pro Glu His Lys 340 345 350 | 1056 |
| ccg ttc atg tcg ctt tcc ggc ctt gaa ccc ttc gtg ctg acc aag gac Pro Phe Met Ser Leu Ser Gly Leu Glu Pro Phe Val Leu Thr Lys Asp 355 360 365 | 1104 |
| att ccc ttc gtc aac gtg ggc gag cgc acc aac gtc acc ggt tcg gcc Ile Pro Phe Val Asn Val Gly Glu Arg Thr Asn Val Thr Gly Ser Ala 370 375 380 | 1152 |
| cgc ttc cgc aag ctc atc act gcc ggc gac tat acg gcg gcg ctg gct Arg Phe Arg Lys Leu Ile Thr Ala Gly Asp Tyr Thr Ala Ala Leu Ala 385 390 395 400 | 1200 |
| gtt gcc cgc gac cag gtg gaa aac ggc gcg cag atc atc gac atc aac Val Ala Arg Asp Gln Val Glu Asn Gly Ala Gln Ile Ile Asp Ile Asn 405 410 415 | 1248 |
| atg gat gag ggc ctg atc gat tcg gaa aag gcg atg gtc gag ttc ctg Met Asp Glu Gly Leu Ile Asp Ser Glu Lys Ala Met Val Glu Phe Leu 420 425 430 | 1296 |
| aac ctc atc gcc gcc gag cct gac att gcc cgt gtg ccc gtc atg atc Asn Leu Ile Ala Ala Glu Pro Asp Ile Ala Arg Val Pro Val Met Ile 435 440 445 | 1344 |
| gac tca tcc aag ttc gag atc atc gag gcc ggc ctg aaa tgc gtg cag Asp Ser Ser Lys Phe Glu Ile Ile Glu Ala Gly Leu Lys Cys Val Gln 450 455 460 | 1392 |
| ggc aaa tcg atc gtc aat tcc att tcg ctg aag gaa ggc gag gag aag Gly Lys Ser Ile Val Asn Ser Ile Ser Leu Lys Glu Gly Glu Glu Lys 465 470 475 480 | 1440 |
| ttt ctc cag cag gct cgg ctc gtc cac aat tac ggt gcg gcg gtt gtc | 1488 |

210

| | |
|---|------|
| Phe Leu Gln Gln Ala Arg Leu Val His Asn Tyr Gly Ala Ala Val Val | |
| 485 490 495 | |
| gtc atg gcc ttt gat gag gtc ggg cag gcg gat acc tat cag cgc aag | 1536 |
| Val Met Ala Phe Asp Glu Val Gly Gln Ala Asp Thr Tyr Gln Arg Lys | |
| 500 505 510 | |
| gtg gaa atc tgc gcg cgc gcc tac aag ctt ctg acc gaa aag gcc ggt | 1584 |
| Val Glu Ile Cys Ala Arg Ala Tyr Lys Leu Leu Thr Glu Lys Ala Gly | |
| 515 520 525 | |
| ctg tct ccg gaa gac atc atc ttc gac ccg aat gtg ttt gcg gta gct | 1632 |
| Leu Ser Pro Glu Asp Ile Ile Phe Asp Pro Asn Val Phe Ala Val Ala | |
| 530 535 540 | |
| acg ggc atc gag gag cac aat aat tac ggc gtg gac ttc atc gag gcc | 1680 |
| Thr Gly Ile Glu Glu His Asn Asn Tyr Gly Val Asp Phe Ile Glu Ala | |
| 545 550 555 560 | |
| acc aag acc atc cgc gaa acc atg ccg ctc acg cat att tcc ggg ggc | 1728 |
| Thr Lys Thr Ile Arg Glu Thr Met Pro Leu Thr His Ile Ser Gly Gly | |
| 565 570 575 | |
| gtt tcc aac ctg tcc ttc tcc ttc cgc ggc aat gag ccg gtg cgt gag | 1776 |
| Val Ser Asn Leu Ser Phe Ser Phe Arg Gly Asn Glu Pro Val Arg Glu | |
| 580 585 590 | |
| gcg atg cat gcc gtg ttc ctc tat cac gcc att cag gtc ggc atg gat | 1824 |
| Ala Met His Ala Val Phe Leu Tyr His Ala Ile Gln Val Gly Met Asp | |
| 595 600 605 | |
| atg ggc atc gtc aac gcc ggg cag ctt gcg gtt tac gac aat atc gat | 1872 |
| Met Gly Ile Val Asn Ala Gly Gln Leu Ala Val Tyr Asp Asn Ile Asp | |
| 610 615 620 | |
| gcg gaa ctg cgc gag gcc tgc gaa gac gtg gtg ctg aac cgc cgc gac | 1920 |
| Ala Glu Leu Arg Glu Ala Cys Glu Asp Val Val Leu Asn Arg Arg Asp | |
| 625 630 635 640 | |
| gat gcc acg gag cgt ctg ctc gag gtg gcg gag cgt ttc cgt ggt acg | 1968 |
| Asp Ala Thr Glu Arg Leu Leu Glu Val Ala Glu Arg Phe Arg Gly Thr | |
| 645 650 655 | |
| ggg gaa aaa cag gcc aag gtg cag gat ctt tcc tgg cgc gag tat ccc | 2016 |
| Gly Glu Lys Gln Ala Lys Val Gln Asp Leu Ser Trp Arg Glu Tyr Pro | |
| 660 665 670 | |
| gtt gaa aag cgg ctg gaa cat gct ctg gtc aac ggc att acc gac tat | 2064 |
| Val Glu Lys Arg Leu Glu His Ala Leu Val Asn Gly Ile Thr Asp Tyr | |
| 675 680 685 | |
| atc gag gcc gat acg gaa gag gca cgc cag cag gcc gcc cgc ccg ctg | 2112 |
| Ile Glu Ala Asp Thr Glu Glu Ala Arg Gln Gln Ala Ala Arg Pro Leu | |
| 690 695 700 | |
| cat gtc atc gaa ggg ccg ctg atg gcc ggt atg aat gtg gtg ggt gac | 2160 |
| His Val Ile Glu Gly Pro Leu Met Ala Gly Met Asn Val Val Gly Asp | |
| 705 710 715 720 | |
| ctg ttc ggt tcc ggc aag atg ttc ctg cca cag gtg gtg aaa tcc gcc | 2208 |
| Leu Phe Gly Ser Gly Lys Met Phe Leu Pro Gln Val Val Lys Ser Ala | |
| 725 730 735 | |

211

| | |
|---|------|
| cgt gtg atg aag cag gcg gtt gcc gtt ctg ctg cct tac atg gaa gag | 2256 |
| Arg Val Met Lys Gln Ala Val Ala Val Leu Leu Pro Tyr Met Glu Glu | |
| 740 745 750 | |
| gaa aag cgc ctg aat ggc ggt tcc gag cgc agt gcc gcc ggc aag gtg | 2304 |
| Glu Lys Arg Leu Asn Gly Gly Ser Glu Arg Ser Ala Ala Gly Lys Val | |
| 755 760 765 | |
| cta atg gcg acc gtg aag ggc gac gtg cac gat atc ggc aag aac atc | 2352 |
| Leu Met Ala Thr Val Lys Gly Asp Val His Asp Ile Gly Lys Asn Ile | |
| 770 775 780 | |
| gtc ggc gtt gtg cta gcc tgc aac aat tac gag atc att gat ctc ggc | 2400 |
| Val Gly Val Val Leu Ala Cys Asn Asn Tyr Glu Ile Ile Asp Leu Gly | |
| 785 790 795 800 | |
| gtg atg gtg ccg acg acg aaa atc ctc gaa acg gcg atc gcc gaa aag | 2448 |
| Val Met Val Pro Thr Thr Lys Ile Leu Glu Thr Ala Ile Ala Glu Lys | |
| 805 810 815 | |
| gtg gat gtg atc ggc ctc tcc ggc ctc atc acc ccg tcg ctg gat gag | 2496 |
| Val Asp Val Ile Gly Leu Ser Gly Leu Ile Thr Pro Ser Leu Asp Glu | |
| 820 825 830 | |
| atg gtg cat gtg gcg gcc gaa atg gag cga cag ggt ttc gac att ccg | 2544 |
| Met Val His Val Ala Ala Glu Met Glu Arg Gln Gly Phe Asp Ile Pro | |
| 835 840 845 | |
| ctg ctg atc ggc ggt gcg acg acc agc cgt gtg cat acg gcg gta aaa | 2592 |
| Leu Leu Ile Gly Gly Ala Thr Thr Ser Arg Val His Thr Ala Val Lys | |
| 850 855 860 | |
| atc cat ccg cgt tac gag cag ggg cag gcg atc tat gtc acc gac gcc | 2640 |
| Ile His Pro Arg Tyr Glu Gln Gly Gln Ala Ile Tyr Val Thr Asp Ala | |
| 865 870 875 880 | |
| tcg cgc gcg gtg ggc gtc gtt tca gcg ctc ctc tcc gaa gag cag aag | 2688 |
| Ser Arg Ala Val Gly Val Val Ser Ala Leu Leu Ser Glu Glu Gln Lys | |
| 885 890 895 | |
| ccc gct tat atc gac ggc atc cga gcc gaa tat gcc aag gtg gcg gaa | 2736 |
| Pro Ala Tyr Ile Asp Gly Ile Arg Ala Glu Tyr Ala Lys Val Ala Glu | |
| 900 905 910 | |
| gcc cat gcc cgc aat gag cgc gaa aag cag cgc ctg ccg ctt tcc cgc | 2784 |
| Ala His Ala Arg Asn Glu Arg Glu Lys Gln Arg Leu Pro Leu Ser Arg | |
| 915 920 925 | |
| gcc cgg gag aat gcg cac aag atc gac tgg tcg agc tac agc gtt gtc | 2832 |
| Ala Arg Glu Asn Ala His Lys Ile Asp Trp Ser Ser Tyr Ser Val Val | |
| 930 935 940 | |
| aag ccg cag ttc ttc ggc acc aag gtt ttt gag acc tat gat ctg gaa | 2880 |
| Lys Pro Gln Phe Phe Gly Thr Lys Val Phe Glu Thr Tyr Asp Leu Glu | |
| 945 950 955 960 | |
| gag ctt tcc cgt tac atc gac tgg acg ccg ttc ttc cag acc tgg gaa | 2928 |
| Glu Leu Ser Arg Tyr Ile Asp Trp Thr Pro Phe Phe Gln Thr Trp Glu | |
| 965 970 975 | |
| ttg aag ggc cgt ttc ccg gcg atc ctt gaa gac gaa aag cag ggc gag | 2976 |

212

| | |
|---|------|
| Leu Lys Gly Arg Phe Pro Ala Ile Leu Glu Asp Glu Lys Gln Gly Glu | |
| 980 985 990 | |
| gcg gcg cgg cag ctt tat gcc gat gcg cag gcc atg ctt gcg aag atc | 3024 |
| Ala Ala Arg Gln Leu Tyr Ala Asp Ala Gln Ala Met Leu Ala Lys Ile | |
| 995 1000 1005 | |
| atc gag gaa aag tgg ttc cga cca cgc gcg gtg atc ggc ttc tgg ccg | 3072 |
| Ile Glu Glu Lys Trp Phe Arg Pro Arg Ala Val Ile Gly Phe Trp Pro | |
| 1010 1015 1020 | |
| gcc aat gcc gtg ggt gac gat atc agg ctc ttt acg gat gaa ggt cgg | 3120 |
| Ala Asn Ala Val Gly Asp Asp Ile Arg Leu Phe Thr Asp Glu Gly Arg | |
| 1025 1030 1035 1040 | |
| aag gaa gag ttg gcg acg ttc ttc acg ctg cgc cag cag ctt tcc aag | 3168 |
| Lys Glu Glu Leu Ala Thr Phe Phe Thr Leu Arg Gln Gln Leu Ser Lys | |
| 1045 1050 1055 | |
| cgc gat ggc cgt ccg aac gtg gcg ctg tcc gat ttc gtc gcg ccc gtc | 3216 |
| Arg Asp Gly Arg Pro Asn Val Ala Leu Ser Asp Phe Val Ala Pro Val | |
| 1060 1065 1070 | |
| gat agc ggc gtt gcc gat tat gtc ggc ggt ttc gtg gta acg gcg ggt | 3264 |
| Asp Ser Gly Val Ala Asp Tyr Val Gly Gly Phe Val Val Thr Ala Gly | |
| 1075 1080 1085 | |
| atc gag gaa gtg gcg att gcc gag cgc ttc gag cgg gcc aat gac gat | 3312 |
| Ile Glu Glu Val Ala Ile Ala Glu Arg Phe Glu Arg Ala Asn Asp Asp | |
| 1090 1095 1100 | |
| tat tcg tcc atc ctc gtc aag gcg ttg gct gac cgt ttt gcc gaa gcc | 3360 |
| Tyr Ser Ser Ile Leu Val Lys Ala Leu Ala Asp Arg Phe Ala Glu Ala | |
| 1105 1110 1115 1120 | |
| ttt gcc gag cgt atg cat gag cgc gtg cgc aag gag ttc tgg ggt tat | 3408 |
| Phe Ala Glu Arg Met His Glu Arg Val Arg Lys Glu Phe Trp Gly Tyr | |
| 1125 1130 1135 | |
| gcg ccg gac gag gct ctt gcc ggt gac gat ctg ata ggc gaa gcc tat | 3456 |
| Ala Pro Asp Glu Ala Leu Ala Gly Asp Asp Leu Ile Gly Glu Ala Tyr | |
| 1140 1145 1150 | |
| gcc ggt atc cgc ccg gca ccg ggt tat ccg gcc cag ccg gac cac acc | 3504 |
| Ala Gly Ile Arg Pro Ala Pro Gly Tyr Pro Ala Gln Pro Asp His Thr | |
| 1155 1160 1165 | |
| gaa aag aag acg ctg ttt gct ctg ctg gac gcc acc aat gcg gcg ggt | 3552 |
| Glu Lys Lys Thr Leu Phe Ala Leu Leu Asp Ala Thr Asn Ala Ala Gly | |
| 1170 1175 1180 | |
| gtg gaa ttg acg gaa agc tat gcg atg tgg ccc ggc tcg tcg gtt tcg | 3600 |
| Val Glu Leu Thr Glu Ser Tyr Ala Met Trp Pro Gly Ser Ser Val Ser | |
| 1185 1190 1195 1200 | |
| ggc ctc tat atc ggc cat ccc gaa agc tat tat ttc ggc gtt gcc aag | 3648 |
| Gly Leu Tyr Ile Gly His Pro Glu Ser Tyr Tyr Phe Gly Val Ala Lys | |
| 1205 1210 1215 | |
| gtg gag cgg gat cag gtt ctc gac tat gcg cgc cgc aag gat atg ccg | 3696 |
| Val Glu Arg Asp Gln Val Leu Asp Tyr Ala Arg Arg Lys Asp Met Pro | |
| 1220 1225 1230 | |

213

gtc aca gag gtg gag cgc tgg ctc ggg ccg gtg ctc aac tac gtg ccg 3744
 Val Thr Glu Val Glu Arg Trp Leu Gly Pro Val Leu Asn Tyr Val Pro
 1235 1240 1245

acc aac ggc gag gag aaa atc gac agc gct gcg tga 3780
 Thr Asn Gly Glu Glu Lys Ile Asp Ser Ala Ala
 1250 1255

<210> 48

<211> 1259

<212> PRT

<213> Agrobacterium tumefaciens

<400> 48

Val Pro Val Phe Asp Asp Leu Phe Gly Pro Glu Gly Ala Lys Arg Asp
 1 5 10 15

Gly Ala Glu Ile Phe Lys Ala Leu Arg Asp Ala Ala Ser Glu Arg Ile
 20 25 30

Leu Ile Leu Asp Gly Ala Met Gly Thr Gln Ile Gln Gly Leu Gly Phe
 35 40 45

Asp Glu Asp His Phe Arg Gly Asp Arg Phe Ile Gly Cys Ala Cys His
 50 55 60

Gln Lys Gly Asn Asn Asp Leu Leu Ile Leu Thr Gln Pro Asp Ala Ile
 65 70 75 80

Glu Glu Ile His Tyr Arg Tyr Ala Met Ala Gly Ala Asp Ile Leu Glu
 85 90 95

Thr Asn Thr Phe Ser Ser Thr Arg Ile Ala Gln Ala Asp Tyr Glu Met
 100 105 110

Glu Asn Ala Val Tyr Asp Leu Asn Arg Glu Gly Ala Ala Ile Val Arg
 115 120 125

Arg Ala Ala Gln Arg Ala Glu Arg Glu Asp Gly Arg Arg Arg Phe Val
 130 135 140

Ala Gly Ala Ile Gly Pro Thr Asn Arg Thr Ala Ser Ile Ser Pro Asp
 145 150 155 160

Val Asn Asn Pro Gly Tyr Arg Ala Val Ser Phe Asp Asp Leu Arg Ile
 165 170 175

Ala Tyr Gly Glu Gln Ile Asp Gly Leu Ile Asp Gly Gly Ala Asp Ile
 180 185 190

Ile Leu Ile Glu Thr Ile Phe Asp Thr Leu Asn Ala Lys Ala Ala Ile
 195 200 205

Phe Ala Cys Glu Glu Arg Phe Glu Ala Lys Gly Ile Arg Leu Pro Val
 210 215 220

Met Ile Ser Gly Thr Ile Thr Asp Leu Ser Gly Arg Thr Leu Ser Gly
 225 230 235 240

Gln Thr Pro Ser Ala Phe Trp Asn Ser Val Arg His Ala Asn Pro Phe

214

| | | |
|--|-----|-----|
| 245 | 250 | 255 |
| Thr Ile Gly Leu Asn Cys Ala Leu Gly Ala Asp Ala Met Arg Pro His 260 265 270 | | |
| Leu Gln Glu Leu Ser Asp Val Ala Asp Thr Phe Val Cys Ala Tyr Pro 275 280 285 | | |
| Asn Ala Gly Leu Pro Asn Glu Phe Gly Gln Tyr Asp Glu Thr Pro Glu 290 295 300 | | |
| Met Met Ala Arg Gln Val Glu Gly Phe Val Arg Asp Gly Leu Val Asn 305 310 315 320 | | |
| Ile Val Gly Gly Cys Cys Gly Ser Thr Pro Glu His Ile Arg Ala Ile 325 330 335 | | |
| Ala Glu Ala Val Lys Asp Tyr Lys Pro Arg Glu Ile Pro Glu His Lys 340 345 350 | | |
| Pro Phe Met Ser Leu Ser Gly Leu Glu Pro Phe Val Leu Thr Lys Asp 355 360 365 | | |
| Ile Pro Phe Val Asn Val Gly Glu Arg Thr Asn Val Thr Gly Ser Ala 370 375 380 | | |
| Arg Phe Arg Lys Leu Ile Thr Ala Gly Asp Tyr Thr Ala Ala Leu Ala 385 390 395 400 | | |
| Val Ala Arg Asp Gln Val Glu Asn Gly Ala Gln Ile Ile Asp Ile Asn 405 410 415 | | |
| Met Asp Glu Gly Leu Ile Asp Ser Glu Lys Ala Met Val Glu Phe Leu 420 425 430 | | |
| Asn Leu Ile Ala Ala Glu Pro Asp Ile Ala Arg Val Pro Val Met Ile 435 440 445 | | |
| Asp Ser Ser Lys Phe Glu Ile Ile Glu Ala Gly Leu Lys Cys Val Gln 450 455 460 | | |
| Gly Lys Ser Ile Val Asn Ser Ile Ser Leu Lys Glu Gly Glu Glu Lys 465 470 475 480 | | |
| Phe Leu Gln Gln Ala Arg Leu Val His Asn Tyr Gly Ala Ala Val Val 485 490 495 | | |
| Val Met Ala Phe Asp Glu Val Gly Gln Ala Asp Thr Tyr Gln Arg Lys 500 505 510 | | |
| Val Glu Ile Cys Ala Arg Ala Tyr Lys Leu Leu Thr Glu Lys Ala Gly 515 520 525 | | |
| Leu Ser Pro Glu Asp Ile Ile Phe Asp Pro Asn Val Phe Ala Val Ala 530 535 540 | | |
| Thr Gly Ile Glu Glu His Asn Asn Tyr Gly Val Asp Phe Ile Glu Ala 545 550 555 560 | | |
| Thr Lys Thr Ile Arg Glu Thr Met Pro Leu Thr His Ile Ser Gly Gly 565 570 575 | | |

215

Val Ser Asn Leu Ser Phe Ser Phe Arg Gly Asn Glu Pro Val Arg Glu
 580 585 590
 Ala Met His Ala Val Phe Leu Tyr His Ala Ile Gln Val Gly Met Asp
 595 600 605
 Met Gly Ile Val Asn Ala Gly Gln Leu Ala Val Tyr Asp Asn Ile Asp
 610 615 620
 Ala Glu Leu Arg Glu Ala Cys Glu Asp Val Val Leu Asn Arg Arg Asp
 625 630 635 640
 Asp Ala Thr Glu Arg Leu Leu Glu Val Ala Glu Arg Phe Arg Gly Thr
 645 650 655
 Gly Glu Lys Gln Ala Lys Val Gln Asp Leu Ser Trp Arg Glu Tyr Pro
 660 665 670
 Val Glu Lys Arg Leu Glu His Ala Leu Val Asn Gly Ile Thr Asp Tyr
 675 680 685
 Ile Glu Ala Asp Thr Glu Glu Ala Arg Gln Gln Ala Ala Arg Pro Leu
 690 695 700
 His Val Ile Glu Gly Pro Leu Met Ala Gly Met Asn Val Val Gly Asp
 705 710 715 720
 Leu Phe Gly Ser Gly Lys Met Phe Leu Pro Gln Val Val Lys Ser Ala
 725 730 735
 Arg Val Met Lys Gln Ala Val Ala Val Leu Leu Pro Tyr Met Glu Glu
 740 745 750
 Glu Lys Arg Leu Asn Gly Gly Ser Glu Arg Ser Ala Ala Gly Lys Val
 755 760 765
 Leu Met Ala Thr Val Lys Gly Asp Val His Asp Ile Gly Lys Asn Ile
 770 775 780
 Val Gly Val Val Leu Ala Cys Asn Asn Tyr Glu Ile Ile Asp Leu Gly
 785 790 795 800
 Val Met Val Pro Thr Thr Lys Ile Leu Glu Thr Ala Ile Ala Glu Lys
 805 810 815
 Val Asp Val Ile Gly Leu Ser Gly Leu Ile Thr Pro Ser Leu Asp Glu
 820 825 830
 Met Val His Val Ala Ala Glu Met Glu Arg Gln Gly Phe Asp Ile Pro
 835 840 845
 Leu Leu Ile Gly Gly Ala Thr Thr Ser Arg Val His Thr Ala Val Lys
 850 855 860
 Ile His Pro Arg Tyr Glu Gln Gly Gln Ala Ile Tyr Val Thr Asp Ala
 865 870 875 880
 Ser Arg Ala Val Gly Val Val Ser Ala Leu Leu Ser Glu Glu Gln Lys
 885 890 895
 Pro Ala Tyr Ile Asp Gly Ile Arg Ala Glu Tyr Ala Lys Val Ala Glu
 900 905 910

216

Ala His Ala Arg Asn Glu Arg Glu Lys Gln Arg Leu Pro Leu Ser Arg
 915 920 925
 Ala Arg Glu Asn Ala His Lys Ile Asp Trp Ser Ser Tyr Ser Val Val
 930 935 940
 Lys Pro Gln Phe Phe Gly Thr Lys Val Phe Glu Thr Tyr Asp Leu Glu
 945 950 955 960
 Glu Leu Ser Arg Tyr Ile Asp Trp Thr Pro Phe Phe Gln Thr Trp Glu
 965 970 975
 Leu Lys Gly Arg Phe Pro Ala Ile Leu Glu Asp Glu Lys Gln Gly Glu
 980 985 990
 Ala Ala Arg Gln Leu Tyr Ala Asp Ala Gln Ala Met Leu Ala Lys Ile
 995 1000 1005
 Ile Glu Glu Lys Trp Phe Arg Pro Arg Ala Val Ile Gly Phe Trp Pro
 1010 1015 1020
 Ala Asn Ala Val Gly Asp Asp Ile Arg Leu Phe Thr Asp Glu Gly Arg
 1025 1030 1035 1040
 Lys Glu Glu Leu Ala Thr Phe Phe Thr Leu Arg Gln Gln Leu Ser Lys
 1045 1050 1055
 Arg Asp Gly Arg Pro Asn Val Ala Leu Ser Asp Phe Val Ala Pro Val
 1060 1065 1070
 Asp Ser Gly Val Ala Asp Tyr Val Gly Gly Phe Val Val Thr Ala Gly
 1075 1080 1085
 Ile Glu Glu Val Ala Ile Ala Glu Arg Phe Glu Arg Ala Asn Asp Asp
 1090 1095 1100
 Tyr Ser Ser Ile Leu Val Lys Ala Leu Ala Asp Arg Phe Ala Glu Ala
 1105 1110 1115 1120
 Phe Ala Glu Arg Met His Glu Arg Val Arg Lys Glu Phe Trp Gly Tyr
 1125 1130 1135
 Ala Pro Asp Glu Ala Leu Ala Gly Asp Asp Leu Ile Gly Glu Ala Tyr
 1140 1145 1150
 Ala Gly Ile Arg Pro Ala Pro Gly Tyr Pro Ala Gln Pro Asp His Thr
 1155 1160 1165
 Glu Lys Lys Thr Leu Phe Ala Leu Leu Asp Ala Thr Asn Ala Ala Gly
 1170 1175 1180
 Val Glu Leu Thr Glu Ser Tyr Ala Met Trp Pro Gly Ser Ser Val Ser
 1185 1190 1195 1200
 Gly Leu Tyr Ile Gly His Pro Glu Ser Tyr Tyr Phe Gly Val Ala Lys
 1205 1210 1215
 Val Glu Arg Asp Gln Val Leu Asp Tyr Ala Arg Arg Lys Asp Met Pro
 1220 1225 1230
 Val Thr Glu Val Glu Arg Trp Leu Gly Pro Val Leu Asn Tyr Val Pro

217

1235

1240

1245

Thr Asn Gly Glu Glu Lys Ile Asp Ser Ala Ala
1250 1255

<210> 49

<211> 2718

<212> DNA

<213> Ralstonia solanacearum

<220>

<221> CDS

<222> (1) .. (2715)

<223> RSOL_GMI1000

<400> 49

atg acc gac cac ctc atg cgc ctc tcc ggc ctc gaa ccg ttc aac atc 48
Met Thr Asp His Leu Met Arg Leu Ser Gly Leu Glu Pro Phe Asn Ile
1 5 10 15

ggc gag gac acg ctg ttc gtc aac gtc ggc gaa cgc acc aac gtc acc 96
Gly Glu Asp Thr Leu Phe Val Asn Val Gly Glu Arg Thr Asn Val Thr
20 25 30

gga tcc aag gcg ttc gcg cgc atg atc ctc aac agc cag ttc gac gag 144
Gly Ser Lys Ala Phe Ala Arg Met Ile Leu Asn Ser Gln Phe Asp Glu
35 40 45

gcg ctc gcc gtg gca cgc cag cag gtc gag aac ggc gcg cag gtc atc 192
Ala Leu Ala Val Ala Arg Gln Gln Val Glu Asn Gly Ala Gln Val Ile
50 55 60

gac atc aac atg gac gag gcc atg ctc gac tcc aag gcg gcg atg gtg 240
Asp Ile Asn Met Asp Glu Ala Met Leu Asp Ser Lys Ala Ala Met Val
65 70 75 80

cgc ttc ctg aac ctg atc gcc tcg gag ccg gac atc gcg cgc gtg ccg 288
Arg Phe Leu Asn Leu Ile Ala Ser Glu Pro Asp Ile Ala Arg Val Pro
85 90 95

atc atg atc gac tcg tcc aag tgg gag gtg atc gag gcc ggc ctg aag 336
Ile Met Ile Asp Ser Ser Lys Trp Glu Val Ile Glu Ala Gly Leu Lys
100 105 110

tgc gtg cag ggc aag gcc atc gtc aac tcg atc tcg ctc aag gaa ggc 384
Cys Val Gln Gly Lys Ala Ile Val Asn Ser Ile Ser Leu Lys Glu Gly
115 120 125

gag gaa cag ttc gcc cac cac gcc aag ctg atc aag cgc tac ggc gcc 432
Glu Glu Gln Phe Ala His His Ala Lys Leu Ile Lys Arg Tyr Gly Ala
130 135 140

gcc gcc gtg gtg atg gcc ttc gac gag cag ggc cag gcc gac acg ttc 480
Ala Ala Val Val Met Ala Phe Asp Glu Gln Gly Gln Ala Asp Thr Phe
145 150 155 160

gcg cgc aag acc gag atc tgc aag cgc agc tat gac ttc ctc gtg aac 528
Ala Arg Lys Thr Glu Ile Cys Lys Arg Ser Tyr Asp Phe Leu Val Asn
165 170 175

cag gtc ggc ttt gcg ccg gaa gac atc atc ttc gat ccg aac atc ttc 576

218

| | |
|---|------|
| Gln Val Gly Phe Ala Pro Glu Asp Ile Ile Phe Asp Pro Asn Ile Phe | |
| 180 185 190 | |
| gcg gtc gcc acc ggc atc gag gag cac aac aac tac gcc gtc gac ttc | 624 |
| Ala Val Ala Thr Gly Ile Glu Glu His Asn Asn Tyr Ala Val Asp Phe | |
| 195 200 205 | |
| atc gag gcc acg cgc tgg atc aag cag aaa ttg ccg cac gcc aag gtg | 672 |
| Ile Glu Ala Thr Arg Trp Ile Lys Gln Lys Leu Pro His Ala Lys Val | |
| 210 215 220 | |
| agc ggc ggc gtg tcg aac gtc tcg ttc tcg ttc cgc ggc aac gac gtg | 720 |
| Ser Gly Gly Val Ser Asn Val Ser Phe Ser Phe Arg Gly Asn Asp Val | |
| 225 230 235 240 | |
| gtg cgc gag gcc atc cac acc gtg ttc ctg tac cac gcc atc ggt gcg | 768 |
| Val Arg Glu Ala Ile His Thr Val Phe Leu Tyr His Ala Ile Gly Ala | |
| 245 250 255 | |
| ggc atg gac atg ggc atc gtc aac gcg ggc cag ttg ggc gtg tac gag | 816 |
| Gly Met Asp Met Gly Ile Val Asn Ala Gly Gln Leu Gly Val Tyr Glu | |
| 260 265 270 | |
| aac ctc gcc ccc gaa ctg cgc gag cgc gtg gaa gac gtg gtg ctc aac | 864 |
| Asn Leu Ala Pro Glu Leu Arg Glu Arg Val Glu Asp Val Val Leu Asn | |
| 275 280 285 | |
| cgc cgc ccg gat gcg acc gac cgc ctg ctg gaa att gcc gac cgc tac | 912 |
| Arg Arg Pro Asp Ala Thr Asp Arg Leu Leu Glu Ile Ala Asp Arg Tyr | |
| 290 295 300 | |
| aag ggc ggc ggc gcc aag cgc gag gag aac ctc gcc tgg cgc cag gag | 960 |
| Lys Gly Gly Gly Ala Lys Arg Glu Glu Asn Leu Ala Trp Arg Gln Glu | |
| 305 310 315 320 | |
| ccg gtg gaa aag cgc ctg gcc cac gcg ctc gtg cac ggc atc acc gac | 1008 |
| Pro Val Glu Lys Arg Leu Ala His Ala Leu Val His Gly Ile Thr Asp | |
| 325 330 335 | |
| tac gtg gtc gaa gac acc gag gaa gtt cgc cag aag atc ttt gcc gcc | 1056 |
| Tyr Val Val Glu Asp Thr Glu Glu Val Arg Gln Lys Ile Phe Ala Ala | |
| 340 345 350 | |
| ggc ggc cgc ccg atc cag gtg atc gag ggc ccg ctg atg gac ggc atg | 1104 |
| Gly Gly Arg Pro Ile Gln Val Ile Glu Gly Pro Leu Met Asp Gly Met | |
| 355 360 365 | |
| aac atc gtc ggc gat ctg ttc ggc gcg ggc aag atg ttc ctg ccg cag | 1152 |
| Asn Ile Val Gly Asp Leu Phe Gly Ala Gly Lys Met Phe Leu Pro Gln | |
| 370 375 380 | |
| gtg gtg aaa tcc gcc cgc gtg atg aag cag gcg gtg gcc cac ctg atc | 1200 |
| Val Val Lys Ser Ala Arg Val Met Lys Gln Ala Val Ala His Leu Ile | |
| 385 390 395 400 | |
| ccg ttc atc gag gaa gag aag cgg cag atc gcg gcc gcc ggc ggc gac | 1248 |
| Pro Phe Ile Glu Glu Glu Lys Arg Gln Ile Ala Ala Ala Gly Gly Asp | |
| 405 410 415 | |
| gtg cgc tcg cgc ggc aag atc gtc atc gcc acc gtg aag ggc gac gtg | 1296 |
| Val Arg Ser Arg Gly Lys Ile Val Ile Ala Thr Val Lys Gly Asp Val | |
| 420 425 430 | |

219

| | |
|---|------|
| cac gac atc ggc aag aac atc gtc acc gtc gtg ctc cag tgc aac aac His Asp Ile Gly Lys Asn Ile Val Thr Val Val Leu Gln Cys Asn Asn 435 440 445 | 1344 |
| ttc gaa gtc gtg aac atg ggc gtg atg gtc ccg tgc aac gag atc ctg Phe Glu Val Val Asn Met Gly Val Met Val Pro Cys Asn Glu Ile Leu 450 455 460 | 1392 |
| gcc aag gcg aag gtc gag ggc gcg gac atc atc ggc ctg tgc ggc ctg Ala Lys Ala Lys Val Glu Gly Ala Asp Ile Ile Gly Leu Ser Gly Leu 465 470 475 480 | 1440 |
| atc aca ccg tgc ctg gaa gag atg gcc tac gtg gcc tcc gag atg cag Ile Thr Pro Ser Leu Glu Glu Met Ala Tyr Val Ala Ser Glu Met Gln 485 490 495 | 1488 |
| cgc gac gag tac ttc cgc gtg aag aag atc ccg ctg ctg atc ggt ggc Arg Asp Glu Tyr Phe Arg Val Lys Lys Ile Pro Leu Leu Ile Gly Gly 500 505 510 | 1536 |
| gcg acc acg agc cgc gtg cac acc gcc gtg aag atc gcg ccc aat tac Ala Thr Thr Ser Arg Val His Thr Ala Val Lys Ile Ala Pro Asn Tyr 515 520 525 | 1584 |
| gaa ggc ccg gtc gtg tac gtg ccc gac gcc tgc cgc tgc gtg agc gtg Glu Gly Pro Val Val Tyr Val Pro Asp Ala Ser Arg Ser Val Ser Val 530 535 540 | 1632 |
| gcc tcc agc ctg ctg tcc gac gag gcc gcc gcg cgc tac atc gaa gag Ala Ser Ser Leu Leu Ser Asp Glu Ala Ala Ala Arg Tyr Ile Glu Glu 545 550 555 560 | 1680 |
| ctg cac gcc gac tac gac cgc atc cgc acc cag cac gcc agc aag aaa Leu His Ala Asp Tyr Asp Arg Ile Arg Thr Gln His Ala Ser Lys Lys 565 570 575 | 1728 |
| gcc atg ccg atg gtg tgc ctg gcc gcc gcg cgc gcc aac aag acc cgg Ala Met Pro Met Val Ser Leu Ala Ala Ala Arg Ala Asn Lys Thr Arg 580 585 590 | 1776 |
| atc gac tgg tgc aac tac acg ccg ccc aag ccc aag ttc gtc ggc cgc Ile Asp Trp Ser Asn Tyr Thr Pro Pro Lys Pro Lys Phe Val Gly Arg 595 600 605 | 1824 |
| cgc gtg ttc cgc aac tac gac ctg aac gag ctc gcg cag tac atc gac Arg Val Phe Arg Asn Tyr Asp Leu Asn Glu Leu Ala Gln Tyr Ile Asp 610 615 620 | 1872 |
| tgg ggc ccg ttc ttc cag acg tgg gac ctg gcc ggc aaa ttc ccc gac Trp Gly Pro Phe Phe Gln Thr Trp Asp Leu Ala Gly Lys Phe Pro Asp 625 630 635 640 | 1920 |
| atc ctc aac gac gcg atc gtc ggc gaa tgc gcc cgc cgc gtg ttc tcc Ile Leu Asn Asp Ala Ile Val Gly Glu Ser Ala Arg Arg Val Phe Ser 645 650 655 | 1968 |
| gac ggc aag agc atg ctc gcg cgc ctg atc gcc gga cgc tgg ctg acg Asp Gly Lys Ser Met Leu Ala Arg Leu Ile Ala Gly Arg Trp Leu Thr 660 665 670 | 2016 |
| gcc aac ggc gtg atc gcg ctg ctg ccg gcc aac acc gtc aac gac gac | 2064 |

220

| | |
|---|------|
| Ala Asn Gly Val Ile Ala Leu Leu Pro Ala Asn Thr Val Asn Asp Asp | |
| 675 680 685 | |
| gac atc gag atc tac acc gac gag acc cgc tcg gaa gtc gcc ctc acc | 2112 |
| Asp Ile Glu Ile Tyr Thr Asp Glu Thr Arg Ser Glu Val Ala Leu Thr | |
| 690 695 700 | |
| tgg cgc aac atc cgc cag cag agc gag cgc ccg atc atc gac ggc gtg | 2160 |
| Trp Arg Asn Ile Arg Gln Gln Ser Glu Arg Pro Ile Ile Asp Gly Val | |
| 705 710 715 720 | |
| atg cgc ccg aac cgc tgc ctg gcg gac ttc atc gcc ccc aag gac acc | 2208 |
| Met Arg Pro Asn Arg Cys Leu Ala Asp Phe Ile Ala Pro Lys Asp Thr | |
| 725 730 735 | |
| ggc atc gcc gat tac atc ggc ctc ttc gcg gtg acg ggc ggc atc ggg | 2256 |
| Gly Ile Ala Asp Tyr Ile Gly Leu Phe Ala Val Thr Gly Gly Ile Gly | |
| 740 745 750 | |
| atc gac aag cgc gaa gcc gcc ttc gaa gcc gac cac gac gac tac agc | 2304 |
| Ile Asp Lys Arg Glu Ala Ala Phe Glu Ala Asp His Asp Asp Tyr Ser | |
| 755 760 765 | |
| gcg atc atg ctc aag gcc ctg gcc gac cgc ttc gcc gaa gcc ttc gcc | 2352 |
| Ala Ile Met Leu Lys Ala Leu Ala Asp Arg Phe Ala Glu Ala Phe Ala | |
| 770 775 780 | |
| gag tgc ctg cac gcc cgt gtg cgc cgc gac ctg tgg ggc tac gcg cag | 2400 |
| Glu Cys Leu His Ala Arg Val Arg Arg Asp Leu Trp Gly Tyr Ala Gln | |
| 785 790 795 800 | |
| gac gaa acg ctc gac aac gac gcg ctg atc cgc gag gaa tac cgc ggc | 2448 |
| Asp Glu Thr Leu Asp Asn Asp Ala Leu Ile Arg Glu Glu Tyr Arg Gly | |
| 805 810 815 | |
| atc cgc ccg gcg ccc ggc tac ccg gcc tgc ccg gag cac acc gtc aag | 2496 |
| Ile Arg Pro Ala Pro Gly Tyr Pro Ala Cys Pro Glu His Thr Val Lys | |
| 820 825 830 | |
| cgc gac ctg ttc cgc gtg ctc gac gcg cag gag atc ggc atg aac ctg | 2544 |
| Arg Asp Leu Phe Arg Val Leu Asp Ala Gln Glu Ile Gly Met Asn Leu | |
| 835 840 845 | |
| acc gag gcg ctg gcg atg aca ccg gcc gcg tcg gtc tcg ggc ttc cag | 2592 |
| Thr Glu Ala Leu Ala Met Thr Pro Ala Ala Ser Val Ser Gly Phe Gln | |
| 850 855 860 | |
| ctg tcg cac ccg gac agc acg tac ttc acg atc ggc aag atc ggc cag | 2640 |
| Leu Ser His Pro Asp Ser Thr Tyr Phe Thr Ile Gly Lys Ile Gly Gln | |
| 865 870 875 880 | |
| gac cag gtg gac gac atg gcc gcg cgc agc ggg gaa gac cgc cgc aat | 2688 |
| Asp Gln Val Asp Asp Met Ala Ala Arg Ser Gly Glu Asp Arg Arg Asn | |
| 885 890 895 | |
| gtg gag cgc gcc ctg gca ccc aac ctg taa | 2718 |
| Val Glu Arg Ala Leu Ala Pro Asn Leu | |
| 900 905 | |

<210> 50

<211> 905

221

<212> PRT

<213> Ralstonia solanacearum

<400> 50

Met Thr Asp His Leu Met Arg Leu Ser Gly Leu Glu Pro Phe Asn Ile
 1 5 10 15

Gly Glu Asp Thr Leu Phe Val Asn Val Gly Glu Arg Thr Asn Val Thr
 20 25 30

Gly Ser Lys Ala Phe Ala Arg Met Ile Leu Asn Ser Gln Phe Asp Glu
 35 40 45

Ala Leu Ala Val Ala Arg Gln Gln Val Glu Asn Gly Ala Gln Val Ile
 50 55 60

Asp Ile Asn Met Asp Glu Ala Met Leu Asp Ser Lys Ala Ala Met Val
 65 70 75 80

Arg Phe Leu Asn Leu Ile Ala Ser Glu Pro Asp Ile Ala Arg Val Pro
 85 90 95

Ile Met Ile Asp Ser Ser Lys Trp Glu Val Ile Glu Ala Gly Leu Lys
 100 105 110

Cys Val Gln Gly Lys Ala Ile Val Asn Ser Ile Ser Leu Lys Glu Gly
 115 120 125

Glu Glu Gln Phe Ala His His Ala Lys Leu Ile Lys Arg Tyr Gly Ala
 130 135 140

Ala Ala Val Val Met Ala Phe Asp Glu Gln Gly Gln Ala Asp Thr Phe
 145 150 155 160

Ala Arg Lys Thr Glu Ile Cys Lys Arg Ser Tyr Asp Phe Leu Val Asn
 165 170 175

Gln Val Gly Phe Ala Pro Glu Asp Ile Ile Phe Asp Pro Asn Ile Phe
 180 185 190

Ala Val Ala Thr Gly Ile Glu Glu His Asn Asn Tyr Ala Val Asp Phe
 195 200 205

Ile Glu Ala Thr Arg Trp Ile Lys Gln Lys Leu Pro His Ala Lys Val
 210 215 220

Ser Gly Gly Val Ser Asn Val Ser Phe Ser Phe Arg Gly Asn Asp Val
 225 230 235 240

Val Arg Glu Ala Ile His Thr Val Phe Leu Tyr His Ala Ile Gly Ala
 245 250 255

Gly Met Asp Met Gly Ile Val Asn Ala Gly Gln Leu Gly Val Tyr Glu
 260 265 270

Asn Leu Ala Pro Glu Leu Arg Glu Arg Val Glu Asp Val Val Leu Asn
 275 280 285

Arg Arg Pro Asp Ala Thr Asp Arg Leu Leu Glu Ile Ala Asp Arg Tyr
 290 295 300

Lys Gly Gly Gly Ala Lys Arg Glu Glu Asn Leu Ala Trp Arg Gln Glu

222

| | | | |
|---|-----|-----|-----|
| 305 | 310 | 315 | 320 |
| Pro Val Glu Lys Arg Leu Ala His Ala Leu Val His Gly Ile Thr Asp | 325 | 330 | 335 |
| Tyr Val Val Glu Asp Thr Glu Glu Val Arg Gln Lys Ile Phe Ala Ala | 340 | 345 | 350 |
| Gly Gly Arg Pro Ile Gln Val Ile Glu Gly Pro Leu Met Asp Gly Met | 355 | 360 | 365 |
| Asn Ile Val Gly Asp Leu Phe Gly Ala Gly Lys Met Phe Leu Pro Gln | 370 | 375 | 380 |
| Val Val Lys Ser Ala Arg Val Met Lys Gln Ala Val Ala His Leu Ile | 385 | 390 | 395 |
| Pro Phe Ile Glu Glu Lys Arg Gln Ile Ala Ala Ala Gly Gly Asp | 405 | 410 | 415 |
| Val Arg Ser Arg Gly Lys Ile Val Ile Ala Thr Val Lys Gly Asp Val | 420 | 425 | 430 |
| His Asp Ile Gly Lys Asn Ile Val Thr Val Val Leu Gln Cys Asn Asn | 435 | 440 | 445 |
| Phe Glu Val Val Asn Met Gly Val Met Val Pro Cys Asn Glu Ile Leu | 450 | 455 | 460 |
| Ala Lys Ala Lys Val Glu Gly Ala Asp Ile Ile Gly Leu Ser Gly Leu | 465 | 470 | 475 |
| Ile Thr Pro Ser Leu Glu Glu Met Ala Tyr Val Ala Ser Glu Met Gln | 485 | 490 | 495 |
| Arg Asp Glu Tyr Phe Arg Val Lys Lys Ile Pro Leu Leu Ile Gly Gly | 500 | 505 | 510 |
| Ala Thr Thr Ser Arg Val His Thr Ala Val Lys Ile Ala Pro Asn Tyr | 515 | 520 | 525 |
| Glu Gly Pro Val Val Tyr Val Pro Asp Ala Ser Arg Ser Val Ser Val | 530 | 535 | 540 |
| Ala Ser Ser Leu Leu Ser Asp Glu Ala Ala Ala Arg Tyr Ile Glu Glu | 545 | 550 | 555 |
| Leu His Ala Asp Tyr Asp Arg Ile Arg Thr Gln His Ala Ser Lys Lys | 565 | 570 | 575 |
| Ala Met Pro Met Val Ser Leu Ala Ala Ala Arg Ala Asn Lys Thr Arg | 580 | 585 | 590 |
| Ile Asp Trp Ser Asn Tyr Thr Pro Pro Lys Pro Lys Phe Val Gly Arg | 595 | 600 | 605 |
| Arg Val Phe Arg Asn Tyr Asp Leu Asn Glu Leu Ala Gln Tyr Ile Asp | 610 | 615 | 620 |
| Trp Gly Pro Phe Phe Gln Thr Trp Asp Leu Ala Gly Lys Phe Pro Asp | 625 | 630 | 635 |
| | | | 640 |

223

Ile Leu Asn Asp Ala Ile Val Gly Glu Ser Ala Arg Arg Val Phe Ser
 645 650 655
 Asp Gly Lys Ser Met Leu Ala Arg Leu Ile Ala Gly Arg Trp Leu Thr
 660 665 670
 Ala Asn Gly Val Ile Ala Leu Leu Pro Ala Asn Thr Val Asn Asp Asp
 675 680 685
 Asp Ile Glu Ile Tyr Thr Asp Glu Thr Arg Ser Glu Val Ala Leu Thr
 690 695 700
 Trp Arg Asn Ile Arg Gln Gln Ser Glu Arg Pro Ile Ile Asp Gly Val
 705 710 715 720
 Met Arg Pro Asn Arg Cys Leu Ala Asp Phe Ile Ala Pro Lys Asp Thr
 725 730 735
 Gly Ile Ala Asp Tyr Ile Gly Leu Phe Ala Val Thr Gly Gly Ile Gly
 740 745 750
 Ile Asp Lys Arg Glu Ala Ala Phe Glu Ala Asp His Asp Asp Tyr Ser
 755 760 765
 Ala Ile Met Leu Lys Ala Leu Ala Asp Arg Phe Ala Glu Ala Phe Ala
 770 775 780
 Glu Cys Leu His Ala Arg Val Arg Arg Asp Leu Trp Gly Tyr Ala Gln
 785 790 795 800
 Asp Glu Thr Leu Asp Asn Asp Ala Leu Ile Arg Glu Glu Tyr Arg Gly
 805 810 815
 Ile Arg Pro Ala Pro Gly Tyr Pro Ala Cys Pro Glu His Thr Val Lys
 820 825 830
 Arg Asp Leu Phe Arg Val Leu Asp Ala Gln Glu Ile Gly Met Asn Leu
 835 840 845
 Thr Glu Ala Leu Ala Met Thr Pro Ala Ala Ser Val Ser Gly Phe Gln
 850 855 860
 Leu Ser His Pro Asp Ser Thr Tyr Phe Thr Ile Gly Lys Ile Gly Gln
 865 870 875 880
 Asp Gln Val Asp Asp Met Ala Ala Arg Ser Gly Glu Asp Arg Arg Asn
 885 890 895
 Val Glu Arg Ala Leu Ala Pro Asn Leu
 900 905

<210> 51

<211> 3645

<212> DNA

<213> Chlorobium tepidum

<220>

<221> CDS

<222> (1) .. (3642)

<223> RCL00420

224

<400> 51

| | |
|---|-----|
| gtg ctc gac ggg gcc atg ggc acc atg atc cag agg cat ggc ctc gac | 48 |
| Val Leu Asp Gly Ala Met Gly Thr Met Ile Gln Arg His Gly Leu Asp | |
| 1 5 10 15 | |
| gaa cag gac tac cgg ggc gag cgt ttc gct tcg cat gac cat ccg ctg | 96 |
| Glu Gln Asp Tyr Arg Gly Glu Arg Phe Ala Ser His Asp His Pro Leu | |
| 20 25 30 | |
| aag ggc aac aac gac ctt ctt gtc atc acc cgg ccc gac atc atc cgt | 144 |
| Lys Gly Asn Asn Asp Leu Leu Val Ile Thr Arg Pro Asp Ile Ile Arg | |
| 35 40 45 | |
| tcg atc cac tgc gac ttc ctc gac gcg ggt gcg gac atc atc gag acc | 192 |
| Ser Ile His Cys Asp Phe Leu Asp Ala Gly Ala Asp Ile Ile Glu Thr | |
| 50 55 60 | |
| tgc acc ttc aac gcc aac ccg atc tcg cag tcg gac tac cag ttg cag | 240 |
| Cys Thr Phe Asn Ala Asn Pro Ile Ser Gln Ser Asp Tyr Gln Leu Gln | |
| 65 70 75 80 | |
| gac ttg acc cgc gag ctg aac gtg gcg gcg gca aag ata gcc cgc tcg | 288 |
| Asp Leu Thr Arg Glu Leu Asn Val Ala Ala Ala Lys Ile Ala Arg Ser | |
| 85 90 95 | |
| gca gcg gac gag ttc acc gca aag act ccc gac aag ccg cgt ttc gtg | 336 |
| Ala Ala Asp Glu Phe Thr Ala Lys Thr Pro Asp Lys Pro Arg Phe Val | |
| 100 105 110 | |
| gcc ggt tcc atc gga ccg acc aac aag acg ctc tcg ctc tcg ccg gac | 384 |
| Ala Gly Ser Ile Gly Pro Thr Asn Lys Thr Leu Ser Leu Ser Pro Asp | |
| 115 120 125 | |
| gtg aac aac ccc ggc ttc cgc gcc gtc acc ttc cag gag atg gtc gat | 432 |
| Val Asn Asn Pro Gly Phe Arg Ala Val Thr Phe Gln Glu Met Val Asp | |
| 130 135 140 | |
| aac tac act gcc cag ctc gaa ggc ttg cac gag ggc ggt gtc gat ctc | 480 |
| Asn Tyr Thr Ala Gln Leu Glu Gly Leu His Glu Gly Gly Val Asp Leu | |
| 145 150 155 160 | |
| ttg ctc gtc gag acg gtg ttc gac aca ctg aac tgc aag gcg gcg ctc | 528 |
| Leu Leu Val Glu Thr Val Phe Asp Thr Leu Asn Cys Lys Ala Ala Leu | |
| 165 170 175 | |
| tac gct atc gag gag tac gcg gtg aaa acc ggc tgg cag gtg ccc gtg | 576 |
| Tyr Ala Ile Glu Glu Tyr Ala Val Lys Thr Gly Trp Gln Val Pro Val | |
| 180 185 190 | |
| atg gtc tcc ggc acg gtg gtg gac gcg agc ggc cgc acc ctc tcc ggc | 624 |
| Met Val Ser Gly Thr Val Val Asp Ala Ser Gly Arg Thr Leu Ser Gly | |
| 195 200 205 | |
| caa acc acc gag gcg ttc tgg att tcg att tcg cac atg ccg agt ctg | 672 |
| Gln Thr Thr Glu Ala Phe Trp Ile Ser Ile Ser His Met Pro Ser Leu | |
| 210 215 220 | |
| ctc tcg gtc ggc ctg aac tgc gca ctc ggc tcc aag cag atg cgc ccc | 720 |
| Leu Ser Val Gly Leu Asn Cys Ala Leu Gly Ser Lys Gln Met Arg Pro | |
| 225 230 235 240 | |
| ttc atc gag gcg ctc tcg aac atc gcc gaa agc tac gtc agc gtc tat | 768 |

225

| | |
|---|------|
| Phe Ile Glu Ala Leu Ser Asn Ile Ala Glu Ser Tyr Val Ser Val Tyr | |
| 245 250 255 | |
| ccc aac gcg ggc ctg ccg aat gag ttc ggc gag tac gac gac tcc ccc | 816 |
| Pro Asn Ala Gly Leu Pro Asn Glu Phe Gly Glu Tyr Asp Asp Ser Pro | |
| 260 265 270 | |
| gag tac atg gcc gcg cag atc gcg ggc ttc gcc gaa tca ggc ttc gtg | 864 |
| Glu Tyr Met Ala Ala Gln Ile Ala Gly Phe Ala Glu Ser Gly Phe Val | |
| 275 280 285 | |
| aac atc gtc ggc ggc tgc tgc ggc acc acg ccg acg cac atc cgc gcc | 912 |
| Asn Ile Val Gly Gly Cys Cys Gly Thr Thr Pro Thr His Ile Arg Ala | |
| 290 295 300 | |
| att gcc gaa gcg gtc aag act ctc ccg ccg aga aag cgc ccc gcc aac | 960 |
| Ile Ala Glu Ala Val Lys Thr Leu Pro Pro Arg Lys Arg Pro Ala Asn | |
| 305 310 315 320 | |
| aag cac gtg ctg agg ctc tcc ggc ctc gaa ccg ctc gtg gtt gac gaa | 1008 |
| Lys His Val Leu Arg Leu Ser Gly Leu Glu Pro Leu Val Val Asp Glu | |
| 325 330 335 | |
| acc acc ggc ttc atc aac gtc ggc gag cgc acc aac gtc acc ggt tcg | 1056 |
| Thr Thr Gly Phe Ile Asn Val Gly Glu Arg Thr Asn Val Thr Gly Ser | |
| 340 345 350 | |
| cgc aag ttc gcc cgc ctc atc aag gag gcc aat tac gac gaa gcg ctc | 1104 |
| Arg Lys Phe Ala Arg Leu Ile Lys Glu Ala Asn Tyr Asp Glu Ala Leu | |
| 355 360 365 | |
| tcc att gcc cgc cag cag gtc gag aac ggc gcg cag gtg atc gac gtg | 1152 |
| Ser Ile Ala Arg Gln Gln Val Glu Asn Gly Ala Gln Val Ile Asp Val | |
| 370 375 380 | |
| aac ctc gac gaa gga atg ctc gac tcc gaa aag gtg atc gtc gaa ttc | 1200 |
| Asn Leu Asp Glu Gly Met Leu Asp Ser Glu Lys Val Ile Val Glu Phe | |
| 385 390 395 400 | |
| ctg aac ctc atc gcc tcc gag cct gag atc gcc aag gtg ccg gtg atg | 1248 |
| Leu Asn Leu Ile Ala Ser Glu Pro Glu Ile Ala Lys Val Pro Val Met | |
| 405 410 415 | |
| atc gac tcg tcg aaa tgg tcg gtc atc gaa aac ggc ctg cgc tgc acc | 1296 |
| Ile Asp Ser Ser Lys Trp Ser Val Ile Glu Asn Gly Leu Arg Cys Thr | |
| 420 425 430 | |
| cag ggc aag agc atc gtc aac tcg atc agc ctc aag gag ggc gag gag | 1344 |
| Gln Gly Lys Ser Ile Val Asn Ser Ile Ser Leu Lys Glu Gly Glu Glu | |
| 435 440 445 | |
| ctg ttc aag gag cgc gct cgc aag atc atg caa tac ggc gcg gcg gcg | 1392 |
| Leu Phe Lys Glu Arg Ala Arg Lys Ile Met Gln Tyr Gly Ala Ala Ala | |
| 450 455 460 | |
| gtg gtc atg gcc ttc gac gag cag ggc cag gcc gac agc ctg cac cgc | 1440 |
| Val Val Met Ala Phe Asp Glu Gln Gly Gln Ala Asp Ser Leu His Arg | |
| 465 470 475 480 | |
| cgc atc gag att tgc agc cgc gcc tac aaa att ctc acc gaa gag gtg | 1488 |
| Arg Ile Glu Ile Cys Ser Arg Ala Tyr Lys Ile Leu Thr Glu Glu Val | |
| 485 490 495 | |

| | |
|---|------|
| ggc ttc ccg ccg gag gac atc atc ttt gac ccg aac gtg ctg acc gtg | 1536 |
| Gly Phe Pro Pro Glu Asp Ile Ile Phe Asp Pro Asn Val Leu Thr Val | |
| 500 505 510 | |
| gcc acc ggc atc gac gag cac aac aac tac gcg ctc gac ttc atc gaa | 1584 |
| Ala Thr Gly Ile Asp Glu His Asn Asn Tyr Ala Leu Asp Phe Ile Glu | |
| 515 520 525 | |
| agc gtg cgc tgg atc aag cag aac ctg ccg cac gcg aag gtc tcc ggc | 1632 |
| Ser Val Arg Trp Ile Lys Gln Asn Leu Pro His Ala Lys Val Ser Gly | |
| 530 535 540 | |
| ggc atc agc aac gtt tcg ttc tcc ttc cgc ggc aac gag ccg gtg cgc | 1680 |
| Gly Ile Ser Asn Val Ser Phe Ser Phe Arg Gly Asn Glu Pro Val Arg | |
| 545 550 555 560 | |
| gag gcg atg cac acc gcg ttc ctc tac cac gcc atc cac gcc ggt ctc | 1728 |
| Glu Ala Met His Thr Ala Phe Leu Tyr His Ala Ile His Ala Gly Leu | |
| 565 570 575 | |
| gac atg ggc atc gtc aac gcc gcc cag ctt ggc atc tac gaa gag atc | 1776 |
| Asp Met Gly Ile Val Asn Ala Ala Gln Leu Gly Ile Tyr Glu Glu Ile | |
| 580 585 590 | |
| gac ccg gag ctt ctt gtc tat gtc gag gac gtg ctg ctg aac cgc cgc | 1824 |
| Asp Pro Glu Leu Leu Val Tyr Val Glu Asp Val Leu Leu Asn Arg Arg | |
| 595 600 605 | |
| gac gac gcc acc gag cgg ctc gtg gcg ttc gct gaa acg atc cgc gac | 1872 |
| Asp Asp Ala Thr Glu Arg Leu Val Ala Phe Ala Glu Thr Ile Arg Asp | |
| 610 615 620 | |
| ggc ggc gaa aag gcc gag gcc aag aac gcc gaa tgg cgc aac gcc ccg | 1920 |
| Gly Gly Glu Lys Ala Glu Ala Lys Asn Ala Glu Trp Arg Asn Ala Pro | |
| 625 630 635 640 | |
| gtc gag gag cgg ctg aaa cac gcg ctc gtc aag ggc atc gtt gac tac | 1968 |
| Val Glu Glu Arg Leu Lys His Ala Leu Val Lys Gly Ile Val Asp Tyr | |
| 645 650 655 | |
| atc gac gag gac acc gaa gag gcc cgc cag ctc tac ccg agt ccg ctg | 2016 |
| Ile Asp Glu Asp Thr Glu Glu Ala Arg Gln Leu Tyr Pro Ser Pro Leu | |
| 660 665 670 | |
| gag gtg atc gag ggg ccg ctc atg aac ggc atg aac cac gtc ggc gac | 2064 |
| Glu Val Ile Glu Gly Pro Leu Met Asn Gly Met Asn His Val Gly Asp | |
| 675 680 685 | |
| ctc ttc gcc gaa ggc aag atg ttc ctg cca cag gtg gtc aaa agc gcc | 2112 |
| Leu Phe Ala Glu Gly Lys Met Phe Leu Pro Gln Val Val Lys Ser Ala | |
| 690 695 700 | |
| cgc gtc atg aag cgc tcg gta gct gcg ctg att ccc tat atc gag gag | 2160 |
| Arg Val Met Lys Arg Ser Val Ala Ala Leu Ile Pro Tyr Ile Glu Glu | |
| 705 710 715 720 | |
| gag aag tcg aaa aac tgc gac acg agc gcc aaa gcc aag gtg ctg ctc | 2208 |
| Glu Lys Ser Lys Asn Cys Asp Thr Ser Ala Lys Ala Lys Val Leu Leu | |
| 725 730 735 | |
| gcc acg gtg aag ggc gac gtg cac gac atc ggc aag aac atc gtg tcg | 2256 |

227

| | |
|---|------|
| Ala Thr Val Lys Gly Asp Val His Asp Ile Gly Lys Asn Ile Val Ser | |
| 740 745 750 | |
| gtg.gtg ctt gcc tgc aac aac ttc gac gtg atc gac atc ggc gtc atg | 2304 |
| Val Val Leu Ala Cys Asn Asn Phe Asp Val Ile Asp Ile Gly Val Met | |
| 755 760 765 | |
| atg cca tgc gac aag att ctc gaa gcg ctg gca gaa cac aag ccc gac | 2352 |
| Met Pro Cys Asp Lys Ile Leu Glu Ala Leu Ala Glu His Lys Pro Asp | |
| 770 775 780 | |
| gtg ctc ggc ctc tcc ggc ctc atc acc ccg tgc ctc gaa gag atg gcg | 2400 |
| Val Leu Gly Leu Ser Gly Leu Ile Thr Pro Ser Leu Glu Glu Met Ala | |
| 785 790 795 800 | |
| cac gtg gcc aaa gag atg gag cgg ctc ggc atg aac att ccg ctc atc | 2448 |
| His Val Ala Lys Glu Met Glu Arg Leu Gly Met Asn Ile Pro Leu Ile | |
| 805 810 815 | |
| atc ggc ggc gcg acc acc tcg aag gtg cac acg gcg gtg aaa ctc gcg | 2496 |
| Ile Gly Gly Ala Thr Thr Ser Lys Val His Thr Ala Val Lys Leu Ala | |
| 820 825 830 | |
| ccc tgc tac ccc agc ggc gcg gta gta cac gtg ctc gac gcc tcg cgc | 2544 |
| Pro Cys Tyr Pro Ser Gly Ala Val Val His Val Leu Asp Ala Ser Arg | |
| 835 840 845 | |
| agc gtg ccg gtg gtc agc aac ctc tgc aac ccc gcc cag cgc gac agc | 2592 |
| Ser Val Pro Val Val Ser Asn Leu Cys Asn Pro Ala Gln Arg Asp Ser | |
| 850 855 860 | |
| tat atc gcg gcg ctg aag gat gag cag gag gcg atg cgc aag agc cac | 2640 |
| Tyr Ile Ala Ala Leu Lys Asp Glu Gln Glu Ala Met Arg Lys Ser His | |
| 865 870 875 880 | |
| gcc gag cgc atg gcg gca aaa aag tac gtc tcg ctc gac gcc gcc cgc | 2688 |
| Ala Glu Arg Met Ala Ala Lys Lys Tyr Val Ser Leu Asp Ala Ala Arg | |
| 885 890 895 | |
| gac aac cgc ctc acc att gac tgg gag gcc gaa acc atc gac aag ccc | 2736 |
| Asp Asn Arg Leu Thr Ile Asp Trp Glu Ala Glu Thr Ile Asp Lys Pro | |
| 900 905 910 | |
| gcc cag act ggc gtc acc gtg ctg gag gat gtc acc gtc ggc gcg ctc | 2784 |
| Ala Gln Thr Gly Val Thr Val Leu Glu Asp Val Thr Val Gly Ala Leu | |
| 915 920 925 | |
| cgc ccg tat atc gac tgg gca mcc ttc ttc tgg agc tgg gag ctg cac | 2832 |
| Arg Pro Tyr Ile Asp Trp Ala Xaa Phe Phe Trp Ser Trp Glu Leu His | |
| 930 935 940 | |
| ggc gtc tat ccg cag att ctg gag gat gaa aag gtc ggc gag gag gca | 2880 |
| Gly Val Tyr Pro Gln Ile Leu Glu Asp Glu Lys Val Gly Glu Glu Ala | |
| 945 950 955 960 | |
| acc aaa ctc ttc aac gac gcc acc gct ctg ctc gac ccg atc gac agc | 2928 |
| Thr Lys Leu Phe Asn Asp Ala Thr Ala Leu Leu Asp Arg Ile Asp Ser | |
| 965 970 975 | |
| gaa aag ctg ctc ggc atc aaa ggc gtg gcg ggc atc ttc ccg gcc aac | 2976 |
| Glu Lys Leu Leu Gly Ile Lys Gly Val Ala Gly Ile Phe Pro Ala Asn | |
| 980 985 990 | |

228

agc atc ggc gac gac atc ttc gtc tat gcg gat gac gag cgc tcg ata 3024
 Ser Ile Gly Asp Asp Ile Phe Val Tyr Ala Asp Asp Glu Arg Ser Ile
 995 1000 1005

atc cgc acc gtg ctg cac acc ctg cgc cag caa ggc gaa aag cac ggc 3072
 Ile Arg Thr Val Leu His Thr Leu Arg Gln Gln Gly Glu Lys His Gly
 1010 1015 1020

gaa gcg aac ctc gcg ctg gcg gac ttc gtg gcc ccg cgc gaa agc ggc 3120
 Glu Ala Asn Leu Ala Leu Ala Asp Phe Val Ala Pro Arg Glu Ser Gly
 1025 1030 1035 1040

gtc aac gac tgg atc ggc tgc ttc acc gta acc gcc gga ctc ggc atc 3168
 Val Asn Asp Trp Ile Gly Cys Phe Thr Val Thr Ala Gly Leu Gly Ile
 1045 1050 1055

cag aat ttg ctc gac gag ttc aca gca gag aac gac gac tac cac cgc 3216
 Gln Asn Leu Leu Asp Glu Phe Thr Ala Glu Asn Asp Asp Tyr His Arg
 1060 1065 1070

atc atg aca cag gcg ctc gcc gac cga ctg gcc gaa gcg ttc gca gag 3264
 Ile Met Thr Gln Ala Leu Ala Asp Arg Leu Ala Glu Ala Phe Ala Glu
 1075 1080 1085

atg ctg cac gaa aag gtg cgc cgc gaa ctc tgg ggc tac gcg ccc ggc 3312
 Met Leu His Glu Lys Val Arg Arg Glu Leu Trp Gly Tyr Ala Pro Gly
 1090 1095 1100

gaa atc ctc ggc aac gaa gag ctg atc gcc gaa aag tac cga ggc atc 3360
 Glu Ile Leu Gly Asn Glu Glu Leu Ile Ala Glu Lys Tyr Arg Gly Ile
 1105 1110 1115 1120

cgc ccc gcc ccc ggc tac ccc gcc tgc ccg gat cac acc gaa aag gca 3408
 Arg Pro Ala Pro Gly Tyr Pro Ala Cys Pro Asp His Thr Glu Lys Ala
 1125 1130 1135

atc atc ttc gac ctg ctc aac gct gaa gcg gcc acc ggc gtc acg ctg 3456
 Ile Ile Phe Asp Leu Leu Asn Ala Glu Ala Ala Thr Gly Val Thr Leu
 1140 1145 1150

acg gaa act ttc gcg atg aac ccc gca gcc tca gtc tgc ggc ctc tac 3504
 Thr Glu Thr Phe Ala Met Asn Pro Ala Ala Ser Val Cys Gly Leu Tyr
 1155 1160 1165

ttc gcc aac ccg gcc tcg aaa tac ttc gta ctc ggc aag att ggt aag 3552
 Phe Ala Asn Pro Ala Ser Lys Tyr Phe Val Leu Gly Lys Ile Gly Lys
 1170 1175 1180

gat cag gtc gaa gac tac gcc aac cgc aaa ggg ctg gaa gta gca gaa 3600
 Asp Gln Val Glu Asp Tyr Ala Asn Arg Lys Gly Leu Glu Val Ala Glu
 1185 1190 1195 1200

gcc gag aag tgg ctc gcg ccc tcg ctg aac tac gat cca gcg 3642
 Ala Glu Lys Trp Leu Ala Pro Ser Leu Asn Tyr Asp Pro Ala
 1205 1210

taa 3645

<210> 52

<211> 1214

229

<212> PRT

<213> Chlorobium tepidum

<220>

<221> unsure

<222> 936 .. 936

<223> All occurrences of Xaa indicate any amino acid

<400> 52

Val Leu Asp Gly Ala Met Gly Thr Met Ile Gln Arg His Gly Leu Asp
 1 5 10 15

Glu Gln Asp Tyr Arg Gly Glu Arg Phe Ala Ser His Asp His Pro Leu
 20 25 30

Lys Gly Asn Asn Asp Leu Leu Val Ile Thr Arg Pro Asp Ile Ile Arg
 35 40 45

Ser Ile His Cys Asp Phe Leu Asp Ala Gly Ala Asp Ile Ile Glu Thr
 50 55 60

Cys Thr Phe Asn Ala Asn Pro Ile Ser Gln Ser Asp Tyr Gln Leu Gln
 65 70 75 80

Asp Leu Thr Arg Glu Leu Asn Val Ala Ala Ala Lys Ile Ala Arg Ser
 85 90 95

Ala Ala Asp Glu Phe Thr Ala Lys Thr Pro Asp Lys Pro Arg Phe Val
 100 105 110

Ala Gly Ser Ile Gly Pro Thr Asn Lys Thr Leu Ser Leu Ser Pro Asp
 115 120 125

Val Asn Asn Pro Gly Phe Arg Ala Val Thr Phe Gln Glu Met Val Asp
 130 135 140

Asn Tyr Thr Ala Gln Leu Glu Gly Leu His Glu Gly Gly Val Asp Leu
 145 150 155 160

Leu Leu Val Glu Thr Val Phe Asp Thr Leu Asn Cys Lys Ala Ala Leu
 165 170 175

Tyr Ala Ile Glu Glu Tyr Ala Val Lys Thr Gly Trp Gln Val Pro Val
 180 185 190

Met Val Ser Gly Thr Val Val Asp Ala Ser Gly Arg Thr Leu Ser Gly
 195 200 205

Gln Thr Thr Glu Ala Phe Trp Ile Ser Ile Ser His Met Pro Ser Leu
 210 215 220

Leu Ser Val Gly Leu Asn Cys Ala Leu Gly Ser Lys Gln Met Arg Pro
 225 230 235 240

Phe Ile Glu Ala Leu Ser Asn Ile Ala Glu Ser Tyr Val Ser Val Tyr
 245 250 255

Pro Asn Ala Gly Leu Pro Asn Glu Phe Gly Glu Tyr Asp Asp Ser Pro
 260 265 270

Glu Tyr Met Ala Ala Gln Ile Ala Gly Phe Ala Glu Ser Gly Phe Val
 275 280 285

230

Asn Ile Val Gly Gly Cys Cys Gly Thr Thr Pro Thr His Ile Arg Ala
 290 295 300
 Ile Ala Glu Ala Val Lys Thr Leu Pro Pro Arg Lys Arg Pro Ala Asn
 305 310 315 320
 Lys His Val Leu Arg Leu Ser Gly Leu Glu Pro Leu Val Val Asp Glu
 325 330 335
 Thr Thr Gly Phe Ile Asn Val Gly Glu Arg Thr Asn Val Thr Gly Ser
 340 345 350
 Arg Lys Phe Ala Arg Leu Ile Lys Glu Ala Asn Tyr Asp Glu Ala Leu
 355 360 365
 Ser Ile Ala Arg Gln Gln Val Glu Asn Gly Ala Gln Val Ile Asp Val
 370 375 380
 Asn Leu Asp Glu Gly Met Leu Asp Ser Glu Lys Val Ile Val Glu Phe
 385 390 395 400
 Leu Asn Leu Ile Ala Ser Glu Pro Glu Ile Ala Lys Val Pro Val Met
 405 410 415
 Ile Asp Ser Ser Lys Trp Ser Val Ile Glu Asn Gly Leu Arg Cys Thr
 420 425 430
 Gln Gly Lys Ser Ile Val Asn Ser Ile Ser Leu Lys Glu Gly Glu Glu
 435 440 445
 Leu Phe Lys Glu Arg Ala Arg Lys Ile Met Gln Tyr Gly Ala Ala Ala
 450 455 460
 Val Val Met Ala Phe Asp Glu Gln Gly Gln Ala Asp Ser Leu His Arg
 465 470 475 480
 Arg Ile Glu Ile Cys Ser Arg Ala Tyr Lys Ile Leu Thr Glu Glu Val
 485 490 495
 Gly Phe Pro Pro Glu Asp Ile Ile Phe Asp Pro Asn Val Leu Thr Val
 500 505 510
 Ala Thr Gly Ile Asp Glu His Asn Asn Tyr Ala Leu Asp Phe Ile Glu
 515 520 525
 Ser Val Arg Trp Ile Lys Gln Asn Leu Pro His Ala Lys Val Ser Gly
 530 535 540
 Gly Ile Ser Asn Val Ser Phe Ser Phe Arg Gly Asn Glu Pro Val Arg
 545 550 555 560
 Glu Ala Met His Thr Ala Phe Leu Tyr His Ala Ile His Ala Gly Leu
 565 570 575
 Asp Met Gly Ile Val Asn Ala Ala Gln Leu Gly Ile Tyr Glu Glu Ile
 580 585 590
 Asp Pro Glu Leu Leu Val Tyr Val Glu Asp Val Leu Leu Asn Arg Arg
 595 600 605
 Asp Asp Ala Thr Glu Arg Leu Val Ala Phe Ala Glu Thr Ile Arg Asp

231

| | | |
|---|-----|-------------|
| 610 | 615 | 620 |
| Gly Gly Glu Lys Ala Glu Ala Lys Asn Ala Glu Trp Arg Asn Ala Pro | | |
| 625 | 630 | 635 640 |
| Val Glu Glu Arg Leu Lys His Ala Leu Val Lys Gly Ile Val Asp Tyr | | |
| | 645 | 650 655 |
| Ile Asp Glu Asp Thr Glu Glu Ala Arg Gln Leu Tyr Pro Ser Pro Leu | | |
| | 660 | 665 670 |
| Glu Val Ile Glu Gly Pro Leu Met Asn Gly Met Asn His Val Gly Asp | | |
| | 675 | 680 685 |
| Leu Phe Ala Glu Gly Lys Met Phe Leu Pro Gln Val Val Lys Ser Ala | | |
| | 690 | 695 700 |
| Arg Val Met Lys Arg Ser Val Ala Ala Leu Ile Pro Tyr Ile Glu Glu | | |
| | 705 | 710 715 720 |
| Glu Lys Ser Lys Asn Cys Asp Thr Ser Ala Lys Ala Lys Val Leu Leu | | |
| | 725 | 730 735 |
| Ala Thr Val Lys Gly Asp Val His Asp Ile Gly Lys Asn Ile Val Ser | | |
| | 740 | 745 750 |
| Val Val Leu Ala Cys Asn Asn Phe Asp Val Ile Asp Ile Gly Val Met | | |
| | 755 | 760 765 |
| Met Pro Cys Asp Lys Ile Leu Glu Ala Leu Ala Glu His Lys Pro Asp | | |
| | 770 | 775 780 |
| Val Leu Gly Leu Ser Gly Leu Ile Thr Pro Ser Leu Glu Glu Met Ala | | |
| | 785 | 790 795 800 |
| His Val Ala Lys Glu Met Glu Arg Leu Gly Met Asn Ile Pro Leu Ile | | |
| | 805 | 810 815 |
| Ile Gly Gly Ala Thr Thr Ser Lys Val His Thr Ala Val Lys Leu Ala | | |
| | 820 | 825 830 |
| Pro Cys Tyr Pro Ser Gly Ala Val His Val Leu Asp Ala Ser Arg | | |
| | 835 | 840 845 |
| Ser Val Pro Val Val Ser Asn Leu Cys Asn Pro Ala Gln Arg Asp Ser | | |
| | 850 | 855 860 |
| Tyr Ile Ala Ala Leu Lys Asp Glu Gln Glu Ala Met Arg Lys Ser His | | |
| | 865 | 870 875 880 |
| Ala Glu Arg Met Ala Ala Lys Lys Tyr Val Ser Leu Asp Ala Ala Arg | | |
| | 885 | 890 895 |
| Asp Asn Arg Leu Thr Ile Asp Trp Glu Ala Glu Thr Ile Asp Lys Pro | | |
| | 900 | 905 910 |
| Ala Gln Thr Gly Val Thr Val Leu Glu Asp Val Thr Val Gly Ala Leu | | |
| | 915 | 920 925 |
| Arg Pro Tyr Ile Asp Trp Ala Xaa Phe Phe Trp Ser Trp Glu Leu His | | |
| | 930 | 935 940 |

232

Gly Val Tyr Pro Gln Ile Leu Glu Asp Glu Lys Val Gly Glu Glu Ala
 945 950 955 960
 Thr Lys Leu Phe Asn Asp Ala Thr Ala Leu Leu Asp Arg Ile Asp Ser
 965 970 975
 Glu Lys Leu Leu Gly Ile Lys Gly Val Ala Gly Ile Phe Pro Ala Asn
 980 985 990
 Ser Ile Gly Asp Asp Ile Phe Val Tyr Ala Asp Asp Glu Arg Ser Ile
 995 1000 1005
 Ile Arg Thr Val Leu His Thr Leu Arg Gln Gln Gly Glu Lys His Gly
 1010 1015 1020
 Glu Ala Asn Leu Ala Leu Ala Asp Phe Val Ala Pro Arg Glu Ser Gly
 1025 1030 1035 1040
 Val Asn Asp Trp Ile Gly Cys Phe Thr Val Thr Ala Gly Leu Gly Ile
 1045 1050 1055
 Gln Asn Leu Leu Asp Glu Phe Thr Ala Glu Asn Asp Asp Tyr His Arg
 1060 1065 1070
 Ile Met Thr Gln Ala Leu Ala Asp Arg Leu Ala Glu Ala Phe Ala Glu
 1075 1080 1085
 Met Leu His Glu Lys Val Arg Arg Glu Leu Trp Gly Tyr Ala Pro Gly
 1090 1095 1100
 Glu Ile Leu Gly Asn Glu Glu Leu Ile Ala Glu Lys Tyr Arg Gly Ile
 1105 1110 1115 1120
 Arg Pro Ala Pro Gly Tyr Pro Ala Cys Pro Asp His Thr Glu Lys Ala
 1125 1130 1135
 Ile Ile Phe Asp Leu Leu Asn Ala Glu Ala Ala Thr Gly Val Thr Leu
 1140 1145 1150
 Thr Glu Thr Phe Ala Met Asn Pro Ala Ala Ser Val Cys Gly Leu Tyr
 1155 1160 1165
 Phe Ala Asn Pro Ala Ser Lys Tyr Phe Val Leu Gly Lys Ile Gly Lys
 1170 1175 1180
 Asp Gln Val Glu Asp Tyr Ala Asn Arg Lys Gly Leu Glu Val Ala Glu
 1185 1190 1195 1200
 Ala Glu Lys Trp Leu Ala Pro Ser Leu Asn Tyr Asp Pro Ala
 1205 1210

<210> 53

<211> 52

<212> DNA

<213> Künstliche Sequenz

<220>

<223> Beschreibung der künstlichen Sequenz:PCR primer

<400> 53

ccccggatcc gctagcggcg cgccggccgg cccggtgtga aataccgcac ag

<210> 54
<211> 53
<212> DNA
<213> Künstliche Sequenz

<220>
<223> Beschreibung der künstlichen Sequenz:PCR primer

<400> 54
tctagactcg agcggccgcg gccggccttt aaattgaaga cgaaagggcc tcg 53

<210> 55
<211> 47
<212> DNA
<213> Künstliche Sequenz

<220>
<223> Beschreibung der künstlichen Sequenz:PCR primer

<400> 55
gagatctaga cccgggggatc cgctagcggg ctgctaaagg aagcgga 47

<210> 56
<211> 38
<212> DNA
<213> Künstliche Sequenz

<220>
<223> Beschreibung der künstlichen Sequenz:PCR primer

<400> 56
gagagggcgcg ccgctagcgt gggcgaagaa ctccagca 38

<210> 57
<211> 34
<212> DNA
<213> Künstliche Sequenz

<220>
<223> Beschreibung der künstlichen Sequenz:PCR primer

<400> 57
gagagggcgcg ccgcgcaaag tcccgttcg tgaa 34

<210> 58
<211> 34
<212> DNA
<213> Künstliche Sequenz

<220>
<223> Beschreibung der künstlichen Sequenz:PCR primer

<400> 58
gagagggcgcg ccgctcaagt cggtaagcc acgc 34

234

<210> 59

<211> 140

<212> DNA

<213> Künstliche Sequenz

<220>

<223> Beschreibung der künstlichen Sequenz:PCR primer

<400> 59

```
tccaatttaa atctcgagag gcctgacgtc gggcccggtta ccacgcgtca tatgactagt 60
tcggacctag ggatatcgtc gacatcgatg ctcttctgcg ttaattaaca attgggatcc 120
tctagaccg ggatttaaat 140
```

<210> 60

<211> 140

<212> DNA

<213> Künstliche Sequenz

<220>

<223> Beschreibung der künstlichen Sequenz:PCR primer

<400> 60

```
gatcatttaa atcccgggtc tagaggatcc caattgttaa ttaacgcaga agagcatcga 60
tgctgacgat atccctaggt ccgaactagt catatgacgc gtggtaccgg gcccgacgtc 120
aggcctctcg agatttaaat 140
```

<210> 61

<211> 33

<212> DNA

<213> Künstliche Sequenz

<220>

<223> Beschreibung der künstlichen Sequenz:PCR primer

<400> 61

```
gagagcggcc gccgatcctt tttaacccat cac 33
```

<210> 62

<211> 32

<212> DNA

<213> Künstliche Sequenz

<220>

<223> Beschreibung der künstlichen Sequenz:PCR primer

<400> 62

```
aggagcggcc gccatcggca ttttcttttg cg 32
```

<210> 63

<211> 5091

<212> DNA

<213> Künstliche Sequenz

<220>

<223> Beschreibung der künstlichen Sequenz:Plasmid

<400> 63

```
gccgcgactg ccttcgcgaa gccttgcccc gcggaaattt cctccaccga gttcgtgcac 60
```

235

```

acccctatgc caagcttctt tcaccctaaa ttcgagagat tggattctta ccgtggaaat 120
tcttcgcaaa aatcgtccccc tgatcgccct tgcgacgttg gcgtcggtgc cgctgggtgc 180
gcttggcttg accgacttga tcagcggccg ctcgatttaa atctcgagag gcctgacgtc 240
gggcccggta ccacgcgtca tatgactagt tcggacctag ggatatcgtc gacatcgatg 300
ctcttctgcg ttaattaaca attgggatcc tctagaccgg ggatttaa atcgctagcggg 360
ctgctaaagg aagcggaaac cgtagaaagc cagtcgcgag aaacgggtgct gaccccggt 420
gaatgtcagc tactgggcta tctggacaag ggaaaacgca agcgcgaaaga gaaagcaggt 480
agcttgacgt gggcttacat ggcgatagct agactggggc gttttatgga cagcaagcga 540
accggaattg ccagctgggg cgccctctgg taaggttggg aagccctgca aagtaaaactg 600
gatggcttct ttgccgccaa ggatctgatg gcgcagggga tcaagatctg atcaagagac 660
aggatgagga tcgtttcgca tgattgaaca agatggattg cagcgaggt ctccggccgc 720
ttgggtggag aggtattcgc gctatgactg ggcaacaacg acaatcggct gctctgatgc 780
cgccgtgttc cggctgtcag cgcagggggc cccggttctt tttgtcaaga ccgacctgtc 840
cgggtgccctg aatgaactgc aggcagggc agcgcggcta tcgtgggtgg ccacgacggg 900
cgctccttgc gcagctgtgc tcgacgttgt cactgaagcg ggaagggact ggctgctatt 960
gggcgaagtg ccggggcagg atctcctgtc atctcacctt gctcctgccg agaaagtatc 1020
catcatggct gatgcaatgc ggcggtgca tacgcttgat ccggctacct gccattcga 1080
ccaccaagcg aaacatcgca tcgagcgagc acgtactcgg atggaagccg gtcttgctga 1140
tcaggatgat ctggacgaag agcatcaggg gctcgcgcca gccgaactgt tcgccaggct 1200
caaggcgcgc atgcccgacg gcgaggatct cgtcgtgacc catggcgatg cctgcttgc 1260
gaatatcatg gtggaaaatg gccgcttttc tggattcatc gactgtggcc ggctgggtgt 1320
ggcggaaccg tatcaggaca tagcgttggc taccggtgat attgctgaag agcttggcgg 1380
cgaatgggct gaccgcttcc tcgtgcttta ccggtatcgc gctccgatt cgcagcgc 1440
cgccctctat cgccctcttg acgagttctt ctgagcggga ctctggggtt cgaatgacc 1500
gaccaagcga cgcccaacct gccatcacga gatttcgatt ccaccgccgc cttctatgaa 1560
aggttgggct tcggaatcgt tttccgggac gccggtgga tgatcctcca gcgcggggat 1620
ctcatgctgg agttcttcgc ccacgctagc ggcgcgccgg ccggcccggt gtgaaatacc 1680
gcacagatgc gtaaggagaa aataccgcac caggcgctct tccgcttctt cgtcactga 1740
ctcgctgcgc tcggtcgctt ggctgcggcg agcggtatca gctcactcaa aggcggtaat 1800
acggttatcc acagaatcag gggataacgc aggaaagaac atgtgagcaa aaggccagca 1860
aaaggccagg aaccgtaaaa aggcgcggtt gctggcggtt tcccataggc tcgcccccc 1920
tgacgagcat caaaaaatc gacgtcaag tcagaggtgg cgaaacccga caggactata 1980
aagataccag gcgtttcccc ctggaagctc cctcgtgcgc tctcctgttc cgaccctgcc 2040
gcttacggga tactgtccg ccttctccc tcggggaagc gtggcgcttt ctcatagtc 2100
acgctgtagg tatctcagtt cgggtgtagt cgttcgctcc aagctgggct gtgtgcagca 2160
acccccgtt cagcccgacc gctgcgcctt atccggtaac tatcgtcttg agtccaacce 2220
ggtaagacac gacttatcgc cactggcagc agccactggt aacaggatta gcagagcgag 2280
gtatgtaggc ggtgctacag agttcttgaa gtgggtggcct aactacggct acactagaag 2340
gacagtattt ggtatctgcg ctctgctgaa gccagttacc ttcggaaaaa gagttggtag 2400
ctcttgatcc ggcaaaacaa ccaccgctgg tagcgggtgg ttttttgtt gcaagcagca 2460
gattacgcgc agaaaaaaag gatctcaaga agatcctttg atcttttcta cggggtctga 2520
cgctcagtg aacgaaaact cacgttaagg gattttggtc atgagattat caaaaaggat 2580
cttcacctag atccttttaa aggccggccg cggccgcgca aagtcggct tcgtgaaaat 2640
tttcgtgcg cgtgattttc cgccaaaaac tttaacgaac gttcgttata atggtgtcat 2700
gaccttcacg acgaagtact aaaattggcc cgaatcatca gctatggatc tctctgatgt 2760
cgcgctggag tccgacgcgc tcgatgctgc cgtcgattta aaaacgggtg tcggattttt 2820
ccgagctctc gatacgacgg acgcgccagc atcacgagac tgggccagtg ccgcgagcga 2880
cctagaaact ctcggtggcg atcttgagga gctggctgac gagctgcgtg ctccggccagc 2940
gccaggagga cgcacagtag tggaggatgc aatcagttgc gcctactcgc gtggcctgat 3000
tctccccgg cctgaccgcg gaggacggcg cgcaaaatat tgctcagatg cgtgtcgtgc 3060
cgagccagc cgcgagcgcg ccaacaaaac ccacgccgag gagctggagg cggctaggtc 3120
gcaaatggcg ctggaagtgc gtcccccgag cgaaattttg gccatggtcg tcacagagct 3180
ggaagcggca gcgagaatta tcgcgatcgt ggcgggtgcc gcaggcatga caaacatcgt 3240
aaatgcgcg tttcgtgtgc cgtggccgcc caggacgtgt cagcgccgc accacctgca 3300
ccgaatcggc agcagcgtcg cgcgtcga aaagcgcacag gcggcaagaa gcgataagct 3360
gcacgaatac ctgaaaaatg ttgaacgccc cgtgagcggg aactcacagg gcgtcggcta 3420
acccccagtc caaacctggg agaaagcgct caaaaatgac tctagcggat tcacgagaca 3480
ttgacacacc ggcttgaaaa ttttcgctg atctgttcga caccatccc gagctcgcgc 3540
tgcatcacg tggctggagc agcgaagacc gccgcgaatt cctcgtcac ctggcgagag 3600
aaaatttcca gggcgacga acccgcgact tcgccagcgc ttggatcaaa gaccgggaca 3660
cggagaaaca cagccgaagt tataccgagt tggttcaaaa tcgcttgccc ggtgccagta 3720
tgttgctctg acgcacgcgc agcacgcagc cgtgcttgc ctggacattg atgtgccag 3780

```

236

```

ccaccaggcc ggcgggaaaa tcgagcacgt aaacccccgag gtctacgcga ttttggagcg 3840
ctggggcacgc ctggaaaaag cgcagccttg gatcggcgtg aatccactga gcgggaaatg 3900
ccagctcatc tggctcattg atccgggtga tgccgcagca ggcatgagca gcccgaatat 3960
gcgcctgctg gctgcaacga ccgaggaaat gacccgcgtt ttcggcgctg accaggcttt 4020
ttcacatagg ctgagccgtg gccactgcac tctccgacga tcccagccgt accgctggca 4080
tgcccagcac aatcgcgctg atcgccatgc tgatcttatg gaggttgctc gcatgatctc 4140
aggcacagaa aaacctaata aacgctatga gcaggagttt tctagcggac gggcacgtat 4200
cgaagcggca agaaaaagcca ctgcggaagc aaaagcactt gccacgcttg aagcaagcct 4260
gccgagcgcc gctgaagcgt ctggagagct gatcgacggc gtccgtgtcc tctggactgc 4320
tccaggggcg gccgcccgtg atgagacggc ttttcgccac gctttgactg tgggatacca 4380
gttaaaagcg gctggtgagc gcctaaaaga caccaagggt catcgagcct acgagcgtgc 4440
ctacaccgtc gctcaggcgg tcggaggagg ccgtgagcct gatctgccgc cggactgtga 4500
ccgccagacg gattggccgc gacgtgtgcg cggctacgtc gctaaaggcc agccagtcgt 4560
ccctgctcgt cagacagaga cgcagagcca gccgaggcga aaagctctgg ccactatggg 4620
aagacgtggc ggtaaaaagg ccgcagaacg ctggaaagac ccaaacagtg agtacgccc 4680
agcacagcga gaaaaactag ctaagtccag tcaacgacaa gctaggaaag ctaaaaggaaa 4740
tcgcttgacc attgcagggt ggtttatgac tgttgaggga gagactggct cgtggccgac 4800
aatcaatgaa gctatgtctg aatttagcgt gtcacgtcag accgtgaata gagacttaa 4860
ggtctgcggg cattgaactt ccacgaggac gccgaaagct tcccagtaaa tgtgccatct 4920
cgtaggcaga aaacggttcc ccgtaggggt ctctctcttg gcctccttcc taggtcgggc 4980
tgattgtctc tgaagctctc taggggggct cacaccatag gcagataacg tccccaccg 5040
gctcgctcgc taagcgcaca aggactgtc ccaaagatct tcaaagccac t 5091

```

<210> 64

<211> 4323

<212> DNA

<213> Künstliche Sequenz

<220>

<223> Beschreibung der künstlichen Sequenz: Plasmid

<400> 64

```

tctctcagcg tatggttgct gcctgagctg tagttgcctt catcgatgaa ctgctgtaca 60
ttttgatacg tttttccgtc accgtcaaaag attgatattat aatccctctac accgttgatg 120
ttcaaagagc tgcctgatgc tgatacgtta acttggtgcag ttgtcagtg ttgtttgccg 180
taatggtttac cggagaaatc agtgtagaat aaacggattt ttccgtcaga tgtaaattgtg 240
gctgaacctg accattcttg tgtttggtct tttaggatag aatcatttgc atcgaatttg 300
tcgctgtctt taaagacgcg gccagcgttt ttccagctgt caatagaagt ttccgccgact 360
ttttgataga acatgtaaat cgatgtgtca tccgcatttt taggatctcc ggctaattgca 420
aagacgatgt ggtagccgtg atagtttgcg acagtgcctg cagcgttttg taatggccag 480
ctgtcccaaa cgtccaggcc ttttgagaaa gagatatttt taattgtgga cgaatcaaat 540
tcgaaactt gatatttttc atttttttgc tgttcaggga tttgcagcat atcatggcgt 600
gtaatatggg aaatgccgta tgtttcctta tatggctttt gggtcgtttc tttcgcaaac 660
gcttgagttg cgcctcctgc cagcagtgcg gtagtaaaag ttaatactgt tgcctgtttt 720
gcaaaccttt tgatgttcat cgttcatgtc tcctttttta tgtactgtgt tagcggctctg 780
cttcttccag ccctcctgtt tgaagatggc aagttagtta cgcacaataa aaaaagacct 840
aaaatatgta aggggtgacg ccaaagtata cactttgcc tttacacatt ttaggtcttg 900
cctgctttat cagtaacaaa cccgcgcgat ttacttttcg acctcattct attagactct 960
cgtttggatt gcaactggtc tattttcttc ttttgttga tagaaaaatc taaaaggatt 1020
tgcagactac gggcctaaag aactaaaaaa tctatctgtt tcttttcatt ctctgtattt 1080
tttatagttt ctggtgcatg ggcataaagt tgccctttta atcacaattc agaaaatate 1140
ataatatctc atttcactaa ataatagtga acggcaggta tatgtgatgg gttaaaaagg 1200
atcggcggcc gctcgattta aatctcgaga ggccgtgacgt cgggcccggg accacgcgtc 1260
atatgactag ttcggacctg gggatatcgt cgacatcgat gctcttctgc gtttaattaac 1320
aattgggac cctagaccc gggatttaaa tcgtagcggg gctgctaaag gaagcggaac 1380
acgtagaaa cagtcgcga gaaacgggtg tgaccccgga tgaatgtcag ctactgggct 1440
atctggacaa gggaaaacgc aagcgcaaa agaaagcagg tagcttgacg tgggcttaca 1500
tggcgatagc tagactgggc ggttttatgg acagcaagcg aaccggaatt gccagctggg 1560
gcgcctctg gtaagggttg gaagccctgc aaagtaaaact ggatggcttt cttgccgcca 1620
aggatctgat ggcgcagggg atcaagatct gatcaagaga caggatgagg atcgtttcgc 1680

```

237

atgattgaac aagatggatt gcacgcaggt tctccggccg cttgggtgga gaggtattc 1740
 ggctatgact gggcacaaca gacaatcggc tgctctgatg ccgccgtgtt ccggctgtca 1800
 gcgcaggggc gcccggttct ttttgtcaag accgacctgt ccggtgccct gaatgaactg 1860
 caggacgagg cagcgcggct atcgtggctg gccacgcagg gcgttccttg cgcagctgtg 1920
 ctcgacgttg tcaactgaagc ggggaaggac tggctgctat tgggcgaagt gccggggcag 1980
 gatctcctgt catctcacct tgctcctgcc gagaaagtat ccatcatggc tgatgcaatg 2040
 cggcgggtgc atacgcttga tccggctacc tgcccattcg accaccaagc gaaacatcgc 2100
 atcgagcgag cagctactcg gatggaagcc ggtcttgtcg atcaggatga tctggacgaa 2160
 gagcatcagg ggctcgcgcc agccgaactg ttcgccagge tcaaggcgcg catgcccagc 2220
 ggcgaggatc tcgtcgtgac ccatggcgat gcctgcttgc cgaatatcat ggtggaaaaat 2280
 ggccgctttt ctggattcat cgaactgtggc cggctgggtg tggcggaccg ctatcaggac 2340
 atagcgttgg ctaccctgta tattgctgaa gagcttggcg gcgaatgggc tgaccgcttc 2400
 ctcgctgctt acggtatcgc cgtccccgat tcgcagcgca tcgccttcta tcgccttctt 2460
 gacgagtctt tctgagcggg actctggggg tcgaaatgac cgaccaagcg acgccaacc 2520
 tgccatcacg agatttcgat tccaccgccg cctctatga aaggttgggc ttcggaatcg 2580
 ttttccggga cgcggctg atgacctcc agcgcgggga tctcatgctg gagtcttctg 2640
 cccacgctag cggcgcgcgc gccggccccg tgtgaaatac cgcacagatg cgtaaggaga 2700
 aaataccgca tcaggcgctc ttcgccttcc tcgctcactg actcgctgcg ctcggctcgtt 2760
 cggctgcggc gagcgggtatc agctcactca aaggcggtaa tacggttatc cacagaatca 2820
 ggggataacg caggaaagaa catgtgagca aaaggccagc aaaaggccag gaaccgtaaa 2880
 aaggccgcgt tgctggcggt tttccatagg ctcgcgcgcc ctgacgagca tcacaaaaat 2940
 cgcagctcaa gtcagaggtg gcgaaaccgc acaggactat aaagatacca ggcgtttccc 3000
 cctggaagct cctcgtgctg ctctcctggt ccgaccctgc cgcttaccgg atacctgtcc 3060
 gcctttctcc cttcgggaag cgtggcgctt tctcatagct cagctgtag gtatctcagt 3120
 tcgggtgtag tcgttcgctc caagctgggc tgtgtgcacg aacccccgt tcagcccagc 3180
 cgctgcgcct tatccggtaa ctatcgtctt gagtccaacc cggtaagaca cgacttatcg 3240
 ccactggcag agccactg taacaggatt agcagagcga ggtatgtagg cgtgctaca 3300
 gagttcttga agtgggtggc taactacggc tacactagaa ggacagtatt tggatatctg 3360
 gctctgctga agccagttac cttcggaaaa agagtggta gctcttgatc cggcaaaaaa 3420
 accaccgctg gtacgggtgg tttttttgtt tgcaagcagc agattacgcg cagaaaaaaa 3480
 ggatctcaag aagatccttt gatcttttct acggggctctg acgctcagtg gaacgaaaaa 3540
 tcacgttaag ggatttttgt catgagatta tcaaaaagga tcttcaccta gatcctttta 3600
 aaggccggcc cggcccgcca tcggcatttt ctttgcgtt tttatttgtt aactgttaat 3660
 tgccttgtt caaggatgct gtctttgaca acagatgttt tcttgccctt gatgttcagc 3720
 aggaagctcg gcgcaaacgt tgattgtttg tctgcgtaga atcctctggt tgtcatatag 3780
 cttgtaatac cgacattgtt tcctttcgtt tgaggtagc cgaagtgtga gtaagtaaag 3840
 gttacatcgt taggatcaag atccattttt aacacaaggc cagttttgtt cagcggcttg 3900
 tatgggccag ttaaagaatt agaaacataa ccaagcatgt aaatatcgtt agacgtaatg 3960
 ccgtcaatcg tcatttttga tccgcgggag tcagtgaaca ggtaccattt gccgttcatt 4020
 ttaaagacgt tcgcgcgttc aatttcactt gttactgtgt tagatgcaat cagcggtttc 4080
 atcacttttt tcagtgtgta atcatcggtt agctcaatca taccgagagc gccgtttgct 4140
 aactcagccg tcggtttttt atcgctttgc agaagttttt gactttcttg acggaagaat 4200
 gatgtgcttt tgccatagta tgctttgtta aataaagatt cttcgcttgc gtagccatct 4260
 tcagttccag tgtttgcttc aaataactaa tatttgtggc ctttatcttc tacgtagtga 4320
 gga 4323

<210> 65

<211> 35

<212> DNA

<213> PCR Primer

<400> 65

gagagagaga cgcgtcccag tggctgagac gcac

35

<210> 66

<211> 34

<212> DNA

<213> PCR Primer

<400> 66

ctctctctgt cgacgaattc aatcttacgg cctg

34

238

<210> 67
<211> 38
<212> DNA
<213> PCR Primer
<400> 67
cggcaccacc gacatcatct tcacctgccc tcgttcg 38

<210> 68
<211> 38
<212> DNA
<213> PCR Primer
<400> 68
cggaacgagg gcaggtgaag atgatgtcgg tgggtccg 38

<210> 69
<211> 31
<212> DNA
<213> PCR Primer
<400> 69
gagactcgag ggaaggtgaa tcgaatttcg g 31

<210> 70
<211> 38
<212> DNA
<213> PCR Primer
<400> 70
gtcccgggga gaacgcacga ttctccaaaa ataatcgc 38

<210> 71
<211> 23
<212> DNA
<213> PCR Primer
<400> 71
gaatcgtgcg ttctccccg gac 23

<210> 72
<211> 22
<212> DNA
<213> PCR Primer
<400> 72
gtagttgacc gagttgatca cc 22

<210> 73
<211> 18
<212> DNA
<213> PCR Primer
<400> 73
ccggcctgga gaagctcg 18

<210> 74
<211> 28
<212> DNA
<213> PCR Primer
<400> 74

239

gagagatatc cctcagcggg cggtgaag

28

<210> 75
 <211> 1266
 <212> DNA
 <213> LysC Mutante
 <220>
 <221> CDS
 <222> (1) .. (1266)
 <223>

<400> 75
 gtg gcc ctg gtc gta cag aaa tat ggc ggt tcc tcg ctt gag agt gcg 48
 Val Ala Leu Val Val Gln Lys Tyr Gly Gly Ser Ser Leu Glu Ser Ala
 1 5 10 15

gaa cgc att aga aac gtc gct gaa cgg atc gtt gcc acc aag aag gct 96
 Glu Arg Ile Arg Asn Val Ala Glu Arg Ile Val Ala Thr Lys Lys Ala
 20 25 30

gga aat gat gtc gtg gtt gtc tgc tcc gca atg gga gac acc acg gat 144
 Gly Asn Asp Val Val Val Val Cys Ser Ala Met Gly Asp Thr Thr Asp
 35 40 45

gaa ctt cta gaa ctt gca gcg gca gtg aat ccc gtt ccg cca gct cgt 192
 Glu Leu Leu Glu Leu Ala Ala Ala Val Asn Pro Val Pro Pro Ala Arg
 50 55 60

gaa atg gat atg ctc ctg act gct ggt gag cgt att tct aac gct ctc 240
 Glu Met Asp Met Leu Leu Thr Ala Gly Glu Arg Ile Ser Asn Ala Leu
 65 70 75 80

gtc gcc atg gct att gag tcc ctt ggc gca gaa gcc caa tct ttc acg 288
 Val Ala Met Ala Ile Glu Ser Leu Gly Ala Glu Ala Gln Ser Phe Thr
 85 90 95

ggc tct cag gct ggt gtg ctc acc acc gag cgc cac gga aac gca cgc 336
 Gly Ser Gln Ala Gly Val Leu Thr Thr Glu Arg His Gly Asn Ala Arg
 100 105 110

att gtt gat gtc act cca ggt cgt gtg cgt gaa gca ctc gat gag ggc 384
 Ile Val Asp Val Thr Pro Gly Arg Val Arg Glu Ala Leu Asp Glu Gly
 115 120 125

aag atc tgc att gtt gct ggt ttc cag ggt gtt aat aaa gaa acc cgc 432
 Lys Ile Cys Ile Val Ala Gly Phe Gln Gly Val Asn Lys Glu Thr Arg
 130 135 140

gat gtc acc acg ttg ggt cgt ggt ggt tct gac acc act gca gtt gcg 480
 Asp Val Thr Thr Leu Gly Arg Gly Gly Ser Asp Thr Thr Ala Val Ala
 145 150 155 160

ttg gca gct gct ttg aac gct gat gtg tgt gag att tac tcg gac gtt 528
 Leu Ala Ala Ala Leu Asn Ala Asp Val Cys Glu Ile Tyr Ser Asp Val
 165 170 175

gac ggt gtg tat acc gct gac ccg cgc atc gtt cct aat gca cag aag 576
 Asp Gly Val Tyr Thr Ala Asp Pro Arg Ile Val Pro Asn Ala Gln Lys
 180 185 190

ctg gaa aag ctc agc ttc gaa gaa atg ctg gaa ctt gct gct gtt ggc 624

240

| | |
|---|------|
| Leu Glu Lys Leu Ser Phe Glu Glu Met Leu Glu Leu Ala Ala Val Gly | |
| 195 200 205 | |
| tcc aag att ttg gtg ctg cgc agt gtt gaa tac gct cgt gca ttc aat | 672 |
| Ser Lys Ile Leu Val Leu Arg Ser Val Glu Tyr Ala Arg Ala Phe Asn | |
| 210 215 220 | |
| gtg cca ctt cgc gta cgc tgc tct tat agt aat gat ccc ggc act ttg | 720 |
| Val Pro Leu Arg Val Arg Ser Ser Tyr Ser Asn Asp Pro Gly Thr Leu | |
| 225 230 235 240 | |
| att gcc ggc tct atg gag gat att cct gtg gaa gaa gca gtc ctt acc | 768 |
| Ile Ala Gly Ser Met Glu Asp Ile Pro Val Glu Glu Ala Val Leu Thr | |
| 245 250 255 | |
| ggc gtc gca acc gac aag tcc gaa gcc aaa gta acc gtt ctg ggt att | 816 |
| Gly Val Ala Thr Asp Lys Ser Glu Ala Lys Val Thr Val Leu Gly Ile | |
| 260 265 270 | |
| tcc gat aag cca ggc gag gct gcg aag gtt ttc cgt gcg ttg gct gat | 864 |
| Ser Asp Lys Pro Gly Glu Ala Ala Lys Val Phe Arg Ala Leu Ala Asp | |
| 275 280 285 | |
| gca gaa atc aac att gac atg gtt ctg cag aac gtc tct tct gta gaa | 912 |
| Ala Glu Ile Asn Ile Asp Met Val Leu Gln Asn Val Ser Ser Val Glu | |
| 290 295 300 | |
| gac ggc acc acc gac atc atc ttc acc tgc cct cgt tcc gac ggc cgc | 960 |
| Asp Gly Thr Thr Asp Ile Ile Phe Thr Cys Pro Arg Ser Asp Gly Arg | |
| 305 310 315 320 | |
| cgc gcg atg gag atc ttg aag aag ctt cag gtt cag ggc aac tgg acc | 1008 |
| Arg Ala Met Glu Ile Leu Lys Lys Leu Gln Val Gln Gly Asn Trp Thr | |
| 325 330 335 | |
| aat gtg ctt tac gac gac cag gtc ggc aaa gtc tcc ctc gtg ggt gct | 1056 |
| Asn Val Leu Tyr Asp Asp Gln Val Gly Lys Val Ser Leu Val Gly Ala | |
| 340 345 350 | |
| ggc atg aag tct cac cca ggt gtt acc gca gag ttc atg gaa gct ctg | 1104 |
| Gly Met Lys Ser His Pro Gly Val Thr Ala Glu Phe Met Glu Ala Leu | |
| 355 360 365 | |
| cgc gat gtc aac gtg aac atc gaa ttg att tcc acc tct gag att cgt | 1152 |
| Arg Asp Val Asn Val Asn Ile Glu Leu Ile Ser Thr Ser Glu Ile Arg | |
| 370 375 380 | |
| att tcc gtg ctg atc cgt gaa gat gat ctg gat gct gct gca cgt gca | 1200 |
| Ile Ser Val Leu Ile Arg Glu Asp Asp Leu Asp Ala Ala Arg Ala | |
| 385 390 395 400 | |
| ttg cat gag cag ttc cag ctg ggc ggc gaa gac gaa gcc gtc gtt tat | 1248 |
| Leu His Glu Gln Phe Gln Leu Gly Gly Glu Asp Glu Ala Val Val Tyr | |
| 405 410 415 | |
| gca ggc acc gga cgc taa | 1266 |
| Ala Gly Thr Gly Arg | |
| 420 | |

<210> 76

<211> 421

241

<212> PRT

<213> LysC Mutante

<400> 76

Val Ala Leu Val Val Gln Lys Tyr Gly Gly Ser Ser Leu Glu Ser Ala
 1 5 10 15

Glu Arg Ile Arg Asn Val Ala Glu Arg Ile Val Ala Thr Lys Lys Ala
 20 25 30

Gly Asn Asp Val Val Val Val Cys Ser Ala Met Gly Asp Thr Thr Asp
 35 40 45

Glu Leu Leu Glu Leu Ala Ala Ala Val Asn Pro Val Pro Pro Ala Arg
 50 55 60

Glu Met Asp Met Leu Leu Thr Ala Gly Glu Arg Ile Ser Asn Ala Leu
 65 70 75 80

Val Ala Met Ala Ile Glu Ser Leu Gly Ala Glu Ala Gln Ser Phe Thr
 85 90 95

Gly Ser Gln Ala Gly Val Leu Thr Thr Glu Arg His Gly Asn Ala Arg
 100 105 110

Ile Val Asp Val Thr Pro Gly Arg Val Arg Glu Ala Leu Asp Glu Gly
 115 120 125

Lys Ile Cys Ile Val Ala Gly Phe Gln Gly Val Asn Lys Glu Thr Arg
 130 135 140

Asp Val Thr Thr Leu Gly Arg Gly Gly Ser Asp Thr Thr Ala Val Ala
 145 150 155 160

Leu Ala Ala Ala Leu Asn Ala Asp Val Cys Glu Ile Tyr Ser Asp Val
 165 170 175

Asp Gly Val Tyr Thr Ala Asp Pro Arg Ile Val Pro Asn Ala Gln Lys
 180 185 190

Leu Glu Lys Leu Ser Phe Glu Glu Met Leu Glu Leu Ala Ala Val Gly
 195 200 205

Ser Lys Ile Leu Val Leu Arg Ser Val Glu Tyr Ala Arg Ala Phe Asn
 210 215 220

Val Pro Leu Arg Val Arg Ser Ser Tyr Ser Asn Asp Pro Gly Thr Leu
 225 230 235 240

242

Ile Ala Gly Ser Met Glu Asp Ile Pro Val Glu Glu Ala Val Leu Thr
 245 250 255

Gly Val Ala Thr Asp Lys Ser Glu Ala Lys Val Thr Val Leu Gly Ile
 260 265 270

Ser Asp Lys Pro Gly Glu Ala Ala Lys Val Phe Arg Ala Leu Ala Asp
 275 280 285

Ala Glu Ile Asn Ile Asp Met Val Leu Gln Asn Val Ser Ser Val Glu
 290 295 300

Asp Gly Thr Thr Asp Ile Ile Phe Thr Cys Pro Arg Ser Asp Gly Arg
 305 310 315 320

Arg Ala Met Glu Ile Leu Lys Lys Leu Gln Val Gln Gly Asn Trp Thr
 325 330 335

Asn Val Leu Tyr Asp Asp Gln Val Gly Lys Val Ser Leu Val Gly Ala
 340 345 350

Gly Met Lys Ser His Pro Gly Val Thr Ala Glu Phe Met Glu Ala Leu
 355 360 365

Arg Asp Val Asn Val Asn Ile Glu Leu Ile Ser Thr Ser Glu Ile Arg
 370 375 380

Ile Ser Val Leu Ile Arg Glu Asp Asp Leu Asp Ala Ala Ala Arg Ala
 385 390 395 400

Leu His Glu Gln Phe Gln Leu Gly Gly Glu Asp Glu Ala Val Val Tyr
 405 410 415

Ala Gly Thr Gly Arg
 420

<210> 77

<211> 5860

<212> DNA

<213> Plasmid

<400> 77

| | |
|---|-----|
| cccgggtacca cgcgtcccag tggtgagac gcatccgcta aagccccagg aacctgtgc | 60 |
| agaaagaaaa cactcctctg gctaggtaga cacagtttat aaaggtagag ttgagcgggt | 120 |
| aactgtcagc acgtagatcg aaaggtgcac aaaggtggcc ctggtcgtac agaaatatgg | 180 |
| cggttcctcg cttgagagtg cggaacgcac tagaaacgtc gctgaacgga tcgttgccac | 240 |

243

| | |
|--|------|
| caagaaggct ggaaatgatg tcgtggttgt ctgctccgca atgggagaca ccacggatga | 300 |
| acttctagaa cttgcagcgg cagtgaatcc cgttccgcca gctcgtgaaa tggatatgct | 360 |
| cctgactgct ggtgagcgta tttctaacgc tctcgtcgcc atggctattg agtcccttgg | 420 |
| cgcagaagcc caatctttca cgggctctca ggctggtgtg ctcaccaccg agcgccacgg | 480 |
| aaacgcacgc attgttgatg tcaactccagg tcgtgtgcgt gaagcactcg atgagggcaa | 540 |
| gatctgcatt gttgctggtt tccaggggtg taataaagaa acccgcgatg tcaccacgtt | 600 |
| gggtcgtggt ggttctgaca ccactgcagt tgcgttggca gctgcttga acgctgatgt | 660 |
| gtgtgagatt tactcggacg ttgacgggtg gtataccgct gaccgcgca tcgttcctaa | 720 |
| tgcacagaag ctggaaaagc tcagcttcga agaaatgctg gaacttgctg ctggttggtc | 780 |
| caagattttg gtgctgcgca gtgttgaata cgctcgtgca ttcaatgtgc cacttcgcgt | 840 |
| acgctcgtct tatagtaatg atcccgccac tttgattgcc ggctctatgg aggatattcc | 900 |
| tgtggaagaa gcagtcctta ccggtgtcgc aaccgacaag tccgaagcca aagtaaccgt | 960 |
| tctgggtatt tccgataagc caggcgagge tgcgaagggt ttccgtgcgt tggctgatgc | 1020 |
| agaaatcaac attgacatgg ttctgcagaa cgtctcttct gtagaagacg gcaccaccga | 1080 |
| catcaccttc acctgcctc gttccgacgg ccgcccgcg atggagatct tgaagaagct | 1140 |
| tcaggttcag ggcaactgga ccaatgtgct ttacgacgac caggtcggca aagtctccct | 1200 |
| cgtgggtgct ggcataaagt ctcaccacgg tgttaccgca gagttcatgg aagctctgcg | 1260 |
| cgatgtcaac gtgaacatcg aattgatttc cacctctgag attcgtattt ccgtgctgat | 1320 |
| ccgtgaagat gatctggatg ctgctgcacg tgcattgcat gagcagttcc agctggcg | 1380 |
| cgaagacgaa gccgtcgttt atgcaggcac cggacgctaa agttttaag gagtagtttt | 1440 |
| acaatgacca ccatacgagt tggtggtgca accggccagg tcggccaggt tatgcgaccc | 1500 |
| cttttggaag agcgcaattt cccagctgac actgttcgtt tctttgcttc cccacgttcc | 1560 |
| gcaggccgta agattgaatt cgtcgacatc gatgctcttc tgcgttaatt aacaattggg | 1620 |
| atcctctaga cccgggattt aaatcgctag cgggctgcta aaggaagcgg aacacgtaga | 1680 |
| aagccagtcc gcagaaacgg tgctgacccc ggatgaatgt cagctactgg gctatctgga | 1740 |
| caagggaaaa cgcaagcgca aagagaaagc aggtagcttg cagtgggctt acatggcgat | 1800 |
| agctagactg ggcggtttta tggacagcaa gcgaaccgga attgccagct ggggcgcct | 1860 |
| ctggttaagg tgggaagccc tgcaaagtaa actggatggc tttcttgccg ccaaggatct | 1920 |
| gatggcgtag gggatcaaga tctgatcaag agacaggatg aggatcgttt cgcattgattg | 1980 |
| aacaagatgg attgcacgca ggttctccgg ccgcttggtt ggagaggcta ttcggctatg | 2040 |
| actgggcaca acagacaatc ggctgctctg atgccgccgt gttccggctg tcagcgacgg | 2100 |

ggcgcccggt tctttttgtc aagaccgacc tgtccggtgc cctgaatgaa ctgcaggacg 2160
aggcagcgcg gctatcgtgg ctggccacga cgggcgttcc ttgcgcagct gtgctcgacg 2220
ttgtcactga agcgggaagg gactggctgc tattgggcga agtgccgggg caggatctcc 2280
tgtcatctca ccttgctcct gccgagaaag tatccatcat ggctgatgca atgcggcggc 2340
tgcatacget tgatccggct acctgcccat tcgaccacca agcgaaacat cgcacgcagc 2400
gagcacgtac tcggatggaa gccggtcttg tcgatcagga tgatctggac gaagagcatc 2460
aggggctcgc gccagccgaa ctgttcgcca ggctcaaggc gcgcacgccc gacggcgagg 2520
atctcgtcgt gacccatggc gatgcctgct tgccgaatat catggtggaa aatggccgct 2580
tttctggatt catcgactgt ggccggctgg gtgtggcgga ccgctatcag gacatagcgt 2640
tggtaccgg tgatattgct gaagagcttg gcggcgaatg ggctgaccgc ttcctcgtgc 2700
tttacggtat cgcgcgtccc gattcgcagc gcacgcctt ctatgcctt cttgacgagt 2760
tcttctgagc gggactctgg ggttcgaaat gaccgaccaa gcgacgccc acctgccatc 2820
acgagatttc gattccaccg ccgccttcta tgaagggttg ggcttcggaa tcgttttccg 2880
ggacgcccgc tggatgatcc tccagcgcg ggatctcatg ctggagtctc tcgccacgc 2940
tagcggcgcg ccggccggcc cgggtgtgaaa taccgcacag atgcgtaagg agaaaatacc 3000
gcacaggcg ctcttccgct tctcgtctca ctgactcgt gcgctcggtc gttcggctgc 3060
ggcgagcgg atcagctcac tcaaaggcgg taatacgggt atccacagaa tcaggggata 3120
acgcaggaaa gaacatgtga gcaaaaggcc agcaaaaggc caggaaaccgt aaaaaggccg 3180
cgttgctggc gtttttccat aggtccgcc cccctgacga gcacacaaa aatcgacgct 3240
caagtcagag gtggcgaaac ccgacaggac tataaagata ccaggcggtt cccctggaa 3300
gctccctcgt gcgctctcct gttccgacce tgccgcttac cggatacctg tccgccttcc 3360
tcccttcggg aagcgtggcg ctttctcata gctcacgctg taggtatctc agttcgggtg 3420
aggctcgttc ctccaagctg ggctgtgtgc acgaaccccc cgttcagccc gaccgctgcg 3480
ccttatccgg taactatcgt cttgagtcca acccgtaag acacgactta tcgccactgg 3540
cagcagccac tggtaacagg attagcagag cgaggatatg aggcggtgct acagagtctc 3600
tgaagtgggt gcctaactac ggctacacta gaaggacagt atttggtatc tgcgctctgc 3660
tgaagccagt taccttcgga aaaagagttg gtagctcttg atccggcaaa caaaccaccg 3720
ctggtagcgg tggttttttt gtttgcaagc agcagattac gcgcagaaaa aaaggatctc 3780
aagaagatcc tttgatcttt tctacggggt ctgacgctca gtggaacgaa aactcacgtt 3840
aagggatttt ggtcatgaga ttatcaaaaa ggatcttcac ctagatcctt ttaaaggccg 3900
gccgcggccg ccacgagcat tttcttttgc gtttttattt gttaactgtt aattgtcctt 3960

gttcaaggat gctgtctttg acaacagatg ttttcttgcc tttgatgttc agcaggaagc 4020
tcggcgcaaa cgttgattgt ttgtctgcgt agaatcctct gtttgtcata tagcttgtaa 4080
tcacgacatt gtttcctttc gcttgaggta cagcgaagtg tgagtaagta aaggttacat 4140
cgttaggatc aagatccatt tttaacacaa ggccagtttt gttcagcggc ttgtatgggc 4200
cagttaaaga attagaaaca taaccaagca tgtaaatac gtttagacgta atgccgtcaa 4260
tcgtcatttt tgatccgcgg gagtcagtga acaggtagca tttgccgttc attttaaaga 4320
cgttcgcggc ttcaatttca tctgttactg tgtagatgc aatcagcggc ttcatacactt 4380
ttttcagtgt gtaatcatcg tttagctcaa tcataccgag agcgccgttt gctaactcag 4440
ccgtgcgttt tttatcgctt tgcagaagtt tttgactttc ttgacggaag aatgatgtgc 4500
ttttgccata gtatgctttg ttaaataaag attcttcgcc ttggtagcca tcttcagttc 4560
cagtgtttgc ttcaataact aagtatttgt ggccctttatc ttctacgtag tgaggatctc 4620
tcagcgtagt gttgtgcct gagctgtagt tgccttcac gatgaactgc tgtacatttt 4680
gatacgtttt tccgtcaccg tcaaagattg atttataatc ctctacaccg ttgatgttca 4740
aagagctgtc tgatgctgat acgttaactt gtgcagttgt cagtgtttgt ttgccgtaat 4800
gtttaccgga gaaatcagt tagaataaac ggatttttcc gtcagatgta aatgtggctg 4860
aacctgacca ttcttggtt tggcttttta ggatagaatc atttgcatcg aatttgctgc 4920
tgtctttaa gacgcggcca gcgtttttcc agctgtcaat agaagtttcg ccgacttttt 4980
gatagaacat gtaaategat gtgtcatccg catttttagg atctccggct aatgcaaaga 5040
cgatgtggta gccgtgatag tttgcgacag tgccgtcagc gttttgtaat ggccagctgt 5100
cccaaacgtc caggcctttt gcagaagaga tatttttaat tgtggacgaa tcaaattcag 5160
aaacttgata tttttcattt ttttgcgtt cagggatttg cagcatatca tggcgtgtaa 5220
tatgggaaat gccgtatgtt tccttatatg gcttttggtt cgtttcttc gcaaacgctt 5280
gagttgcgcc tcctgccagc agtgccgtag taaagggtta tactgttgct tgttttgcaa 5340
actttttgat gttcatcggt catgtctcct tttttatgta ctgtgttagc ggtctgcttc 5400
ttccagccct cctgtttgaa gatggcaagt tagttacgca caataaaaaa agacctaaaa 5460
tatgtaaggg gtgacgcaa agtatacact ttgcccttta cacatttttag gtcttgccgtg 5520
ctttatcagt aacaaaccg cgcgatttac ttttcgacct cattctatta gactctcggt 5580
tggattgcaa ctggtctatt ttctctttt gttgataga aaatcataaa aggatttgca 5640
gactacgggc ctaagaact aaaaaatcta tctgtttctt ttcattctct gtatttttta 5700
tagtttctgt tgcagggca taaagttgcc tttttaatca caattcagaa aatatcataa 5760
tatctcattt cactaaataa tagtgaacgg caggtatatg tgatgggtta aaaaggatcg 5820

246

gcggccgctc gatttaaacc tcgagaggcc tgacgtcggg 5860

<210> 78

<211> 5860

<212> DNA

<213> Plasmid

<400> 78

cccggtagca cgcgtccagc tggtgagac gcatccgcta aagccccagg aaccctgtgc 60
agaaagaaaa cactcctctg gctaggtaga cacagtttat aaaggtagag ttgagcgggt 120
aactgtcagc acgtagatcg aaaggtgcac aaaggtggcc ctggctgtac agaaatatgg 180
cggttcctcg cttgagagtg cggaacgcac tagaaacgct gctgaacgga tcgttgccac 240
caagaaggct ggaaatgatg tcgtggttgt ctgctccgca atgggagaca ccacggatga 300
acttctagaa cttgcagcgg cagtgaatcc cgttccgcca gctcgtgaaa tggatatgct 360
cctgactgct ggtgagcgtg tttctaacgc tctcgtcgcc atggctattg agtcccttgg 420
cgcagaagcc caatctttca cgggctctca ggctgggtgtg ctcaccaccg agcggccagg 480
aaacgcacgc attgttgatg tcaactccagg tcgtgtgcgt gaagcactcg atgagggcaa 540
gatctgcatt gttgctggtt tccagggtgt taataagaa acccgcatg tcaccacgtt 600
gggtcgtggt gggtctgaca ccactgcagt tgcgttgcca gctgctttga acgctgatgt 660
gtgtgagatt tactcggacg ttgacggtgt gtataccgct gacccgcgca tcgttcctaa 720
tgacacagaag ctggaaaagc tcagcttcga agaaatgctg gaacttgctg ctggttgctc 780
caagattttg gtgctgcgca gtgttgaata cgtcgtgca ttcaatgtgc cacttcgctg 840
acgtcgtct tatagtaatg atccccgcac ttgattgcc ggctctatgg aggatattcc 900
tgtggaagaa gcagtcctta ccggtgtcgc aaccgacaag tccgaagcca aagtaaccgt 960
tctgggtatt tccgataagc caggcgaggc tgcaagggtt ttccgtgctg tggctgatgc 1020
agaaatcaac attgacatgg ttctgcagaa cgtctcttct gtagaagacg gcaccaccga 1080
catcatcttc acctgccctc gttccgacgg ccgcccgcg atggagatct tgaagaagct 1140
tcaggttcag ggcaactgga ccaatgtgct ttacgacgac caggtcggca aagtctccct 1200
cgtgggtgct ggcataaggt ctcacccagg tgttaccgca gattcatgg aagctctgag 1260
cgatgtcaac gtgaacatcg aattgatttc cactctgag attcgtattt ccgtgctgat 1320
ccgtgaagat gatctggatg ctgctgcacg tgcattgcat gagcagttcc agctgggagg 1380
cgaagacgaa gccgtcgttt atgcaggcac cggacgctaa agttttaag gagtagtttt 1440
acaatgacca ccacgcaggt tgttggtgca accggccagg tcggccagggt tatgcgcacc 1500
cttttggaag agcgaattt cccagctgac actgttcggt tctttgcttc cccacgttcc 1560
gcaggccgta agattgaatt cgtcgacatc gatgctcttc tgcgttaatt aacaattggg 1620

247

| | |
|--|------|
| atcctctaga cccgggattt aaatcgctag cgggctgcta aaggaagcgg aacacgtaga | 1680 |
| aagccagtcc gcagaaacgg tgctgacccc ggatgaatgt cagctactgg gctatctgga | 1740 |
| caagggaaaa cgcaagcgca aagagaaagc aggtagcttg cagtgggctt acatggcgat | 1800 |
| agctagactg ggcggtttta tggacagcaa gcgaaccgga attgccagct ggggcgccct | 1860 |
| ctggttaagg tgggaagccc tgcaaagtaa actggatggc tttcttgccg ccaaggatct | 1920 |
| gatggcgag gggatcaaga tctgatcaag agacaggatg aggatcggtt cgcattgattg | 1980 |
| aacaagatgg attgcacgca ggttctccgg ccgcttgggt ggagaggcta ttcggctatg | 2040 |
| actgggcaca acagacaatc ggctgctctg atgccgccgt gttccggctg tcagcgagg | 2100 |
| ggcgcccggg tctttttgtc aagaccgacc tgtccgggtg cctgaatgaa ctgcaggacg | 2160 |
| aggcagcgcg gctatcgtag ctggccacga cgggcgttcc ttgcgcagct gtgctcgacg | 2220 |
| ttgtcactga agcgggaagg gactggctgc tattgggcga agtgccgggg caggatctcc | 2280 |
| tgctcatctca ccttgctcct gccgagaaag tatccatcat ggctgatgca atgcggcggc | 2340 |
| tgcatagct tgatccggct acctgcccac tcgaccacca agcgaaacat cgcacgcagc | 2400 |
| gagcacgtac tcggatggaa gccgggtcttg tcgatcagga tgatctggac gaagagcatc | 2460 |
| aggggctcgc gccagccgaa ctgttcgcca ggctcaaggc gcgcagccc gacggcgagg | 2520 |
| atctcgtcgt gacccatggc gatgctgct tgccgaatat catggtggaa aatggccgct | 2580 |
| tttctggatt catcgactgt ggccggctgg gtgtggcgga ccgctatcag gacatagcgt | 2640 |
| tggtaccg tgatattgct gaagagcttg gcggcgaatg ggctgaccgc ttcctcgtgc | 2700 |
| tttacggtat cgcgctccc gattcgcagc gcatcgctt ctatcgctt cttgacgagt | 2760 |
| tcttctgagc gggactctgg ggttcgaaat gaccgaccaa gcgacgcca acctgccatc | 2820 |
| acgagatttc gattccaccg ccgccttcta tgaaagggtg ggcttcggaa tegttttccg | 2880 |
| ggacgccggc tggatgatcc tccagcgcg ggatctcatg ctggagttct tcgcccacgc | 2940 |
| tagcggcgcg ccggccggcc cgggtgtgaa taccgcacag atgcgtaagg agaaaatacc | 3000 |
| gcatcaggcg ctcttccgct tcctcgctca ctgactcgt gcgctcggtc gttcggtgc | 3060 |
| ggcgagcgg atcagctcac tcaaaggcgg taatacgggt atccacagaa tcaggggata | 3120 |
| acgcaggaaa gaacatgtga gcaaaaggcc agcaaaaggc caggaaccgt aaaaaggccg | 3180 |
| cgttgctggc gtttttccat aggtccgcgc cccctgacga gcatcacaaa aatcgacgt | 3240 |
| caagtcagag gtggcgaaac ccgacaggac tataaagata ccaggcggtt cccctggaa | 3300 |
| gtccctcgt gcgctcctt gttccgacct tgccgcttac cggatacctg tccgccttcc | 3360 |
| tcccttcggg aagcgtggcg ctttctcata gctcacgctg taggtatctc agttcggtgt | 3420 |
| aggtcgttcg ctccaagctg ggctgtgtgc acgaaccccc cgttcagccc gaccgctgcg | 3480 |

ccttatccgg taactatcgt cttgagtcca acccggttaag acacgactta tcgccactgg 3540
cagcagccac tggtaacagg attagcagag cgaggatgt aggcggtgct acagagttct 3600
tgaagtgggtg gcctaactac ggctacacta gaaggacagt atttggtatc tgcgctctgc 3660
tgaagccagt taccttcgga aaaagagttg gtagctcttg atccggcaaa caaaccaccg 3720
ctggtagcgg tgggtttttt gtttgcaagc agcagattac gcgcagaaaa aaaggatctc 3780
aagaagatcc tttgatcttt tctacggggt ctgacgctca gtggaacgaa aactcacgtt 3840
aagggatttt ggtcatgaga ttatcaaaaa ggatcttcac ctagatcctt ttaaaggccg 3900
gccgcggccg ccateggcatt tttcttttgc gtttttattt gttaactgtt aattgtcctt 3960
gttcaaggat gctgtctttg acaacagatg ttttcttgcc tttgatgttc agcaggaagc 4020
tcggcgcaaa cgttgattgt ttgtctgcgt agaatcctct gtttgtcata tagcttgtaa 4080
tcacgacatt gtttcttttc gcttgaggta cagcgaagtg tgagtaagta aaggttacat 4140
cgttaggatc aagatccatt ttaacacaa ggccagtttt gtccagcggc ttgtatgggc 4200
cagttaaaga attagaaaca taaccaagca tgtaaatac gttagacgta atgccgtcaa 4260
tcgtcatttt tgatccgcgg gagtcagtga acaggtacca tttgccgttc attttaaaga 4320
cgttcgcgcg ttcaatttca tctgttactg tgttagatgc aatcagcggg ttcacactt 4380
ttttcagtgt gtaatcatcg tttagctcaa tcataccgag agcgccgttt gctaactcag 4440
ccgtgcgttt tttatcgctt tgcagaagtt ttgactttc ttgacggaag aatgatgtgc 4500
ttttgccata gtatgctttg ttaaataaag attcttcgcc ttggtagcca tcttcagttc 4560
cagtgtttgc ttcaaatact aagtatttgt ggcctttatc ttctacgtag tgaggatctc 4620
tcagcgtatg gttgtgcct gagctgtagt tgccttcac gatgaactgc tgtacatttt 4680
gatacgtttt tccgtcaccg tcaaagattg atttataatc ctctacaccg ttgatgttca 4740
aagagctgtc tgatgctgat acgttaactt gtgcagttgt cagtgtttgt ttgccgtaat 4800
gtttaccgga gaaatcagtg tagaataaac ggatttttcc gtcagatgta aatgtggctg 4860
aacctgacca ttcttgtgtt tgggtcttta ggatagaatc atttgcatcg aatttgtcgc 4920
tgtctttaa gacgcggcca gcgtttttcc agctgtcaat agaagtctcg ccgacttttt 4980
gatagaacat gtaaactgat gtgtcatccg catttttagg atctccggct aatgcaaaga 5040
cgatgtggta gccgtgatag tttgcgacag tgccgtcagc gttttgtaat ggccagctgt 5100
cccaaacgtc caggcctttt gcagaagaga tatttttaat tgtggacgaa tcaaattcag 5160
aaacttgata tttttcattt ttttgcgtgt cagggatttg cagcatatca tggcgtgtaa 5220
tatgggaaat gccgtatgtt tccttatatg gcttttggtt cgtttcttcc gcaaacgctt 5280
gagttgcgcc tcctgccagc agtgcggtag taaagggtta tactgttgct tgttttgcaa 5340

249

actttttgat gttcatcggt catgtctcct tttttatgta ctgtgttagc ggtctgcttc 5400
 ttccagccct cctgtttgaa gatggcaagt tagttacgca caataaaaaa agacctaaaa 5460
 tatgtaaggg gtgacgcaa agtatacact ttgcccttta cacatttttag gtcttgccgt 5520
 cttttatcagt aacaaacccg cgcgatttac ttttcgacct cattctatta gactctcggt 5580
 tggattgcaa ctggtctatt ttctcttttt gtttgataga aaatcataaa aggatttgca 5640
 gactacgggc ctaaagaact aaaaaatcta tctgtttctt ttcatctctt gtatttttta 5700
 tagtttctgt tgcattggca taaagttgcc tttttaatca caattcagaa aatatcataa 5760
 tatctcattt cactaaataa tagtgaacgg caggatatatg tgatgggtta aaaaggatcg 5820
 gcggccgctc gatttaaate tcgagaggcc tgacgtcggg 5860

<210> 79

<211> 8787

<212> DNA

<213> Plasmid

<400> 79

tcgaggggaag gtgaatcgaa tttcggggct ttaaagcaaa aatgaacagc ttggtctata 60
 gtggctaggt accctttttt ttttggacac atgtaggggt gccgaaacaa agtaatagga 120
 caacaacgct cgaccgcat tatttttggga gaatcgtgcg ttctccccgg gacgtccac 180
 gacggcgccg accgggcaga ggcaaagccg acagccgctg cactctaggg agccctttca 240
 tggcctcgtc gccatccacc ccgcccgcg acaccgcac ccgctgtcc gccctccgag 300
 aggcctcgc caccgcgtg gtggtcgccg acggcgccat gggcaccatg ctccaggccc 360
 agaacccac gctggacgac ttccagcagc tcgaaggggt caacgaggtc ctgaacctca 420
 cccggcccga catcgtcgc tcggtgcacg aggagtactt cgcggccggc gtcgactgcg 480
 tcgagaccaa caccttcggc gccaaccaact ccgccctggg cgagtacgac atccccgagc 540
 gcgtccacga actgtccgag gccggcgccc gcgtcgccc cgaggtegcc gacgagttcg 600
 gcgcccgcga cggccggcag cgctgggtgc tgggtccat gggccccggc accaagctcc 660
 ccaccctcgg ccacgccccg tacaccgtcc tgcgcgacgc ctaccagcgc aacgccgagg 720
 gactggctgc gggggcgcg gacgcactgc tggtgagac cagcaggac ctgctccaga 780
 ccaaggctc ggtgctcggc gcccggcgcg ccctggacgt cctcggcctc gacctgccgc 840
 tcatcgtgtc cgtcaccgtc gagaccaccg gcaccatgct gctcggctcg gagatcggcg 900
 ccgcgtcac cgcgtggaa ccgctcggca tcgacatgat cggcctgaac tgcgccaccg 960
 gccccgcga gatgagcgag cacctgcgt acctcgcgcg gcactcccgc atcccgctga 1020
 cctgcatgcc caacgccggt ctgccgtcc tcggcaagga cggcgccac taccgctga 1080
 ccgcgccga gctggccgac gcacacgaga cttcgtgcg cgagtacggc ctgtccctgg 1140

| | |
|--|------|
| tcggcggctg ctgcggcacc acgcccagac acctgcgcca ggctgctcgag cgggtccggg | 1200 |
| acaccgcccc caccgcacgc gaccgcgcgc ccgagcccgg cgccgcctcg ctctaccaga | 1260 |
| ccgtgccctt ccgccaggac acctcctacc tggccatcgg cgagcgcacc aacgccaacg | 1320 |
| ggccaagaa gttccgcgag gccatgctgg acggccgctg ggacgactgc gtcgagatgg | 1380 |
| cccgcgacca gatccgcgaa ggcgcgcaca tgctcgacct ctgcgtcgac tacgtcggcc | 1440 |
| gggacggcgt cgccgacatg gaggaactgg ccggccgggt cgccaccgcc tccaegctgc | 1500 |
| cgatcgtcct cgactccacc gaggtcgacg tcatccgggc cggcctggag aagctcggcg | 1560 |
| gccgcgcggt gatcaactcg gtcaactacg aggacggcgc cggccccgag tcccggttcg | 1620 |
| cccgcgtcac gaagctcgcc cgggagcacg ggcgcgcgt gatcgcgctg accatcgacg | 1680 |
| aggtgggaca ggcccgacc gccgagaaga aggtcgagat cgccgaacgg ctcatcgacg | 1740 |
| acctcaccgg caactggggc atccacgagt ccgacatcct cgctcgactgc ctgacctca | 1800 |
| ccatctgcac cgccaggag gagtcccgca aggacggcct ggccaccatc gagggcatcc | 1860 |
| gggaactcaa gcggcgccac ccggacgtgc agaccacgt cggcctgtcg aacatctcct | 1920 |
| tcggcctcaa ccggccgcc cgcatcctgc tcaactccgt cttcctcgac gaatgcgtca | 1980 |
| aggccggcct ggactcggcc atcgtgcacg cgagcaagat cctgccgac gcccgcttcg | 2040 |
| acgaggagca ggtcaccacc gccctcgact tgatctacga ccgccgccgc gagggtacg | 2100 |
| acccctgca aaagctcatg cagctcttcg agggcgccac cgccaagtcg ctgaaggcct | 2160 |
| ccaaggccga ggaactggcc gccctccgc tggaggagcg cctcaagcgc cgcacatcg | 2220 |
| acggcgagaa gaacggcctc gaacaggacc tcgacgagge cctccgggag cggccggccc | 2280 |
| tcgagatcgt caacgacacc ctgctcgacg gtatgaaggc cgtcggcgag ctgttcggct | 2340 |
| ccggccagat gcagctgcgc ttctgtctcc agtcgcgcga ggcatgaag acccggtgg | 2400 |
| cccacctgga gccgcacatg gagaagaccg acgacgacgg caagggcacg atcgtgctgg | 2460 |
| ccaccgtccg cggcgacgtc cagcacatcg gcaagaacct cgtcgacatc atcctgtcca | 2520 |
| acaacggcta caacgtcgtc aacctcggca tcaagcagcc cgtctccgcg atcctggaag | 2580 |
| cggccgacga gcaccgggccc gacgtcatcg gcatgtccgg cctcctcgtc aagtcacgg | 2640 |
| tgatcatgaa ggagaacctg gaggagctga accagcgcaa gctggccgcc gactaccgg | 2700 |
| tcatcctcgg cggcgccgcc ctcaccaggc cctacgtcga acaggacctg cagagatct | 2760 |
| acgacggcga ggtccgctac gcccgcgacg ccttcgaggc cctgcgcctc atggacgccc | 2820 |
| tcatcggcat caagcgcggc gtgcccggcg ccaagctgcc ggagctgaag cagcgccggg | 2880 |
| tcggggccgc caccgtcgag atcgacgagc gccccgagga aggccacgtc cgctccgacg | 2940 |
| tcgccaccga caaccgggtc ccgacccgc ccttcgcgg caccgcgtc gtcaagggca | 3000 |

251

tccagctcaa ggagtacgcc tcctggctcg acgagggcgc cctcttcaag ggccagtggg 3060
gcctcaagca ggccccgacc ggcgaggac cctcctacga ggaactggc gagtccgagg 3120
gccggccgcg gctgcgcggc ctgctcgacc ggctccagac ggacaacctt ttggaggcgg 3180
ccgtgggtcta cggctacttc ccctgctct ccaaggacga cgacctgatc gtcctcgacg 3240
acgacggcaa cgaacgcacc cgcttcacct tcccccgcca gcgcgcggc cggcgctgt 3300
gcctggccga cttcttcgc cgaggaggt cggcgagac cgacgtggc ggcttccagg 3360
tcgtcacctg cggctccgc atcggcgagg agacggccc catgttcgag gccaacgct 3420
accgcgacta tctcgagctg cacggcctgt ccgtgcagct cgccgagcc ctcgccgagt 3480
actggcacgc gcgcgtgcgc tcggaactcg gcttcgccgg ggaggaccg gccgagatgg 3540
aggacatgtt cgccctgaag taccggggtg cccgcttct cctcggctac ggcgcctgcc 3600
ccgacctgga ggaccgcgc aagatcgccg ccctgctgga gcccgagcgc atcggcgctc 3660
acctatccga ggagttccag ctccaccccg agcagtcac cgacgccatc gtcattccacc 3720
acccggaggc caagtacttc aacgcccgt gagggatatt gtcgacatc atgctcttct 3780
gcgttaatta acaattggga tcctctagac ccgggattta aatcgctagc gggctgctaa 3840
aggaagcggg acacgtagaa agccagtccg cagaaacggt gctgacccg gatgaatgtc 3900
agctactggg ctatctggac aagggaaaac gcaagcgcaa agagaaagca ggtagcttgc 3960
agtgggctta catggcgata gctagactgg gcggttttat ggacagcaag cgaaccggaa 4020
ttgccagctg gggcgccctc tggtaagggt ggaagccct gcaaagtaaa ctggatggct 4080
ttcttgccgc caaggatctg atggcgagg ggatcaagat ctgatcaaga gacaggatga 4140
ggatcgtttc gcatgattga acaagatgga ttgcacgcag gttctccggc cgcttgggtg 4200
gagaggctat tcggctatga ctgggcacaa cagacaatcg gctgctctga tgccgcctg 4260
ttccggctgt cagcgcaggg gcgcccgtt ctttttgtca agaccgacct gtccggtgcc 4320
ctgaatgaac tgcaggacga ggcagcgcg ctatcgtggc tggccacgac gggcgttcct 4380
tgcgacgtg tgctcgagct tgtcaactga gcgggaagg actggctgct attgggcgaa 4440
gtgcggggc aggatctcct gtcattctac cttgctcctg ccgagaaagt atccatcatg 4500
gctgatgcaa tgcggcggt gcatacgctt gatccgcta cctgccatt cgaccacaa 4560
gcgaaacatc gcatcgagc agcacgtact cggatggaag ccggtcttgt cgatcaggat 4620
gatctggacg aagagcatca ggggctcgc ccagccgaac tgctcgccag gctcaaggcg 4680
cgcatgcccg acggcgagga tctcgtcgtg acccatggcg atgcctgctt gccgaatatt 4740
atggtggaaa atggccgctt ttctggattc atcactgtg gccggctggg tgtggcgac 4800
cgctatcagg acatagcgtt ggctacccgt gatattgctg aagagcttgg cggcgaatgg 4860

gctgaccgct tcctcgtgct ttacggtatc gccgctcccg attcgcagcg catcgccttc 4920
tategccttc ttgacgagtt cttctgagcg ggactctggg gttcgaaatg accgaccaag 4980
cgacgcccaa cctgccatca cgagatttcg attccaccgc cgccttctat gaaagggttg 5040
gcttcggaat cgttttcccg gacgccggct ggatgaccc cagcgcggg gatctcatgc 5100
tggagtcttt cgcccacgct agcggcgcg cgccggccc ggtgtgaaat accgcacaga 5160
tgcgtaagga gaaaataccg catcaggcgc tcttcgctt cctcgcctac tgactcgtg 5220
cgctcggctg ttcggctcgc gcgagcggta tcagctcact caaaggcgg aatacggta 5280
tccacagaat caggggataa cgcaggaaag aacatgtgag caaaaggcca gcaaaaggcc 5340
aggaaccgta aaaaggccgc gttgctggcg tttttccata ggctccgccc ccctgacgag 5400
catcacaaaa atcgacgctc aagtcagagg tggcgaaacc cgacaggact ataaagatac 5460
caggcgtttc cccctggaag ctccctcgtg cgctctcctg ttccgacct gccgcttacc 5520
ggatacctgt cgcctttct ccttcggga agcgtggcg tttctcatag ctacgctgt 5580
aggatatctca gttcgggtgta ggtcgctcgc tccaagctgg gctgtgtgca cgaaccccc 5640
gttcagccc accgctcgc cttatccgt aactatcgtc ttgagtcca cccggtaga 5700
cacgacttat cgccactggc agcagccact ggtaacagga ttagcagagc gaggtatgta 5760
ggcgggtgcta cagagttctt gaagtgggtg cctaactacg gctacactag aaggacagta 5820
tttggtatct gcgctctgct gaagccagtt accttcggaa aaagagttgg tagctcttga 5880
tccggcaaac aaaccaccgc tggtagcggg ggtttttttg tttgcaagca gcagattacg 5940
cgcagaaaaa aaggatctca agaagatcct ttgatcttt ctacggggtc tgacgctcag 6000
tggaacgaaa actcacgta agggattttg gtcagagat tatcaaaaag gatcttcacc 6060
tagatccttt taaaggccgg cgccggccgc gcaaagtcct gcttcgtgaa aattttcgtg 6120
ccgctgatt ttccgcaaaa aactttaacg aacgttcgtt ataatggtgt catgaccttc 6180
acgacgaagt actaaaattg gcccgatca tcagctatgg atctctctga tgcgcgctg 6240
gagtcgcagc cgtcgcagtc tgccgtcgat ttaaaaacgg tgatcggatt tttccgagct 6300
ctcgatacga cggacgcgcc agcatcacga gactgggcca gtgccgcgag cgacctagaa 6360
actctcgtgg cggatcttga ggagctggt gacgagctgc gtgctcgcc agcgcagga 6420
ggacgcacag tagtgaggga tgcaatcagt tgcgcctact gcggtggcct gattcctccc 6480
cggcctgacc cgcgaggacg gcgcgcaaaa tattgtcag atgcgtgtcg tgccgcagcc 6540
agccgcgagc gcgccaacaa acgccacgcc gaggagctgg aggcggctag gtcgcaaatg 6600
gcgctggaag tgcgtccccc gacgcaaat ttggccatgg tcgtcacaga gctggaagcg 6660
gcagcgagaa ttatcgcgat cgtggcggtg cccgcaggca tgacaaacat cgtaaatgcc 6720

253

| | |
|--|------|
| gcgtttcgtg tgccgtggcc gcccaggacg tgtcagcgcc gccaccacct gcaccgaatc | 6780 |
| ggcagcagcg tcgcgcgtcg aaaaagcgca caggcgga gaagcgataa gctgcacgaa | 6840 |
| tacctgaaaa atgttgaacg ccccgtagc ggtaactcac agggcgtcgg ctaacccccca | 6900 |
| gtccaaacct gggagaaagc gctcaaaaat gactctagcg gattcacgag acattgacac | 6960 |
| accggcctgg aaatttttcg ctgatctgtt cgacacccat cccgagctcg cgctgcgac | 7020 |
| acgtggctgg acgagcgaag accgcccga attcctcgct cactgggca gagaaaattt | 7080 |
| ccagggcagc aagaccgcg acttcgccag cgcttgatc aaagaccgg acacggagaa | 7140 |
| acacagccga agttataccg agttggttca aaatcgcttg cccggtgcca gtatgttgct | 7200 |
| ctgacgcacg cgcagcacgc agccgtgctt gtcctggaca ttgatgtgcc gagccaccag | 7260 |
| gccggcggga aaatcgagca cgtaaaccac gaggtctacg cgatttttga gcgctgggca | 7320 |
| cgcttgaaa aagcgccagc ttggatcggc gtgaatccac tgagcgggaa atgccagctc | 7380 |
| atctggctca ttgatccggt gtatgccga gcaggcatga gcagccgaa tatgcgctg | 7440 |
| ctggctgcaa cgaccgagga aatgaccgc gtttctggcg ctgaccaggc tttttcacat | 7500 |
| aggctgagcc gtggccactg cactctccga cgatcccagc cgtaccgctg gcatgcccag | 7560 |
| cacaatcgcg tggatcgctt agctgatctt atggagggtg ctcgcatgat ctcaggcaca | 7620 |
| gaaaaacctt aaaaacgcta tgagcaggag ttttctagcg gacgggcacg tatcgaagcg | 7680 |
| gcaagaaaag ccaactgcgga agcaaaagca cttgccacgc ttgaagcaag cctgccgagc | 7740 |
| gccgctgaag cgtctggaga gctgatcgac ggcgtccgtg tcctctggac tgctccaggg | 7800 |
| cgtgccgccc gtgatgagac ggcttttcgc cacgctttga ctgtgggata ccagttaaaa | 7860 |
| gcggctggtg agcgcctaaa agacaccaag ggtcatcgag cctacgagcg tgccctacacc | 7920 |
| gtcgtcagg cggtcggagg aggccgtgag cctgatctgc cgccggactg tgaccgccag | 7980 |
| acggattggc cgcgacgtgt gcgcggctac gtcgctaaag gccagccagt cgtccctgct | 8040 |
| cgtcagacag agacgcagag ccagccgagg cgaaaagctc tggccactat gggaagacgt | 8100 |
| ggcggtaaaa aggccgcaga acgctggaaa gacccaaaca gtgagtacgc ccgagcacag | 8160 |
| cgagaaaaac tagctaagtc cagtcaacga caagctagga aagctaaagg aaatcgcttg | 8220 |
| accattgcag gttggtttat gactgttgag ggagagactg gctcgtggcc gacaatcaat | 8280 |
| gaagctatgt ctgaatttag cgtgtcacgt cagaccgtga atagagcact taaggctctgc | 8340 |
| gggcattgaa cttccacgag gacgccgaaa gcttcccagt aaatgtgcca tctcgtaggc | 8400 |
| agaaaaacgg tccccgtag ggtctctctc ttggcctcct ttctaggtcg ggctgattgc | 8460 |
| tcttgaagct ctctaggggg gctcacacca taggcagata acgttcccca ccggctcgcc | 8520 |
| tcgtaagcgc acaaggactg ctcccaaaga tcttcaaagc cactgccgcg actgccttcg | 8580 |

cgaagccttg ccccgcgga atttctcca ccgagttcgt gcacaccct atgccaagct 8640
tctttcacc taaattcgag agattggatt cttaccgtgg aaattcttcg caaaaatcgt 8700
cccctgacg cccttgcgac gttggcgctg gtgccgctgg ttgcgcttgg cttgaccgac 8760
ttgatcagcg gccgctcgat ttaaate 8787

**This Page is Inserted by IFW Indexing and Scanning
Operations and is not part of the Official Record**

BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images include but are not limited to the items checked:

- ☐ BLACK BORDERS
- ☐ IMAGE CUT OFF AT TOP, BOTTOM OR SIDES
- ☒ FADED TEXT OR DRAWING
- ☒ BLURRED OR ILLEGIBLE TEXT OR DRAWING
- ☐ SKEWED/SLANTED IMAGES
- ☐ COLOR OR BLACK AND WHITE PHOTOGRAPHS
- ☐ GRAY SCALE DOCUMENTS
- ☐ LINES OR MARKS ON ORIGINAL DOCUMENT
- ☒ REFERENCE(S) OR EXHIBIT(S) SUBMITTED ARE POOR QUALITY
- ☐ OTHER: _____

IMAGES ARE BEST AVAILABLE COPY.

As rescanning these documents will not correct the image problems checked, please do not report these problems to the IFW Image Problem Mailbox.